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OM nucleic - nucleic search, using sw model

Run on: April 21, 2005, 21:13:15 ; Search time 2021.2 Seconds
(without alignments)
813.555 Million cell updates/sec

Title: US-10-766-691-9
Perfect score: 1041
Sequence: 1 acggaagtgatgaaaatt.....aggactctccgctcaaaagt 1041

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9168763 seqs, 789795712 residues 18337526
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents NA New.*
1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
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11: /cgn2_6/ptodata/1/pna/US14_NEW_COMB.seq.*
12: /cgn2_6/ptodata/1/pna/US15_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	729.6	70.1	1618	2 PCT-US05-03526-3
2	572	54.9	1400	10 US-11-060-756-23
3	572	54.9	1400	10 US-11-060-756-4295
4	567.4	54.5	600	10 US-11-060-756-22
5	567.4	54.5	600	10 US-11-060-756-4294
6	368	35.4	600	10 US-11-060-756-1500
7	368	35.4	600	10 US-11-060-756-1501
8	368	35.4	600	10 US-11-060-756-5772
9	368	35.4	600	10 US-11-060-756-5773
10	343.8	33.0	1175	10 US-11-060-756-3884
11	343.8	33.0	1175	10 US-11-060-756-3885
12	343.8	33.0	1175	10 US-11-060-756-8156
13	343.8	33.0	1175	10 US-11-060-756-8157
14	285.6	27.4	600	10 US-11-060-756-37
15	285.6	27.4	600	10 US-11-060-756-38
16	285.6	27.4	600	10 US-11-060-756-4309
17	285.6	27.4	600	10 US-11-060-756-4310
18	241.2	23.2	1993	2 PCT-US05-03526-1
19	202.6	19.5	1513	2 PCT-US05-03526-2
20	177.4	17.0	1158	8 US-10-450-763-6133
21	177.2	17.0	3399	2 PCT-US05-03526-4

22	176.2	16.9	1400	10	US-11-060-756-523	Sequence 523, App
23	176.2	16.9	1400	10	US-11-060-756-4795	Sequence 4795, App
24	153.4	14.7	1323	10	US-11-060-756-373	Sequence 373, App
25	153.4	14.7	1323	10	US-11-060-756-374	Sequence 374, App
26	153.4	14.7	1323	10	US-11-060-756-4645	Sequence 4645, App
27	153.4	14.7	1323	10	US-11-060-756-4646	Sequence 4646, App
28	151	14.5	1522	9	US-11-085-606-1008	Sequence 1008, App
29	151	14.5	1522	9	US-11-085-606-1012	Sequence 1012, App
30	146.2	14.0	1184	9	US-11-099-266-92	Sequence 92, Appl
31	146.2	14.0	1184	10	US-11-036-196-1727	Sequence 1727, App
32	142.6	13.7	600	10	US-11-060-756-3309	Sequence 3309, App
33	142.6	13.7	600	10	US-11-060-756-7581	Sequence 7581, App
34	134.8	12.9	1161	1	PCT-US05-10257-245	Sequence 245, App
35	134.8	12.9	1825	7	US-10-122-851-313	Sequence 313, App
36	133.2	12.8	1089	1	PCT-US05-10257-244	Sequence 244, App
37	116.2	11.2	1738	8	US-10-450-763-5885	Sequence 5885, App
38	115	11.0	1400	10	US-11-060-756-241	Sequence 241, App
39	115	11.0	1400	10	US-11-060-756-242	Sequence 242, App
40	115	11.0	1400	10	US-11-060-756-4513	Sequence 4513, App
41	115	11.0	1400	10	US-11-060-756-4514	Sequence 4514, App
42	112	10.8	1311	7	US-10-489-448-837	Sequence 837, App
43	111.6	10.7	909	7	US-10-932-182A-81516	Sequence 81516, A
44	111.2	10.7	837	2	PCT-US05-07748-92	Sequence 92, Appl
45	111	10.7	1310	7	US-10-525-647-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
PCT-US05-03526-3
; Sequence 3, Application PC/TUS0503526
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: MEWS AS MODIFIERS OF BRANCHING MORPHOGENESIS AND METHODS OF USE
; FILE REFERENCE: EX05-003C-PC
; CURRENT APPLICATION NUMBER: PCT/US05/03526
; CURRENT FILING DATE: 2005-01-27
; PRIOR APPLICATION NUMBER: US60/539,835
; PRIOR FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 1618
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US05-03526-3

Query Match 70.1%; Score 729.6; DB 2; Length 1618;
Best Local Similarity 84.6%; Pred. No. 6.2e-143;
Matches 893; Conservative 0; Mismatches 49; Indels 114; Gaps 2;

QY	4	GAAAGTATGAAAAATTAGCTAGCACTGGAGAGGGTCTTATGGGTTGTATTCAATGTC	63
DB	496	GACCCGTATGAAAAATTAGCTAGCACTGGAGAGGGTCTTATGGGTTGTATTCAATGTC	555
QY	64	AGAAACAAACCTCTGGCAAGTAGTAGCTTTAAAAAATTGTGGATCTGAAGATCAT	123
DB	556	AGAAACAAACCTCTGGCAAGTAGTAGCTTTAAAAAATTGTGGATCTGAAGATCAT	615
QY	124	CCTGTTGTGAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACATCCA	183
DB	616	CCTGTTGTGAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACATCCA	675
QY	184	AATCTTGTGAACCTCATCGAGGTCTTCCAGGAAAAAGAAAAATGCATTAGTTTGTAA	243
DB	676	AATCTTGTGAACCTCATCGAGGTCTTCCAGGAAAAAGAAAAATGCATTAGTTTGTAA	735
QY	244	TACTGTGATCATACACATTTTAAATGAGCTGGAAAGAACCCAAATGGAGTGTCTGATGA	303
DB	736	TACTGTGATCATACACATTTTAAATGAGCTGGAAAGAACCCAAATGGAGTGTCTGATGA	795
QY	304	GTGATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTGCATATACATA--	361

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Db 796 AGCATCTGGGCGCTCTCAGAGAGTGTGCTCATCTGTTCCAGGTAGCTCCGAAAAATAAT 855
Qy 362 -----ACTGATTTACAGAGATATAAAACCTGAAATATTTCTAATACT 405
Db 856 CAAATAATATGATCTTACAGTGTATTTACAGAGATATAAAACCTGAAATATTTCTAATACT 915
Qy 406 AAGCAAGGATAAATCAAGATTTGACTCTGGGTTTCACAAATTCGATTTCCAGGAGAT 465
Db 916 AAGCAAGGATAAATCAAGATTTGACTCTGGGTTTCACAAATTCGATTTCCAGGAGAT 975
Qy 466 GCCTACACCGATATGATAGTACAGAGATGATACCGAGCTCCTGAACTTTCTGTTGGGAGAT 525
Db 976 GCCTACACCGATATGATAGTACAGAGATGATACCGAGCTCCTGAACTTTCTGTTGGGAGAT 1035
Qy 526 ACTCAGTATGTTCTTCAGTCGATATATGAGGCTATGTTGGTGTGTTTTCGAGAGCTCCTG 585
Db 1036 ACTCAGTATGTTCTTCAGTCGATATATGAGGCTATGTTGGTGTGTTTTCGAGAGCTCCTG 1095
Qy 586 ACAGGCCAGCACTGCGCTGGAAATCAGATGTGACCAACTTTATCTGATAATCAGA 645
Db 1096 ACAGGCCAGCACTGCGCTGGAAATCAGATGTGACCAACTTTATCTGATAATCAGA 1155
Qy 646 ACACCTAGTAGAGACGGGGTTTCGCCATGTTGACCAAGCTGCTCTCGAACTCTTGACGTCA 705
Db 1156 ACACCT----- 1160
Qy 706 AGTGATCCACCTGCGGTAGCCTCTCAAAGTGTGGAATTAACAGAAATAATCCCAAGA 765
Db 1161 -----AGCAAAATAATCCCAAGA 1179
Qy 766 CATCAATCAATCTTTAAAGTAAAGCGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAA 825
Db 1180 CATCAATCAATCTTTAAAGTAAAGCGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAA 1239
Qy 826 GACATGGAACCTCTTGAGGAAAGTTCTCAGATGTTTCATCTGTTGGCTCTGAACTTTCATG 885
Db 1240 GACATGGAACCTCTTGAGGAAAGTTCTCAGATGTTTCATCTGTTGGCTCTGAACTTTCATG 1299
Qy 886 AAGGGGTGTTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTCTCTGGAGAGC 945
Db 1300 AAGGGGTGTTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTCTCTGGAGAGC 1359
Qy 946 TCCTACTTTGATCTTTTCAAGAGCCCAAAATTAAGAAAGACACGTAATGAAGGAAGA 1005
Db 1360 TCCTACTTTGATCTTTTCAAGAGCCCAAAATTAAGAAAGACACGTAATGAAGGAAGA 1419
Qy 1006 AACAGAAGACGCCAACAGGTACTTCCGCTCAAAAGT 1041
Db 1420 AACAGAAGACGCCAACAGGTACTTCCGCTCAAAAGT 1455

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RESULT 2

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US-11-060-756-23
; Sequence 23, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens

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Query Match. 54.9%; Score 572; DB 10; Length 1400;
Best Local Similarity 100.0%; Pred. No. 3.9e-110;

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Matches 572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 454 ATTCAGAGAGATGCCCTACACCGATTTAGCTTACAGATGGTACCGAGCTCCTGAACTT 513
Db 478 ATTCAGAGAGATGCCCTACACCGATTTAGCTTACAGATGGTACCGAGCTCCTGAACTT 537
Qy 514 CTCTGCGGAGATACCTCAGTATGTTCTTCAGTCGATATATGAGGCTATTTGGTGTGTTTTT 573
Db 538 CTCTGCGGAGATACCTCAGTATGTTCTTCAGTCGATATATGAGGCTATTTGGTGTGTTTTT 597
Qy 574 GCAGAGCTCCTGACAGGCCAGCCACTGTGGCTTGGAAATCAGATGTGACCAACTTTAT 633
Db 598 GCAGAGCTCCTGACAGGCCAGCCACTGTGGCTTGGAAATCAGATGTGACCAACTTTAT 657
Qy 634 CTGATATCAGACACCTAGTAGAGACGGGTTTCGCCATGTTCCACAGGCTGCTCTCGAA 693
Db 658 CTGATATCAGACACCTAGTAGAGACGGGTTTCGCCATGTTCCACAGGCTGCTCTCGAA 717
Qy 694 CTCTTGACGCTCAAGTGATCCACCTGCGGTAGCCTCTCAAAGTGTGGAATTAACAGGAAAA 753
Db 718 CTCTTGACGCTCAAGTGATCCACCTGCGGTAGCCTCTCAAAGTGTGGAATTAACAGGAAAA 777
Qy 754 TTAATCCCAAGACATCAATCAATCTTTAAAGTAAAGCGGTTTTTCCATGGCATCAGTATA 813
Db 778 TTAATCCCAAGACATCAATCAATCTTTAAAGTAAAGCGGTTTTTCCATGGCATCAGTATA 837
Qy 814 CCTGAGCCAGACACATGGAACCTCTTGAGGAAAGTTCTCAGATGTTCACTCTGTGGCT 873
Db 838 CCTGAGCCAGACACATGGAACCTCTTGAGGAAAGTTCTCAGATGTTCACTCTGTGGCT 897
Qy 874 CTGAACTTTCATGAAGGGGTGCTCTGAAGATGAATCCAGATGACAGATTAACTGTTCCCAA 933
Db 898 CTGAACTTTCATGAAGGGGTGCTCTGAAGATGAATCCAGATGACAGATTAACTGTTCCCAA 957
Qy 934 CTCTGAGAGCTCTTACTTTGATTTCTTTTCAAGAGCCCAAAATTAAGAAAGACACGT 993
Db 958 CTCTGAGAGCTCTTACTTTGATTTCTTTTCAAGAGCCCAAAATTAAGAAAGACACGT 1017
Qy 994 AATGAGGAGAAACAGAGACGCCAACACGT 1025
Db 1018 AATGAGGAGAAACAGAGACGCCAACACGT 1049

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RESULT 3

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US-11-060-756-4295
; Sequence 4295, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4295
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens

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Query Match 54.9%; Score 572; DB 10; Length 1400;
Best Local Similarity 100.0%; Pred. No. 3.9e-110;

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Matches 572; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 454 ATTCAGAGAGATGCCCTACACCGATTTAGCTTACAGATGGTACCGAGCTCCTGAACTT 513
Db 478 ATTCAGAGAGATGCCCTACACCGATTTAGCTTACAGATGGTACCGAGCTCCTGAACTT 537
Qy 514 CTCTGCGGAGATACCTCAGTATGTTCTTCAGTCGATATATGAGGCTATTTGGTGTGTTTTT 573
Db 538 CTCTGCGGAGATACCTCAGTATGTTCTTCAGTCGATATATGAGGCTATTTGGTGTGTTTTT 597

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Qy 574 GCAGAGCTCTGACAGCGCAGCCACTGTGGCTCGAAATACAGATGTGGACCAACTTTAT 633
Db 598 GCAGAGCTCTGACAGCGCAGCCACTGTGGCTCGAAATACAGATGTGGACCAACTTTAT 657
Qy 634 CTGATATCAGAACACTAGTAGACAGCGGGTTTCGCCATGTGTGACACAGGCTGTCTCGAA 693
Db 658 CTGATATCAGAACACTAGTAGACAGCGGGTTTCGCCATGTGTGACACAGGCTGTCTCGAA 717
Qy 694 CTCCTGACGTCAAGTGATCCACCTGCGCTAGCCTCTCAAAAGTGTGGAATTTACAGGAAAA 753
Db 718 CTCCTGACGTCAAGTGATCCACCTGCGCTAGCCTCTCAAAAGTGTGGAATTTACAGGAAAA 777
Qy 754 TTAATCCAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATA 813
Db 778 TTAATCCAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATA 837
Qy 814 CCTGAGCCAGAGACATGGAACCTCTTGAGGAAAAGTTCTCAGATGTTCATCCTGTGGCT 873
Db 838 CCTGAGCCAGAGACATGGAACCTCTTGAGGAAAAGTTCTCAGATGTTCATCCTGTGGCT 897
Qy 874 CTGAATCTTCATGAAGGGGTGCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCTCAA 933
Db 898 CTGAATCTTCATGAAGGGGTGCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCTCAA 957
Qy 934 CTCCTGAGAGCTCCTACTTTGATTTCTTTCAAGAGCCCAAAATTAAGAAAGACGCT 993
Db 958 CTCCTGAGAGCTCCTACTTTGATTTCTTTCAAGAGCCCAAAATTAAGAAAGACGCT 1017
Qy 994 AATGAAGAGAAACAGACAGCGCCACAGCT 1025
Db 1018 AATGAAGAGAAACAGACAGCGCCACAGCT 1049
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RESULT 4

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US-11-060-756-22
; Sequence 22, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-22
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Query Match 54.5%; Score 567.4; DB 10; Length 600;
Best Local Similarity 98.4%; Pred. No. 3.2e-109;
Matches 562; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
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Qy 471 CACCGATTATGTAGCTACGAGATGGTACCGAGCTCTCGAACTCTTGTGGAGATCTCA 530
Db 1 CACCGATTATGTAGCTACGAGATGGTACCGAGCTCTCGAACTCTTGTGGAGATCTCA 60
Qy 531 GTATGGTTCTTCAGTCGATATATGGGCTATTGGTTGTTGTTTTCAGAGCTCCTGACAGG 590
Db 61 GTATGGTTCTTCAGTCGATATATGGGCTATTGGTTGTTGTTTTCAGAGCTCCTGACAGG 120
Qy 591 CCAGCCACTGTGGCTCGAAATACAGATGTGGAACAACTTTATCTGATAATCAGAACACT 650
Db 121 CCAGCCACTGTGGCTCGAAATACAGATGTGGAACAACTTTATCTGATAATCAGAACACT 180
Qy 651 AGTAGAGACGGGGTTTCGCCATGTGTGACAGGCTGGTCTCGAACTCTTGTGAGTCAAGTGA 710
Db 181 AGTAGAGACGGGGTTTCGCCATGTGTGACAGGCTGGTCTCGAACTCTTGTGAGTCAAGTGA 240
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Qy 711 TCACCTGCCGTAGCCTCTCAAAAGTGTGGAATTTACAGGAAAATTAATCCAGACATCA 770
Db 241 TCACCTGCCGTAGCCTCTCAAAAGTGTGGAATTTACAGGAAAATTAATCCAGACATCA 300
Qy 771 ATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACAT 830
Db 301 ATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACAT 360
Qy 831 GGAAACTCTTTGAGGAAAAGTTCTCAGATGTTCATCTGTGGCTCTGAATCTTCATGAAGGG 890
Db 361 GGAAACTCTTTGAGGAAAAGTTCTCAGATGTTCATCTGTGGCTCTGAATCTTCATGAAGGG 420
Qy 891 GTCTCTGAACATGAATCCAGATGACAGATTAACCTGTTCCTCAACTCTCTGAGAGCTCTTA 950
Db 421 GTCTCTGAACATGAATCCAGATGACAGATTAACCTGTTCCTCAACTCTCTGAGAGCTCTTA 480
Qy 951 CTTTGATTTCTTTCAAGAGGCCCAAAATTAAGAAAGACAGCTAATGAAGAAAGACAG 1010
Db 481 CTTTGATTTCTTTCAAGAGGCCCAAAATTAAGAAAGACAGCTAATGAAGAAAGACAG 540
Qy 1011 AAGACGCCAACAGGTACTTCCGCTCAAAAGT 1041
Db 541 AAGACGCCAACAGGTACTCCKMSGCTCRWRWKT 571
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RESULT 5

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US-11-060-756-4294
; Sequence 4294, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4294
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-4294
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Query Match 54.5%; Score 567.4; DB 10; Length 600;
Best Local Similarity 98.4%; Pred. No. 3.2e-109;
Matches 562; Conservative 9; Mismatches 0; Indels 0; Gaps 0;
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Qy 471 CACCGATTATGTAGCTACGAGATGGTACCGAGCTCTCGAACTCTTGTGGAGATCTCA 530
Db 1 CACCGATTATGTAGCTACGAGATGGTACCGAGCTCTCGAACTCTTGTGGAGATCTCA 60
Qy 531 GTATGGTTCTTCAGTCGATATATGGGCTATTGGTTGTTGTTTTCAGAGCTCCTGACAGG 590
Db 61 GTATGGTTCTTCAGTCGATATATGGGCTATTGGTTGTTGTTTTCAGAGCTCCTGACAGG 120
Qy 591 CCAGCCACTGTGGCTCGAAATACAGATGTGGAACAACTTTATCTGATAATCAGAACACT 650
Db 121 CCAGCCACTGTGGCTCGAAATACAGATGTGGAACAACTTTATCTGATAATCAGAACACT 180
Qy 651 AGTAGAGACGGGGTTTCGCCATGTGTGACAGGCTGGTCTCGAACTCTTGTGAGTCAAGTGA 710
Db 181 AGTAGAGACGGGGTTTCGCCATGTGTGACAGGCTGGTCTCGAACTCTTGTGAGTCAAGTGA 240
Qy 711 TCACCTGCCGTAGCCTCTCAAAAGTGTGGAATTTACAGGAAAATTAATCCAGACATCA 770
Db 241 TCACCTGCCGTAGCCTCTCAAAAGTGTGGAATTTACAGGAAAATTAATCCAGACATCA 300
Qy 771 ATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACAT 830
Db 301 ATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACAT 360
Qy 831 GGAAACTCTTTGAGGAAAAGTTCTCAGATGTTCATCTGTGGCTCTGAATCTTCATGAAGGG 890
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; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5773
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-5773

Query Match      35.4%; Score 368; DB 10; Length 600;
Best Local Similarity 81.9%; Pred. No. 1e-67;
Matches 480; Conservative 0; Mismatches 10; Indels 96; Gaps 1

Qy 438 GTTTGCGCAAAATTCGTATTCAGAGAGATGCCCTACACCGATTATGTAGCTACGAGATGGTA 497
Db |||||
9 GATTGTGTCATTTTGCAGTTTCAGGAGATGCCCTACACCGATTATGTAGCTACGAGATGGTA 68
Qy 498 CCGAGCTCCTGGAACCTCTTGTGGGAGATACCTCAGTATGGTTCTTCAGTCGATATATGGC 557
Db |||||
69 CCGAGCTCCTGGAACCTCTTGTGGGAGATACCTCAGTATGGTTCTTCAGTCGATATATGGC 128
Qy 558 TATTGGTTGTGTTTTTTCAGAGCTCCTGCAGAGCCAGCCACTGTGGCCCTGGAATAATCAGA 617
Db |||||
129 TATTGGTTGTGTTTTTTCAGAGCTCCTGCAGAGCCAGCCACTGTGGCCCTGGAATAATCAGA 188
Qy 618 TGTGGACCAACTTTATCTGATTAATCAGAAACACTAGTAGAGACGGGGTTTCGCCATGTTGA 677
Db |||||
189 TGTGGACCAACTTTATCTGATTAATCAGAAACACT----- 221
Qy 678 CAGGCTGGTCTCGAACTCTTTCAGTCAAGTGATCCACCTGCCGTAGCCTCTCAAAGTGC 737
Db 222 ----- 221

Qy 738 TGGAAATTACAGGAAAAATTAATCCAGACACATCAATCAATCTTTAAAAAGTAAACGGGTTTTT 797
Db |||||
222 -----AGGAAAAATTAATCCAGACACATCAATCAATCTTTAAAAAGTAAACGGGTTTTT 272
Qy 798 CCATGGCATCAGTATACCTGAGCAGAGACATCGAAACTCTTGAGGAAAAAGTTCTCAGA 857
Db 273 CCATGGCATCAGTATACCTGAGCAGAGACATCGAAACTCTTGAGGAAAAAGTTCTCAGA 332
Qy 858 TGTTTCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGCAG 917
Db 333 TGTTTCATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGCAG 392
Qy 918 ATTAACCTGTTCCAACTCCTCGAGAGCTCCTACTTTTGATTCTTTTCAAGAGGCCCAAT 977
Db 393 ATTAACCTGTTCCAACTCCTCGAGAGCTCCTACTTTTGATTCTTTTCAAGAGGCCCAAT 452
Qy 978 TAAAGAAAAAGCAGTAAATGAAGGAGAAAAACAGAAAGCGCAACAG 1023
Db 453 TAAAGAAAAAGCAGTAAATGAAGGAGAAAAACAGAAAGCGCAACAG 498

RESULT 10
US-11-060-756-3884
; Sequence 3884, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles
; TITLE OF INVENTION: Target Genes
; FILE REFERENCES: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3884
; LENGTH: 1175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-3884

Query Match      33.0%; Score 343.8; DB 10; Length 1175;

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Qy	121	GATCTCTGTTGTTAAGAAATATGACCATPAGAGAAATACGTATGTTGAGCAATTTAAACAT	180
Db	152	GACCCGTGTCATAAAGAAAATGCCCCCTTCGGGAAATCCGAATGCTCAAGCAACTCAAGCAT	211
Qy	181	CCAAATCTTGTGAACCTCATCGAGGTGTTTCAGGAGAAAAGGAAAATGCATTTAGTTTTT	240
Db	212	CCCAACCTTGTAACTCTCTGGAAGTCTTCAGAGGAAACGAGGGCTTCACCTGGTGTTT	271
Qy	241	GAATACGTGTGATCATACACTTTTTTAATGAGCTGGAAAGAAAACCCAAATGGAGTGTCTGAT	300
Db	272	GAAATATTGTGACCAACACAGTTCTCCATGAGTTGGACAGATACCAAAGAGGGGTACCAGAA	331
Qy	301	GGAGTGATCAAAAGCGTATTATGGCAAAACACTTCAAGCTCTTAAATTCTGTGTCATATACAT	360
Db	332	CATCTCGTGAAGAGCATTAACCTTGGCAGACACTGCAAGCTGTAAATTTTTTGGCCATAAACAC	391
Qy	361	AACCTGATTTCAGAGATATAAAACCTGAAAAATATTCTAATAACTAAGCAAGGAATAATC	420
Db	392	AATTGCATACATAGAGACGTGAAGCCAGNAANAATATCCTCATCAGNAACACTTCCGTGATT	451
Qy	421	AAGATTGTGACTTCGGGTTTGCAAAATTCGTATT---CCAGGAGATGCCTACACCGAT	477
Db	452	AAGCTTTGTGACTTTTGGATTTTCTCGGCTTTTGACTGGACCCAGTGACTACTATATCAGAC	511
Qy	478	TATGTAGCTACGAGATGTCACGAGCTCCTGAACTTCTTGTGGGAGATACTCAGTATGTT	537
Db	512	TACGTGGCTACGAGTGTGACCGCTCCCTCGAGCTGCTGGTGGGGGACACGCAGTACCGC	571
Qy	538	TCCTTCAGTCGATATATGGCTATTGTTGTGTTTTTTCAGAGACTCTCTGACAGGCCAGCCA	597
Db	572	CCCCCGGTGGATGTTTGGCAATTGGCTGTGCTTTGCTGAGCTGCTGTTCAGGAGTGCTCT	631
Qy	598	CTGTGGCCCTGGAAAATACAGATGTGGACCAACTTTTATCTGATAATCAGAAACACTAGTAGA	656
Db	632	CTGTGGCCAGGAAAATCCGATGTGTGATCAGCTGTATCTCATTPAGGAAGACCTTTGGGGGA	690

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RESULT 13
US-11-060-756-8157
; Sequence 8157, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8157
; LENGTH: 1175
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-8157

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QY	181	CCAAATCTTGTAACCTCATCGAGGTGTTTCAGGAGAAAAAGAAAAATGCATTAGTTTTT	241
QY <th>212</th> <th>CCCAACCTTGTAAACCTCTCGAAGTCTTCAGGAGGAAACGGAGGCTTCACCTGGTGT</th> <th>271</th>	212	CCCAACCTTGTAAACCTCTCGAAGTCTTCAGGAGGAAACGGAGGCTTCACCTGGTGT	271
DB <th>241</th> <th>GAATACTGTGATCATATACACTTTTAAATGAGCTGGGAAAGAAACCCAAATCGAGTGTGCTGAT</th> <th>300</th>	241	GAATACTGTGATCATATACACTTTTAAATGAGCTGGGAAAGAAACCCAAATCGAGTGTGCTGAT	300
DB <th>272</th> <th>GAATATTTGTGACCACACACAGTTCTCCATGAGTTGGACAGATACCAAAGAGGGGTACCA</th> <th>331</th>	272	GAATATTTGTGACCACACACAGTTCTCCATGAGTTGGACAGATACCAAAGAGGGGTACCA	331
QY <th>301</th> <th>GGAGTGATCAAAGCGGTATTATGGCAAAACACTTCGAAGCTCTTAAATCTTGTCATATACAT</th> <th>360</th>	301	GGAGTGATCAAAGCGGTATTATGGCAAAACACTTCGAAGCTCTTAAATCTTGTCATATACAT	360
DB <th>332</th> <th>CATCTCGTGAAGAGCATAACTTGGCAGACACTGCAAGCTGTAAATTTTTTGCCTATAAACAC</th> <th>391</th>	332	CATCTCGTGAAGAGCATAACTTGGCAGACACTGCAAGCTGTAAATTTTTTGCCTATAAACAC	391
QY <th>361</th> <th>AACGTGATTTCAGAGATATAAACCCTGAAAATATTTCTAATAACTTAAGCAAGGAATAATC</th> <th>420</th>	361	AACGTGATTTCAGAGATATAAACCCTGAAAATATTTCTAATAACTTAAGCAAGGAATAATC	420
DB <th>392</th> <th>AATTGCATACATAGACAGCTGAAGCCAGAAAATATCCTCATCAGAAAACATTTCCGTGAT</th> <th>451</th>	392	AATTGCATACATAGACAGCTGAAGCCAGAAAATATCCTCATCAGAAAACATTTCCGTGAT	451
QY <th>421</th> <th>AAGATTGTGACTTCGGGTTTGCAAAATTCGTATTTTCCAGGAGATGCGCTACACCGAT</th> <th>477</th>	421	AAGATTGTGACTTCGGGTTTGCAAAATTCGTATTTTCCAGGAGATGCGCTACACCGAT	477
DB <th>452</th> <th>AAGCTTTGTGACTTTGGATTTTGCTCGGCTTTTGACTGACCGAGTGACTACTATACAGAC</th> <th>511</th>	452	AAGCTTTGTGACTTTGGATTTTGCTCGGCTTTTGACTGACCGAGTGACTACTATACAGAC	511
QY <th>478</th> <th>TATGTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTTGGGAGATACCTCAGTATGT</th> <th>537</th>	478	TATGTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTTGGGAGATACCTCAGTATGT	537
DB <th>512</th> <th>TACGTGGCTACAGGTGATCGGCTCCCTGAGCTGCTGGTGGGGGACACGCACTACGGC</th> <th>571</th>	512	TACGTGGCTACAGGTGATCGGCTCCCTGAGCTGCTGGTGGGGGACACGCACTACGGC	571
QY <th>538</th> <th>TCCTCAGTCGATATATGGGCTATTGGTTGTGTTTTCAGAGAGCTCCTGACAGGCCAGCCA</th> <th>597</th>	538	TCCTCAGTCGATATATGGGCTATTGGTTGTGTTTTCAGAGAGCTCCTGACAGGCCAGCCA	597
DB <th>572</th> <th>CCCCCGGTGGATGTTTGGGCAATTTGGCTGTGTCTTTGCTGAGCTCTGTCAAGAGTGCTC</th> <th>631</th>	572	CCCCCGGTGGATGTTTGGGCAATTTGGCTGTGTCTTTGCTGAGCTCTGTCAAGAGTGCTC	631
QY <th>598</th> <th>CTGTGGCTCGAAAATCAGATGTCGACCAACTTTATCTGATAATCAGAAACACTAGTAGA</th> <th>656</th>	598	CTGTGGCTCGAAAATCAGATGTCGACCAACTTTATCTGATAATCAGAAACACTAGTAGA	656
DB <th>632</th> <th>CTGTGGCCAGGAAATCGGATGTGATCAGCTGTATCTGATTAGGAAGACCTTTGGGGA</th> <th>690</th>	632	CTGTGGCCAGGAAATCGGATGTGATCAGCTGTATCTGATTAGGAAGACCTTTGGGGA	690
RESULT 14			
US-11-060-756-37			
; Sequence 37, Application US/11060756			
; GENERAL INFORMATION:			
; APPLICANT: Wyeth			
; APPLICANT: Mounts, William Martin			
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles			
; TITLE OF INVENTION: Target Genes			
; FILE REFERENCE: AM101083 (031896-042000)			
; CURRENT APPLICATION NUMBER: US/11/060,756			
; CURRENT FILING DATE: 2005-02-18			
; NUMBER OF SEQ ID NOS: 303284			
; SOFTWARE: PatentIn version 3.2			
; SEQ ID NO 37			
; LENGTH: 600			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US-11-060-756-37			
Query Match 27.4%; Score 285.6; DB 10; Length 600;			
Best Local Similarity 94.3%; Pred. No. 1.4e-50;			
Matches 283; Conservative 12; Mismatches 5; Indels 0; Gaps 0			
QY <th>740</th> <th>GAATTTACAGGAAAAATTAATCCCAAGACATCAATCAATCTTTAAAAAGTAAACGGTTTTTCC</th> <th>799</th>	740	GAATTTACAGGAAAAATTAATCCCAAGACATCAATCAATCTTTAAAAAGTAAACGGTTTTTCC	799
DB <th>49</th> <th>GAACTACTGGAATAATTAATCCCAAGACATCAATCAATCTTTAAAAAGTAAACGGTTTTTCC</th> <th>108</th>	49	GAACTACTGGAATAATTAATCCCAAGACATCAATCAATCTTTAAAAAGTAAACGGTTTTTCC	108
QY <th>800</th> <th>ATGGCATCAGTATACCTGAGCCAGAGACATGGAAACTCTTTGAGGAAAAGTTCTCAGATG</th> <th>859</th>	800	ATGGCATCAGTATACCTGAGCCAGAGACATGGAAACTCTTTGAGGAAAAGTTCTCAGATG	859
DB <th>109</th> <th>ATGGCATCAGTATACCTGAGCCAGAGACATGGAAACTCTTTGAGGAAAAGTTCTCAGATG</th> <th>168</th>	109	ATGGCATCAGTATACCTGAGCCAGAGACATGGAAACTCTTTGAGGAAAAGTTCTCAGATG	168
QY <th>860</th> <th>TTCACTCTGTGGCTCTGAACTTTCATGAAGGGGTGCTGAAGATGATCCAGATGACAGAT</th> <th>919</th>	860	TTCACTCTGTGGCTCTGAACTTTCATGAAGGGGTGCTGAAGATGATCCAGATGACAGAT	919
DB <th>169</th> <th>TTCACTCTGTGGCTCTGAACTTTCATGAAGGGGTGCTGAAGATGATCCAGATGACAGAT</th> <th>228</th>	169	TTCACTCTGTGGCTCTGAACTTTCATGAAGGGGTGCTGAAGATGATCCAGATGACAGAT	228
QY <th>920</th> <th>TAACTGTGTCCCACTCCTGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCAATTA</th> <th>979</th>	920	TAACTGTGTCCCACTCCTGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCAATTA	979
DB <th>229</th> <th>TAACTGTGTCCCACTCCTGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCAATTA</th> <th>288</th>	229	TAACTGTGTCCCACTCCTGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCAATTA	288
QY <th>980</th> <th>AAAGAAAAGCACTGTAATGAAGGAGAAACAGAAAGCGCAACAGGTACTTTCGCTCAAAA</th> <th>103</th>	980	AAAGAAAAGCACTGTAATGAAGGAGAAACAGAAAGCGCAACAGGTACTTTCGCTCAAAA	103

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Db      289 AAGAAAAGCACGTATGAGGAGAAACAGAGAGCCCAACAGRWWCWDMBGYTSVCWV 348
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RESULT 15
US-11-060-756-38
; Sequence 38, Application US/11060756
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-38

Query Match      27.4%; Score 285.6; DB 10; Length 600;
Best Local Similarity 94.3%; Pred. No. 1.4e-50;
Matches 283; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

QY      740 GAATTACAGGAAATTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGTTTTTTC 799
Db      49  GAACACTAGGAAATTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGTTTTTTC 108

QY      800 ATGGCATCAGTATACCTGAGCCAGAGACATGGAAACTCTTTGAGGAAAAGTTCTCAGATG 859
Db      109 ATGGCATCAGTATACCTGAGCCAGAGACATGGAAACTCTTTGAGGAAAAGTTCTCAGATG 168

QY      860 TTCATCTGTGGCTCTGAACCTTCAATGAAGGGGTCTCTGAAGATGAATCCAGATGACAGAT 919
Db      169 TTCATCTGTGGCTCTGAACCTTCAATGAAGGGGTCTCTGAAGATGAATCCAGATGACAGAT 228

QY      920 TAACCTGTTCCCAACTCTGGAGAGCTCTTACTTTGATTTCTTTCAAGAGGCCCAATTA 979
Db      229 TAACCTGTTCCCAACTCTGGAGAGCTCTTACTTTGATTTCTTTCAAGAGGCCCAATTA 288

QY      980 AAGAAAAGCACGTAAATCAAGGAGAAACAGAGAGCCCAACAGGTACTTCCGCTCAAAA 1039
Db      289 AAGAAAAGCACGTAAATCAAGGAGAAACAGAGAGCCCAACAGRWWCWDMBGYTSVCWV 348

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Job time : 2026.2 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 21, 2005, 20:26:40 ; Search time 3325.85 Seconds
(without alignments)
11914.206 Million cell updates/sec

Title: US-10-766-691-9
Perfect score: 1041
Sequence: 1 atggaagatgataaaatt.....aggtacttcgctcaaaagt 1041

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	360.2	34.6	689	6	BY752739 BY752739
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9	298.4	28.7	824	5	B0221831 603750354
10	295.6	28.4	536	5	BU686325 UI-CF-DU1
11	289.2	27.8	597	5	BP016186 BP016186
12	284.6	27.3	825	6	CB315094 AGENCOURT
13	269.8	25.9	565	6	CB400506 OSTF177F1
14	258.6	24.8	731	2	AW106692 um32d03.y
15	255	24.5	718	1	AA286088 vc33b05.i
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18	248.8	23.9	806	7	CK472415 AGENCOURT
19	247.6	23.8	504	5	BX304025 BX304025
20	243.8	23.4	1956	3	AY383681 Rattus no
21	239	23.0	485	2	AV960213 AV960213
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23	230.2	22.1	1462	9	AY412140 Homo sapi
24	223.8	21.5	688	5	BW241505 BW241505

25	221.8	21.3	2572	3	AK030598
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31	210.8	20.2	627	6	BY716459
32	210.6	20.2	500	5	BP187523
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35	209.4	20.1	380	5	BY075395
36	202.2	19.4	2005	3	AK090045
37	202.2	19.4	2769	3	AK045036
38	200.6	19.2	1893	3	AK050990
39	199.6	19.2	600	5	BW352155
C 40	199	19.1	295	1	AA626859
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45	190	18.3	754	7	CK358920

ALIGNMENTS

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CB169554/c
LOCUS CB169554 695 bp mRNA linear EST 30-JAN-2003
DEFINITION RUC603000752.R1 CSEQFXN20 testes Bos taurus cDNA, mRNA sequence.
ACCESSION CB169554
VERSION CB169554.1 GI:28155681
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 695)
AUTHORS Adelson,D.L. and Gill,C.A.
TITLE Bovine ESTs (Adelson and Gill)
JOURNAL Unpublished (2003)
COMMENT Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471, USA
Tel: 9798452616
Fax: 9798456970
Email: david.adelson@tamu.edu.
Location/Qualifiers
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/db_xref="taxon:9913"
/tissue_type="testes"
/clone_lib="CSEQFXN20 testes"
/note="Organ: testes; Vector: pBluescript SK+; Site_1: NotI; Site_2: EcoRI; sequence 5' of the insert (5'-NNN...NNNinsert)
GCGAATTCGAGCTCCACCGCGTGGCGCGCGCTCGAG. Sequence 3' of the inserts (AAGAATTCGATATCAAGCTTATGATACCGTCGACCTCGAG. normalized Rd 1 library, sequenced 3' with M13R primer."

FEATURES
source
Tel: 9798452616
Fax: 9798456970
Email: david.adelson@tamu.edu.
Location/Qualifiers

Query Match 46.2%; Score 480.6; DB 6; Length 695;
Best Local Similarity 92.8%; Pred. No. 5.4e-97;
Matches 504; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

Qy 1 ATGGAAGATGAAAAATTAGCTTAAGCTGGAGAGGGTCTTATGGGTGTATTCAA 60
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Db 543 ATGGGAAGATGAAAAATTAGCTTAAGCTGGAGAGGGTCTTATGGGTGTATTCAA 484

RESULT 2
 BY733578
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS

BY733578 670 bp mRNA linear EST 17-DEC-2002
 BY733578 RIKEN full-length enriched, 16 days neonate male
 diencephalon Mus musculus cDNA clone G630052E12.5, mRNA sequence.
 BY733578
 BY733578.1 GI:27146705
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 670)
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
 Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
 Batalov, S., Baisel, K. W., Blake, J. A., Bradt, D., Brusnic, V.,
 Chochia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,
 Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T.,
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
 Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
 Kawaji, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,
 Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
 Numata, K., Okido, T., Pavan, W. J., Perte, G., Pesole, G.,
 Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
 Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
 Sandelin, A., Schneider, C., Simple, C. A., Setou, M., Shimada, K.,
 Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
 Vexardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y.,
 Wells, C., Wilming, L. G., Wyshaw-Boris, A., Yanagisawa, M., Yang, I.,
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
 Hayatsu, N., Hirozane-Kitakawa, T., Konno, H., Nakamura, M.,
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,

FEATURES

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 625 GTTGCACACAGGTGTCACGAGCCGCGAATCTTCTGTGGGAGACA 670

RESULT 3

BY752739

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

BY752739 689 bp mRNA linear EST 17-DEC-2002
 CNA clone P30014106 5', mRNA sequence.
 BY752739
 BY752739.1 GI:27183802
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 689)
 Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaide, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
 Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusci, V.,
 Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
 Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
 Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
 Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
 Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
 Maltas, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
 Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
 Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
 Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,
 Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
 Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
 Verardo, R., Wagner, L., Walstedt, C., Wang, Y., Watanabe, Y.,
 Wells, C., Wilming, L.G., Wyshaw-Boris, A., Yanagisawa, M., Yang, I.,
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
 Hayata, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 22354683
 12466851
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,
 Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,
 Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,
 Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,
 Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N.,
 Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,
 Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Computational Analysis of Full-length Mouse cDNAs Compared with
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 RIKEN integrated sequence analysis (RISA) system--384-format
 10 (11), 1757-1771 (2000)
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Tissues were provided by Kirk W. Beisel (Boys Town National
 Research Hospital 555 North 30th Street Omaha, NE 68131 USA) whose
 assistance we gratefully acknowledge.
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.

FEATURES

source

Location/Qualifiers
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 409 GAGTACTGTGATCACACGCTGTTAAACGAGCTGGAGAGAAACCCAAACGGAGTTCTGAT 468
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Db 648 TGTGCCACCAGTGGTACCGAGCCCCCGA 676

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KINASE KKIALRE (HUMAN); mRNA sequence.
ACCESSION AI385966
VERSION AI385966.1 GI:4199429
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 500)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, J.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:307801
This read is a RESEQUENCE of a previously sequenced mouse clone
correct orientation
Seq primer: -40RP from Gibco
High quality sequence stop: 339.
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-5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor
sequence: 5' CTCAGTGTCTTTTCTTTT 3'"

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Best Local Similarity 82.3%; Pred. No. 4.4e-64;
Matches 408; Conservative 0; Mismatches 84; Indels 4; Gaps 2;
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Db 2 GAAATAGCCCTGCGGAAATCCGTATGCTGAAG---TTGAACACCAACCTCGTGAA 58
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QY 615 AGATGTGGACCAACTT 630
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RESULT 5
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LOCUS Mus musculus adult male testis cDNA, RIKEN full-length enriched
DEFINITION library, clone:493341107 product:cyclin-dependent kinase-like 1
(CDC2-related kinase), full insert sequence.
ACCESSION AK016781
VERSION AK016781.1 GI:12855701
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
JOURNAL 99279253
MEDLINE PUBMED 10349636
REFERENCE 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
AUTHORS Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
JOURNAL prepare full-length cDNA libraries for rapid discovery of new genes
MEDLINE Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 20499374
REFERENCE 3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
AUTHORS Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer

```

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4

The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5

The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 1691)

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H.,
Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y.,
Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K.,
Hiraoka, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Izawa, M.,
Kasakawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K.,
Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C.,
Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,
Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y.,
Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T.,
Tejima, Y., Toya, Y., Yamamura, T., Yasunishi, A., Yoshida, K.,
Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216]

PLEASE visit our web site (http://genome.gsc.riken.jp/) for further
details.

cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues. First strand cDNA was primed with a primer
[5'-GAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse transcriptase
and subsequently enriched for full-length by cap-trapper. Second
strand cDNA was prepared with the primer adapter of sequence [5'-
GAGAGAGATTCGAGTAAATTAATTAATCCCCCCCCC 3']. cDNA was cleaved
with BamHI and XhoI. cDNA of size comprised longer than 7 kb was
selected before cloning. Vector: a modified pBluescript KS(+) after
bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3'
end: BamHI. Host: DH10B.

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Matches 461; Conservative 0; Mismatches 195; Indels 3; Gaps 1;

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Db 477 CCTCTCGTGAAGAACATAAATGTCAGACACTGCGAGGCTGTAAATTTCTGCATATAAAT 536

Qy 361 AACTGTATTCCACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATATTC 420

Db 537 AACTGTCATACACAGAGAGCTGAGACCGGAAATATTTCTATCACCACCAACAGCTACGCCATT 596

Qy 421 AAGATTGTGACTTCGGGTTTGGCAAAATCTTGATTT---CCAGAGAGATCCCTACACCGAT 477

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Qy 538 TCTTCAGTCGATATATGGCTATTGGTTGGTTTTTTCAGAGCTCTTCACAGAGCCAGCCA 597

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RESULT 6

CK482747

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CK482747 757 bp mRNA linear EST 14-JAN-2004
AGENCOURT 17606510 NIH_MGC_235 Rattus norvegicus cDNA clone
IMAGE:71110321 5', mRNA sequence.

CK482747

CK482747.1 GI:40827095

EST.

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 757)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaaps-r@mail.nih.gov
Tissue Procurement: Howard Jacobs
CDNA Library Preparation: Express Genomics
DNA Sequencing Arranged by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLNL1977 row: e column: 07
High quality sequence stop: 695.

FEATURES

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/note="Organ: kidney; Vector: pExpress-1; Site_1: EcorV; Site_2: NotI; RNA obtained from pooled kidney tissue from a mix of male and female animals at 8 wk old. Tissues were snap-frozen before RNA extraction and purification (TRI-reagent method). cDNA was primed using oligo-dT primer: 5'-pGACTGTTCTAGTCGAGCGCGCC(T)25-3' and cloned into the EcorV/NotI sites of pExpress-1. Size-selection >1.4kb resulted in an average insert size of 2.2 kb. This primary library is non-normalized (normalized primary library is NIH MGC 236) and was constructed by Express Genomics (Frederick, MD). Note: this is a NIH_MGC library."

ORIGIN

Query Match 30.4%; Score 316.8; DB 7; Length 757;
Best Local Similarity 70.4%; Pred. No. 2.5e-60;
Matches 439; Conservative 0; Mismatches 182; Indels 3; Gaps 1;
QY 1 ATGGAAAGTAGTAAAGAAATAGCTAAGACTGAGAGAGGCTTATGGGGTGTATTCAAA 60
DB 103 ATGGAAAGTAACGAAAGAAATGGAAGATTGGAAGAGTTCCATGGGTAGTGTTCAG 162
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DB 703 CTGTGGCCAGGAAATCGAATGTG 726

RESULT 7

AA061797
LOCUS
DEFINITION

938 bp mRNA linear EST 03-FEB-1997
mi34h09.r1 Stratagene mouse testis (#937308) Mus musculus cDNA
clone IMAGE:513953 5', similar to gb:X66358 SERINE/THREONINE-PROTEIN
KINASE KXIALRE (HUMAN);, mRNA sequence.

AA061797

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AA061797.1 GI:1555606

Mus musculus

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 938)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,

Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,

Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,

Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and

Waterston, R.

The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@wustl.edu

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MG1:307801

Seq primer: -28ml3 rev1 ET from Amersham

High quality sequence stop: 442.

Location/Qualifiers

1..938

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/note="Organ: testis; Vector: pBluescript SK-; Site_1:

EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:

Oligo dT. Average insert size: 1.0 kb; Uni-ZAP XR Vector;

-5' adaptor sequence: 5' GAATTCGGCAGG 3' -3' adaptor

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

ORIGIN

Query Match 30.4%; Score 316.8; DB 1; Length 938;
Best Local Similarity 82.9%; Pred. No. 2.5e-60;
Matches 398; Conservative 0; Mismatches 77; Indels 5; Gaps 3;
QY 135 GAATAATGACTAAGAGAAATACGTATGTTGAACAAATTAACCAATCTGTGAA 194
DB 1 GAAATAAGCCCTCGGGAAATCCGTATGCTGAAG---TTGAAACACCCCAACCTCGTGA 57
QY 195 CCTCATCGAGTGTTCAGGAGAAAAGAAATGCATTAGTTTTCGAATCTGTGATCA 254

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Db      58 CCTCATCGAGTGTTCAGAGAAAGAGAAAGATGCACTAGTCTTTTGGTACTGTGATCA 117
      255 TACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTCCTGATGGAGTGATCAAAAG 314
      118 CACACTGTTAAACGAGCTGGAGAGAAACCCAAACGGAGTTCCTGATGGAGTGATTAAG 177
      315 CGTATTATGGCAACACTTCAAGCTCTTAAATTCCTGTCATATACATACTGATTCACAG 374
      178 TGTGCTATGGCAAAACCCCTTCAAGCCCTTAACTTCTGTCAAGACACAAATGTTATTCATCG 237
      375 AGATATAAAACCTGAAATATTTCTAAATACTAAGCAAGGAATAATCAAGATTTCGTGACTT 434
      238 GGATGTAAACCTGAAACATCTCTTAATACCAAGCAAGGATGATAAGATTGTGACTT 297
      435 CGGTTTGGCACAATTTCTGATTCCAGGAGATGCCCTACACCGATTATGTAGTACGAGATG 494
      298 TGGATTGGCACGAATCTTAATCCAGGAGAGCCCTACACAGACTATGTGGCCACCGGTG 357
      495 GTACCGAGCTCTGAACCTCTTGTGGGAGATACCTCAGTATGTTCTTCAGTTCGATATATG 554
      358 GTACCGAGCCCGCAACTTCTCGTGGGAGACACGAAAGTACGGTTCTCTGTAGACGTGTG 417
      555 GGCTATTGGTGTGTTTTCAGAGCTCCTCAGAGCCAGCCACTGTGGCTCGAAATC 614
      418 GGCCGTGGCTGTGTTTTCAGAG-CTCCTGACGGGTGAG-CACTGTGGCCGGGAAACC 475

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RESULT 8
AV986182 598 bp mRNA linear EST 14-MAR-2002
LOCUS AV986182 Nori Satoh unpublished cDNA library, larva Ciona
DEFINITION intestinalis cDNA clone cilv41b18 5', mRNA sequence.
ACCESSION AV986182
VERSION AV986182.1 GI:19475050
KEYWORDS EST.
SOURCE Ciona intestinalis
ORGANISM Ciona intestinalis
REFERENCE 1 (bases 1 to 598)
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
TITLE Expressed genes in Ciona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoheascidian.zool.kyoto-u.ac.jp.

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FEATURES
source
1..598
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cilv41b18"
/tissue_type="whole animal"
/dev_stage="larva"
/clone_lib="Nori Satoh unpublished cDNA library, larva"

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ORIGIN
Query Match 29.5%; Score 306.8; DB 2; Length 598;
Best Local Similarity 70.7%; Pred. No. 4.4e-58;
Matches 423; Conservative 0; Mismatches 172; Indels 3; Gaps 1;

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Qy      11 ATGAAAATTAGCTAAGACTGGAGAGGGTCTTATGGGGTTGTATTCAAATGCGAAACA 70
      1 ATGAGAAGATAGGTAAGATAGGGAAGGATCTTATGGCATTTGTTAAATGTCCGAACC 60
      71 AAACCTCTGGACAAGTAGTACTGTGTTAAAAATTTGGGAATCTGAAGATGATCTCTGTG 130
      61 GTGACTTCGGGACAAATTGTGGCCATCAAAAAATTTGTGAGTCAGAAGATGACCCGCTGA 120

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Qy      131 TTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAATCTTGT 190
      121 TCAGAAAATCGCGCTCGAGGAAATCAGAATGTTAAAGCAATTTGAAACACAATAACTTGG 180
      191 TGAACCTCATCGAGGTGTTCAAGGAGAAAAGGAAAAATGCATTTTAAAGTATTTTGAATAC 250
      181 TGAACCTGATTTGAAGTTCCTCGTGAANAACGCAATTTACATCTTTGTTGCGATTTGTG 240
      251 ATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGATGAGATGATCA 310
      241 ATCATACAGTTTAAATGAATTTGGACAAACACATGAGAGGAGTACCAAGAACATCATGTTA 300
      311 AAGCGTATTATGGCAAAACACTTCAAGCTCTTAATTTCTGTCATATACATACTGATTC 370
      301 AACGTATTGTTGGCAAGTTCCTCAAGCTGTTCACCTTTTGCATTCAGCAATAAATGTATAC 360
      371 ACAGAGATATAAAACCTGAAAATATTCTAATACTAAGCAAGGAATAATCAAGATTGTTG 430
      361 ATCGTGATGTAAACACAGAGACATATTATCAATAGCAAGGTGTTATCAAGTTGTG 420
      431 ACTTCGGGTTTGCACAAATTTCTGA---TTCAGGAGATGCTACACCGATTATGTAGCTA 487
      421 ACTTTGGAATTTGCAAGAATTTTAACTGGTCTCTGCGACGATTACACCGACTATGTGSCCA 480
      488 CGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACCTCAGTATGTTCTTTCAGTGC 547
      481 CTAGTGGTACAGACACCTGAGCTCCTCGTGGGGACACTCAGTATGGCCCTCCAGTGG 540
      548 ATATATGGGCTATTGGTGTGTTTTCAGAGCTCCTGACAGGCCACCGCTGTGGCC 605
      541 ATGTGTGGGCAATAGGTTCGTATTTTCCGAGTTGTTGTGCGGACAGGCATTATATGGCC 598

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RESULT 9
BU221831 824 bp mRNA linear EST 25-NOV-2002
LOCUS BU221831 603750354F1 CSEQCHN04 Gallus gallus cDNA clone CHEST66113 5', mRNA
DEFINITION sequence.
ACCESSION BU221831
VERSION BU221831.1 GI:25410266
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
REFERENCE 1 (bases 1 to 824)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

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FEATURES
source
1..824
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="CHEST66113"
/tissue_type="whole embryo"
/dev_stage="20-21"
/lab_hosts="DH10B"
/clone_lib="CSEQCHN04"

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Db      297 TAACTGTTCCTCAACTCTCTGAGAGCTCTACTTTGATCTTTTCAAGAGGCCCAATTA 238
Qy      980 AAAGAAAAGCAGTAATGAAGGAAGAAACAGAGAAGCAGCAACAGGTACTTCCGCTCAAAA 1039
Db      237 AAAGAAAAGCAGTAATGAAGGAAGAAACAGAGAAGCAGCAACAGGTACTTCCGCTCAAAA 178
Qy      1040 GT 1041
Db      177 GT 176

RESULT 11
LOCUS   BP016186
DEFINITION BP016186 Nori Satoh unpublished cDNA library, young adult Ciona
EST. BP016186.1 GI:19507663
ACCESSION BP016186
VERSION
KEYWORDS
SOURCE   Ciona intestinalis
ORGANISM Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 597)
Satoch.N., Satoch.Y., Kohara,Y. and Shin-i,T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoch@ascidian.zool.kyoto-u.ac.jp.

FEATURES             source
    source
    1..597
        /organism="Ciona intestinalis"
        /mol_type="mRNA"
        /db_xref="taxon:7719"
        /clone="ciad64e08"
        /tissue_type="whole animal"
        /dev_stage="young adult"
        /clone_lib="Nori Satoh unpublished cDNA library, young
        adult"

ORIGIN
Query Match      27.8%; Score 289.2; DB 5; Length 597;
Best Local Similarity 71.0%; Pred. No. 3.8e-54;
Matches 397; Conservative 0; Mismatches 159; Indels 3; Gaps 1;

Qy      2 TGAAGAAAGTATGAAAATTAGCTAAGACTGGAGAAGGCTCTTATGGGGTTGTATTCAAAAT 61
Db      38 TGGAGAAATATGAGAAGATAGTAAAGATAGGGAAGGATCTTATGGCATTTGTGTTAAAT 97
Qy      62 GCAGAAACAAACCTCTGGCAAGTAGTAGCTGTATAAAAAATTTGTGGAATCTGAAGATG 121
Db      98 GTCGGAACCGTGACTCGGGCAAAATTTGGGCCATCAAAAAATTTGTGAGTCAGAAGATG 157
Qy      122 ATCTGTGTTTGAAGAAATAGCATAAGAGAAATACGTATGTTTGAAGCAATTAAACATC 181
Db      158 ACCCGCTGATCAAGAAAATCGCGCTGAGGGAATTCAGAATGTTTAAAGCAATTGAACACA 217
Qy      182 CAAATCTTGTGAACCTCATCGAGGTGTTTCAGAGAAAAAGGAAATGCATTTAGTTTGTG 241
Db      218 ATAATCTGTGTAACCTGATTGAAGTTTTCGTCGAAAACGCAATTTACATCTGTGTG 277
Qy      242 AATACTGTGATCATACATCTTTTAAATGAGCTGGAAAGAAACCCCAATGGAGTTGCTGATG 301
Db      278 AGTATTGTGATCATACAGTTTAAATGAATTGGACAAACACATGAGAGGAGTACCAAGAC 337
Qy      302 GAGTGATCAAAAGCGTTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCATATACATA 361

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Db      338 ATCATGTTAAACGTATTGTTTGGCAAGTCTTCAAGCTGTTCACTTTTGCATCAGATA 397
Qy      362 ACTGTATTTCACAGAGATATAAAACCTGAAATATTCTTAATAACTAAGCAAGGAATAATCA 421
Db      398 ATTGTATACATCGTGATGTAATAAACCCAGAGAACAATATTAACTACCTAAGCAAGGTGTTATCA 457
Qy      422 AGATTGTGATCTCGGTTTGGCAAAATTTCTGA---TTCCAGGAGATGCCCTACACCGATT 478
Db      458 AGTTGTGTGACTTTGGATTTCGAAGAATTTTAACTGGTCTCTGGCGCAGCATTTACACCGACT 517
Qy      479 ATGTAGCTACAGAGATGTCACGAGCTCCTGAACCTTCTTGTGGGAGATACTCAGTATGTT 538
Db      518 ATGTGGCCACTAGTGTGTACAGAGCACCTGAGCTCTCTGTCGGGACACACTCAGTATGGCC 577
Qy      539 CTTCAAGTCGATATATGGGC 557
Db      578 CTNCAAGTGGATGTGTGGGC 596

RESULT 12
LOCUS   CB315094
DEFINITION AGENCOURT 11526413 NICHDRr.Pit1 Rattus norvegicus cDNA clone
IMAGE:6888377 5', mRNA sequence.
ACCESSION CB315094
VERSION CB315094.1 GI:28838974
KEYWORDS EST.
SOURCE   Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 825)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: John C. Marshall, M.D., Ph.D
cDNA Library Preparation: CLONTECH
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC3144 row: i column: 16
High-quality sequence stop: 468.

FEATURES             source
    source
    1..825
        /organism="Rattus norvegicus"
        /mol_type="mRNA"
        /db_xref="taxon:10116"
        /clone="IMAGE:6888377"
        /tissue_type="Pituitary"
        /lab_host="DH10B"
        /clone_lib="NICHDRr.Pit1"
        /notes="Vector: pDNR-LIB; Site 1: Sfil; Site 2: Sfil; 5'
        and 3' adaptors were used in cloning as follows: 5'
        adaptor sequence: 5'-CACGCCATATGGGC-3' and 3' adaptor
        sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-dr(30)BN-3'
        (where B = A, C, or G and N = A, C, G, or T). Average
        insert size 1.23 kb (range 0.5-4.0 kb). 15/15 colonies
        contained inserts by PCR. This library was enriched for
        full-length clones and was constructed by Clontech
        Laboratories (Palo Alto, CA)."

ORIGIN
Query Match      27.3%; Score 284.6; DB 6; Length 825;
Best Local Similarity 70.9%; Pred. No. 4.1e-53;
Matches 455; Conservative 0; Mismatches 90; Indels 97; Gaps 2;

Qy      361 AACTGTATTACAGAGATATAAAACCTGAAATATTCTTAATAACTAAGCAAGGAATAATC 420

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Db	96	AGCTGTATCATCGGACGTAAAAACCGAAACATCTCTAATAGCCAAGCAGGTGATA	155
Qy	421	AAGATTGTGACTTCGGGTTCACAAATCTGTATTCAGGAGATGCTACACCGATTAT	480
Db	156	AAGATTGTGACTTCGGATTTCACGAAATCTTAATTCAGGAGATGCTACACAGACTAT	215
Qy	481	GTAGCTACAGATGTGTACCGAGCTCCTGAACTTCTTTGGGAGATACTCAGTATGGTTCT	540
Db	216	GTTGCCACAGGTGTGTACGAGCCCTGAACTTCTGTGGGAGACACGAATACGGCTCC	275
Qy	541	TCAGTCCGATATATGGCTATTGGTTGTCTTTTCAGAGCTCCTGTGACGCCAGCCACTG	600
Db	276	TCGTGTGACATATGGCTGTCCGCTGTGTGTTTTGCAGAGCTCTGTACCCGTGAGCCACTC	335
Qy	601	TGGCCTGGAAATACAGATGTGGACCAACTTATCTGATAATCAGAACACTAGTAGAGCG	660
Db	336	TGGCCAGGAAATACAGATGTGGACCAACTTATCTGATCATCAGGACATT-----	385
Qy	661	GGGTTTGGCCATGTTGACAGGCTGGTCTCGAACTCTTGACGTCAAGTCACTCACTGCC	720
Db	386	-----	385
Qy	721	GTAGCTCTCAAGTGTGGAAATACAGGAAAAATTAATCCAGACATCAATCAATCTTT	780
Db	386	-----GGGAAAGCTGATCCCAAGGCATCAGTCTATCTTT	419
Qy	781	AAAAATAACGGGTTTTTCCATGGCATCAGTATACCTTGAGCCAGACAGATGGAACCTTT	840
Db	420	AAAACTAACCAAGTTTTTCCGTGGCATCAGCATCCCGAAACCTTGAGACATGGAGCTCTT	479
Qy	841	GAGGAAAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAATTCATG-AAAGGGGTGTCTGAA	899
Db	480	GAGAAAAAATTTCTCAAAATGTTTCAGCCCTATGGCTTTAAGTTTCATGAAAGGGGTCTGAA	539
Qy	900	GATGAATCCAGATCACAGATTAACCTGTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTC	959
Db	540	GATGATCCTGATGAGAGGCTGACCTGTGCCCACTGTTGGACAGTACTACTTCGAGTC	599
Qy	960	TTTTCAAGAGCCCAAAATTAAGAAAAAGCAAGTAAATGAAGG	1001
Db	600	TTTTCAAGAGACCAATGAAAGAAAAAGCCCGCAATGAGG	641

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFclone cloning project : Contact david_hill@fci.harvard.edu or marc_vidal@fci.harvard.edu
POLYA=No.

[illegible]

ORIGIN

Query Match	25.9%	Score 269.8	DB 6	Length 565
Best Local Similarity	67.6%	Prod. No. 8.4e-50		
Matches 379	Conservative 0	Mismatches 182	Indels 0	Gaps 0
QY	31	GGAGAGGGCTCTTATGGGTTGTATTCAATCCAGAAACAACCTCTGGCAAGTAGTA	90	
Db				
QY	5	GGTGAAGTTTCATATGGAGTTGTATATAAATGTAATAATAGGATACCTGGCAAAATGTGTG	64	
Db				
QY	91	GCTGTTAAAAAATTTGTGGAATCTGAAGATGATCTGTTGTTAAAGAAAAATAGCACTAAGA	150	
Db				
QY	65	GCAATCAAAAAGTTTGTGAAAATCTGAAGATGATCCGATATAATAAGAAAAATTCGCTACGG	124	
Db				
QY	151	GAATACGTATGTTGAAGCAATTAATAACAATCCAAATCTTGTGAACCTCATCGAGGTGTTTC	210	
Db				
QY	125	GAATACAGAAATGCTGAAGCAACTGAACAATCAAAATTTGGTTGGATTCATTTGAAGTGTTC	184	
Db				
QY	211	AGGAGAAAAGGAAATGCATTTAGTTTTTGAATACTGTGATCATACACTTTTAAATGAG	270	
Db				
QY	185	AAACGGAAACGGAAACCTCATCTCGCTTTGAACTTTGTGATCGAACTGTACTTTCAGAG	244	
Db				
QY	271	CTGGAAAGAAACCCAAATGGAGTTGCTGATGGAGTGATCAAAAGCGTATTATTGGCAAAACA	330	
Db				
QY	245	TTGGAGAGAAATCCCGATGGAGTTAAACGATGAACTCATATAAGAAAAATAATTTATCAATTG	304	
Db				
QY	331	CTTCAAGCTCTTAAATTTCTGTCAATACATAAATCTGATTCACACAGATATAAAACCTGAA	390	
Db				
QY	305	CTAGAAGCTCTTAAATTTCTGTCAAGTCACAAATGTATTCATCGAGATGTGAACCGGAA	364	
Db				
QY	391	AATATCTTAATTAATCAAGCAGGAATTAATCAAGATTTGTGACTTCGGTTTGCACAAATTT	450	
Db				
QY	365	AACATTTTCTTGACACGGAATGATCAAGTGAACCTTGAGATTTTCGGATTTGCTCGAATA	424	
Db				
QY	451	CTGATTTCCAGGAGATGCCCTACACCGATTTATGTAGCTACGAGATGGTACCGAGCTCCTGAA	510	
Db				
QY	425	ATAAAACACGACGGAATATGTACTGACTATGTGSCAACTCGTTTGGTACCGTAGTCAGAA	484	
Db				
QY	511	CTTCTGTGGGAGATCACTCAGATGGTTCTTCAGTCGATATATGGGCTATGTGGTTGTGTT	570	
Db				
QY	485	CTTCTGGTCGGTGATGTTTCAATATGGGCCACCTGTAGACATTTGGGCTGTAGGATGTGTA	544	
Db				
QY	571	TTTGCAGAGCTCCTGCACAGGC	591	
Db				
QY	545	TATGGGAGCTGTTGACTGGC	565	
Db				

RESULT 14
AW106692
LOCUS
DEFINITION

AW106692 731 bp mRNA linear EST 20-OCT-1999
um32d03.y1 Sugano mouse kidney mKia Mus musculus cDNA clone
IMAGE:2236229 5', similar to gb:U66358 SERINE/THREONINE-PROTEIN
KINASE KITALRE (HUMAN); mRNA sequence.

ACCESSION AW106692
 VERSION AW106692.1 GI:6077492
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 731)
 AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
 TITLE The WashU-NCI Mouse EST Project 1999
 JOURNAL Unpublished (1999)
 COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:1006441
 Seq primer: custom primer used
 High quality sequence stop: 433.
 Location/Qualifiers
 1..731
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="CS7BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:2236229"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="Sugano mouse kidney mklia"
 /note="Organ: Kidney; Vector: pME18S-FL3; Site_1: DralII (CAGCTGTG); Site_2: DralII (CAGCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DralII adaptor [GTGTGGCTACTGG], digested vector (5' site CAGCTGTG, 3' site CAGCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCGTCTTAAAGCTGCG and 3' end primer CGACCTGCAGCTCGAGCACA."
 ORIGIN
 Query Match 24.8%; Score 258.6; DB 2; Length 731;
 Best Local Similarity 66.9%; Pred. No. 2.7e-47;
 Matches 382; Conservative 0; Mismatches 186; Indels 3; Gaps 1;
 QY 5 AAAAGTATGAAATATAGCTAAGACTGAGAGGGTCTTATGCGGTGTGTTTCAAAATGCA 64
 DB |||||
 QY 156 AAATATGAAAAAATTTGGAAGATTTGGAAGAGGCTCTATGCGGTGTGTTTCAAGTGA 215
 DB |||||
 QY 65 GAAACAAACCTCTGGACAAGTAGTGTGTTAAAAAATTTGTGGAATCTGAAGATGATC 124
 DB |||||
 QY 216 GAAACAGGGACACGGTTCAGATCGTGGCCATCAAGAGGTTTCTGGAAACCGAAGTACC 275
 DB |||||
 QY 125 CTGTTGTTAAGAAAATAGCACTAGAGAAATACGTATGTTGAAGCAATTAACATCAA 184
 DB |||||
 QY 276 CTGTATGAAGAAAATCGCCCTTCGAGAAATCCGCATGCTCAAGCACTCAAGCACCCCA 335
 DB |||||
 QY 185 ATCTGTGTAACCTCATCAGGTGTTTCAGGAGAAAAAGAAAATGCAATTTAGTTTGAAT 244
 DB |||||
 QY 336 ACCTGGTCACTCTCTGGAAGTCTTCGGAGAGACGGAGGCTTCACCTGGTGTTCAGT 395
 DB |||||
 QY 245 ACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCCAATGGAGTTGCTGATGAG 304
 DB |||||

Db 396 ACTCGACCAACACGGTCTTCACAGCTGGATCGGTATCAGAGGGGGTACCAGAGCCTC 455
 QY |||||
 QY 305 TGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTGCATATACATACT 364
 DB |||||
 Db 456 TCGTGAAGAACATAACTTGGCAGACACTGCAGGCGTGTAAATTTCTGCCATAAACATACT 515
 QY |||||
 QY 365 GTATTACAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAATCAAGA 424
 DB |||||
 Db 516 GCATACACAGAGAGTGAAGCGGAAAATATTCTCATCACCAAAACAGTCACGCCATTAAGC 575
 QY |||||
 QY 425 TTTGTGACTTCGGGTTTGCAAAATTTCTGATT---CCAGGAGATGCTTACACCCGATTATG 481
 DB |||||
 Db 576 TCTGTGACTTTGGGTCGACGGCTCTCACTGACCAANGTACTACTACACAGACTACN 635
 QY |||||
 QY 482 TAGCTACGAGATGGTACCGAGCTCTCGAACTTCTTGTGGGAGATACCTCAGTATGTTCTT 541
 DB |||||
 Db 636 GTGCCACCCCGTGTACTGTCTCACCCGAGCTGTAGTTGGAGACACGACGATTTGGTCCC 695
 QY |||||
 QY 542 CAGTCGATATATGGGCTATTGGTTGTGTTT 572
 DB |||||
 Db 696 CTGTAGATGTCTGGGCAATTGGCTGTGTGT 726

RESULT 15

AA286088

LOCUS

DEFINITION

vc33b05.r1 Barstead MPLRBI Mus musculus cDNA clone IMAGE:776337 5'

similar to gb:X66358 SERINE/THREONINE-PROTEIN KINASE KIALRE

(HUMAN);, mRNA sequence.

AA286088

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 718)
 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:469193
 Seq primer: -28ml3 rev2 ET from Amersham
 High quality sequence stop: 424.
 Location/Qualifiers
 1..718
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="BALB/c"
 /db_xref="taxon:10090"
 /clone="IMAGE:776337"
 /sex="mixed"
 /tissue_type="Kidney"
 /dev_stage="6 weeks"
 /lab_host="DH10B"
 /clone_lib="Barstead MPLRBI"
 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTACGAATCTGAAGTGGAGCGGCCCTTTTTTTTTTTTTTTTTTTTTT

3']; double-stranded cDNA was ligated to Eco RI adaptors
[CATGGATTCCGGTACC], digested with Not I and cloned into the
Not I and Eco RI sites of the modified pTVT3 vector.
Library constructed by Bob Barstead."

ORIGIN

Query Match	24.5%	Score 255;	DB 1;	Length 718;
Best Local Similarity	67.9%	Pred. No. 1.7e-46;		
Matches 416;	Conservative 0;	Mismatches 190;	Indels 7;	Gaps 4;

QY	1	ATCGAAAGTATGAAATTTAGCTAAGACTTGAGAGAGGCTCTTATGGGTTCTATTTCAAA	60
Db	109	ATGGAAAAATATGAAAAAATGGAAGATTGGAGAGGCTCTTATGGGTTCTATTTCAAA	168
QY	61	TGCAGAAACAAACCTCTCGACAAGTAGTAGCTTTTAAAAATTTCTGGAATCTGAAGAT	120
Db	169	TGCAGAAACAGGGACACGGGTGAGATCGTGGCCATCAAGAGTTTCTGGAAACCCGAAGAT	228
QY	121	GATCCTGTTGTTAAGAAATAGCACTTAAGAGAAATACGTAATGTTGAAGCAATTAACACAT	180
Db	229	GACCTGTGTCATAAAGAAATCGCCCTTCAGAAATCCGCATGCTCAAGCACTCAAGCAC	288
QY	181	CCAAATCTTTGTGAACCTCATCGAGTGTTCAGAGAAAGGAAAAATGCAATTTAGTTTTT	240
Db	289	CCCAACTGTCTCACTCTCGAAGTCTTCCGGAG-AAAGCGAGGCTTCACCTGGTGTTC	347
QY	241	GAATAGTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT	300
Db	348	GAGTACTCGGACACACAGGTGCTTCACGAGCTGGATCGGTA-TCAGAGGGGGTACAGAG	406
QY	301	GGAGTATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTAATTAACCAAGGATATC	360
Db	407	CCTCTCGTGAAGACATAAATTTGGCAGACACTGCAGGCTGTAAATTTCTGCCATAAACAT	466
QY	361	AACTGTATTTCACAGAGATATAAACTCGAAATATTCTAATACTTAACCAAGGATATC	420
Db	467	AACTGCATACACAGAGACGTCGAGCCGGAATATTCTCATTAACCAAGTCAAGCCATT	526
QY	421	AAGATTGTGACTTCGGGTTTGCA----CAAATTCGATTCAGGAGATGCTACACCGA	476
Db	527	AAGCTCTGTGACTTTGGGGTTTCGAACGGCTTCTCACTGGACACAGGTGACTACTACACGA	586
QY	477	TTATGTAGCTAGAGATGGTACCGAGCTCCTGAAGCTTCTTGTGGGAGATCTCAGTATGG	536
Db	587	CTACGTGGCCACCCGGTGTACCCGTCACCGAGCTGCTAGTGGGAGACACGCGAGTATGG	646
QY	537	TTCTTCAGTCGATATATGGGCTATTGGTTGTGTTTTTTCAGAGCTCCTGACAGCCAGCC	596
Db	647	TCCCCCTGTAGATGTCTGGGC-ATGGCTGTGTGTTGCTGAGTTACTGTCCGAGTGCC	705
QY	597	ACTGTGGCCTGGA	609
Db	706	TCTATGGCAAGGA	718

Search completed: April 22, 2005, 01:23:04
Job time : 3334.85 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 21, 2005, 23:37:20 ; Search time 3944.37 Seconds
(without alignments)
1602.273 Million cell updates/sec

Title: US-10-766-691-9

Perfect score: 1041

Sequence: 1 atggaagatgataaaatt.....aggtacttcgctcaaaagt 1041

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5633728 seqs, 303525691 residues

Total number of hits satisfying chosen parameters: 11267456

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09D_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09E_PUBCOMB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1041	100.0	1041	US-10-766-691-9	Sequence 9, Appli
2	1025	98.5	1068	US-10-766-691-3	Sequence 3, Appli
3	839	80.6	945	US-10-766-691-11	Sequence 11, Appli
4	823	79.1	972	US-10-766-691-5	Sequence 5, Appli
5	821	78.9	1790	US-10-766-691-5	Sequence 30, Appli
6	762.8	73.3	1678	US-10-333-314-30	Sequence 6, Appli
7	709	68.1	1819	US-10-250-889-6	Sequence 13, Appli
8	645.6	62.0	887	US-10-766-691-13	Sequence 3, Appli
9	645.6	62.0	882	US-09-834-496A-3	Sequence 1, Appli
10	454.4	43.7	561	US-09-834-496A-1	Sequence 1, Appli
11	454.4	43.7	594	US-10-766-691-7	Sequence 7, Appli

12	343.8	33.0	1363	10	US-09-960-706-1079	Sequence 1079, Ap
13	343.8	33.0	1612	17	US-10-363-616-146	Sequence 146, App
14	343.8	33.0	2944	18	US-10-357-930-24573	Sequence 24573, A
15	251.8	24.2	1701	16	US-10-174-794-5	Sequence 5, Appli
16	251.8	24.2	3080	16	US-10-174-794-3	Sequence 3, Appli
17	241.2	23.2	2095	17	US-10-369-022-21	Sequence 21, Appli
18	241.2	23.2	2095	18	US-10-757-262-107	Sequence 107, App
19	202.6	19.5	1513	18	US-10-620-052A-33	Sequence 33, Appli
20	162	15.6	1635	14	US-10-072-036-112	Sequence 112, App
21	162	15.6	1635	14	US-10-072-036-114	Sequence 114, App
22	161.6	15.5	1297	11	US-09-969-034-4494	Sequence 4494, Ap
23	161.6	15.5	1297	16	US-10-295-681-28	Sequence 28, Appli
24	160.4	15.4	2213	17	US-10-440-464-137	Sequence 137, App
25	160.4	15.4	2213	17	US-10-641-643-1037	Sequence 1037, Ap
26	160.4	15.4	2734	18	US-10-723-860-7854	Sequence 7854, Ap
27	160	15.4	1322	9	US-09-925-300-324	Sequence 324, App
28	158.4	15.2	1297	16	US-10-295-681-30	Sequence 30, Appli
29	155.6	14.9	2213	16	US-10-295-681-40	Sequence 40, Appli
30	154.2	14.8	1050	9	US-09-954-456-84	Sequence 84, Appli
31	154.2	14.8	1050	9	US-09-954-456-718	Sequence 718, App
32	154.2	14.8	1050	9	US-09-954-456-1165	Sequence 1165, Ap
33	154.2	14.8	1050	11	US-09-968-007A-985	Sequence 985, App
34	154.2	14.8	1050	15	US-10-177-293-40	Sequence 40, Appli
35	154.2	14.8	1050	16	US-10-204-041-7	Sequence 7, Appli
36	154.2	14.8	1050	17	US-10-172-118-668	Sequence 668, App
37	154.2	14.8	1050	17	US-10-189-266-4	Sequence 4, Appli
38	154.2	14.8	1050	17	US-10-342-887-668	Sequence 668, App
39	154.2	14.8	1050	18	US-10-723-860-2447	Sequence 2447, Ap
40	154.2	14.8	1050	19	US-10-843-641A-3111	Sequence 3111, Ap
41	154.2	14.8	1050	19	US-10-843-641A-3745	Sequence 3745, Ap
42	154.2	14.8	1050	19	US-10-843-641A-4192	Sequence 4192, Ap
43	154.2	14.8	1050	19	US-10-843-641A-7455	Sequence 7455, Ap
44	154.2	14.8	1235	18	US-10-733-878-420	Sequence 420, App
45	154.2	14.8	1235	18	US-10-751-736-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-766-691-9
; Sequence 9, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10766,691
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-9

Query Match 100.0%; Score 1041; DB 19; Length 1041;
Best Local Similarity 100.0%; Pred. No. 6.6e-266;
Matches 1041; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGGAAGATGATAAAATTAGCTAACGACGAGAGGCTTATGGGTGATTCAA 60
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Db 1 ATGAAAAGTATGAAAAATAGCTAAGACTGGAGAGGCTCTTATGGGTTGTTATTCAA 60
QY 61 TGAGAAACAAACCTCTGACAGTAGTAGCTGTAAAAATTTGTGGAATCTGAAGAT 120
Db 61 TGAGAAACAAACCTCTGACAGTAGTAGCTGTAAAAATTTGTGGAATCTGAAGAT 120
QY 121 GATCTGTTGTTAAGAAAATAGCAGTCTAAGAGAAATACGTATCTGAAGCAATTAACAAAT 180
Db 121 GATCTGTTGTTAAGAAAATAGCAGTCTAAGAGAAATACGTATCTGAAGCAATTAACAAAT 180
QY 181 CCAATCTGTTGAACTCTAAGCTGTTGAGGAAAGAAAGCAATTAACAAATTAACAAAT 240
Db 181 CCAATCTGTTGAACTCTAAGCTGTTGAGGAAAGAAAGCAATTAACAAATTAACAAAT 240
QY 241 GAATAGTGTGATCATACACTTTTAATGAGCTGGAAGAAAGCAATTAACAAATTAACAAAT 300
Db 241 GAATAGTGTGATCATACACTTTTAATGAGCTGGAAGAAAGCAATTAACAAATTAACAAAT 300
QY 301 GGAGTGTCAAAAGCGTATTAATGAGCTGGAAGAAAGCAATTAACAAATTAACAAAT 360
Db 301 GGAGTGTCAAAAGCGTATTAATGAGCTGGAAGAAAGCAATTAACAAATTAACAAAT 360
QY 361 AACTGTATTCAGAGATATTAACCTGGAAGAAAGCAATTAACAAATTAACAAATTAAC 420
Db 361 AACTGTATTCAGAGATATTAACCTGGAAGAAAGCAATTAACAAATTAACAAATTAAC 420
QY 421 AAGATTTGTGACTTGGGTTTGCACAACTCTGAGCTTAAATCTGTCATATACAT 480
Db 421 AAGATTTGTGACTTGGGTTTGCACAACTCTGAGCTTAAATCTGTCATATACAT 480
QY 481 GTAGTACAGATGGTACCGAGCTCTGAACTCTTGTGGGAGATATCTCAGTATGGTTCT 540
Db 481 GTAGTACAGATGGTACCGAGCTCTGAACTCTTGTGGGAGATATCTCAGTATGGTTCT 540
QY 541 TCAGTTCGATATATGGGTTTGCACAACTCTGAGCTTAAATCTGTCATATACAT 600
Db 541 TCAGTTCGATATATGGGTTTGCACAACTCTGAGCTTAAATCTGTCATATACAT 600
QY 601 TGGCTCGGAAATCAGATGTGGACCACTTATCTGATTAATCTGATTAATCTGATTAATCTGAT 660
Db 601 TGGCTCGGAAATCAGATGTGGACCACTTATCTGATTAATCTGATTAATCTGATTAATCTGAT 660
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; Sequence 3, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-766-691-3

Query Match 98.5%; Score 1025; DB 19; Length 1068;
Best Local Similarity 100.0%; Pred. No. 1.2e-261;
Matches 1025; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAAGTATGAAAAATAGCTAAGACTGGAGAGGCTCTTATGGGTTGTTATTCAA 60
Db 1 ATGAAAAGTATGAAAAATAGCTAAGACTGGAGAGGCTCTTATGGGTTGTTATTCAA 60
QY 61 TGAGAAACAAACCTCTGAGCAAGTAGTAGCTGTAAAAATTTGTGGAATCTGAAGAT 120
Db 61 TGAGAAACAAACCTCTGAGCAAGTAGTAGCTGTAAAAATTTGTGGAATCTGAAGAT 120
QY 121 GATCTGTTGTTAAGAAAATAGCAGTCTAAGAGAAATACGTATCTGAAGCAATTAACAAAT 180
Db 121 GATCTGTTGTTAAGAAAATAGCAGTCTAAGAGAAATACGTATCTGAAGCAATTAACAAAT 180
QY 181 CCAATCTGTTGAACTCTCATCGAGCTGTTGAGCAAGAAAGCAATTAACAAATTAACAAAT 240
Db 181 CCAATCTGTTGAACTCTCATCGAGCTGTTGAGCAAGAAAGCAATTAACAAATTAACAAAT 240
QY 241 GAATAGTGTGATCATACACTTTTAATGAGCTGGAAGAAAGCAATTAACAAATTAACAAAT 300
Db 241 GAATAGTGTGATCATACACTTTTAATGAGCTGGAAGAAAGCAATTAACAAATTAACAAAT 300
QY 301 GGAGTGTCAAAAGCGTATTAATGAGCTGGAAGAAAGCAATTAACAAATTAACAAAT 360
Db 301 GGAGTGTCAAAAGCGTATTAATGAGCTGGAAGAAAGCAATTAACAAATTAACAAAT 360
QY 361 AACTGTATTCAGAGATATTAACCTGGAAGAAAGCAATTAACAAATTAACAAATTAAC 420
Db 361 AACTGTATTCAGAGATATTAACCTGGAAGAAAGCAATTAACAAATTAACAAATTAAC 420
QY 421 AAGATTTGTGACTTGGGTTTGCACAACTCTGAGCTTAAATCTGTCATATACAT 480
Db 421 AAGATTTGTGACTTGGGTTTGCACAACTCTGAGCTTAAATCTGTCATATACAT 480
QY 481 GTAGTACAGATGGTACCGAGCTCTGAACTCTTGTGGGAGATATCTCAGTATGGTTCT 540
Db 481 GTAGTACAGATGGTACCGAGCTCTGAACTCTTGTGGGAGATATCTCAGTATGGTTCT 540
QY 541 TCAGTTCGATATATGGGTTTGCACAACTCTGAGCTTAAATCTGTCATATACAT 600
Db 541 TCAGTTCGATATATGGGTTTGCACAACTCTGAGCTTAAATCTGTCATATACAT 600
QY 601 TGGCTCGGAAATCAGATGTGGACCACTTATCTGATTAATCTGATTAATCTGATTAATCTGAT 660
Db 601 TGGCTCGGAAATCAGATGTGGACCACTTATCTGATTAATCTGATTAATCTGATTAATCTGAT 660
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Qy 661 GGGTTTCCCATGTTGACCAAGCTGGTCTCGAACTCTTGAGCTCAAGTGAATCCACCTGCC 720
Db 661 GGGTTTCCCATGTTGACCAAGCTGGTCTCGAACTCTTGAGCTCAAGTGAATCCACCTGCC 720
Qy 721 GTAGCTCTCAAGTGTCTGGAATACAGGAAATTAATCCCAAGACATCAATCAATCTTT 780
Db 721 GTAGCTCTCAAGTGTCTGGAATACAGGAAATTAATCCCAAGACATCAATCAATCTTT 780
Qy 781 AAAAGTAAACGGGTTTTCATGCGATCAGTATACCTGAGCCAGAGACATGGAACCTCTT 840
Db 781 AAAAGTAAACGGGTTTTCATGCGATCAGTATACCTGAGCCAGAGACATGGAACCTCTT 840
Qy 841 GAGGAAAGTTCTCAGATGTTTCATCTGCTGCTCGAATTCATGAGGGGTGCTGAAG 900
Db 841 GAGGAAAGTTCTCAGATGTTTCATCTGCTGCTCGAATTCATGAGGGGTGCTGAAG 900
Qy 901 ATGAATCCAGATGACAGATTAACCTGTTCCCACTCTCTGGAGAGCTCTCTACTTTGATTCT 960
Db 901 ATGAATCCAGATGACAGATTAACCTGTTCCCACTCTCTGGAGAGCTCTCTACTTTGATTCT 960
Qy 961 TTTCAAGAGGCCCAAAATTAAGAAAGAACGACGTAATGAAGGAAGAAACAGAGACGCCAA 1020
Db 961 TTTCAAGAGGCCCAAAATTAAGAAAGAACGACGTAATGAAGGAAGAAACAGAGACGCCAA 1020
Qy 1021 CAGGT 1025
Db 1021 CAGGT 1025

RESULT 3
US-10-766-691-11
; Sequence 11, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: Lex-0046-USA
; CURRENT APPLICATION NUMBER: US/10/766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 945
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-11

Query Match 80.6%; Score 839; DB 19; Length 945;
Best Local Similarity 90.8%; Pred. No. 3e-212;
Matches 945; Conservative 0; Mismatches 0; Indels .96; Gaps 1;

Qy 1 ATGGAAGAAGTATGAAAAATTAGCTAAGACTGAGAGAGGGTCTTATGGGGTTGTATCCAA 60
Db 1 ATGGAAGAAGTATGAAAAATTAGCTAAGACTGAGAGAGGGTCTTATGGGGTTGTATCCAA 60
Qy 61 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTTGTGGAACTCTGAAGAT 120
Db 61 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTTGTGGAACTCTGAAGAT 120
Qy 121 GATCCTCTGTTAGAAAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACAT 180
Db 121 GATCCTCTGTTAGAAAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACAT 180
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Qy 181 CCAAACTTTGTGAACCTCATCGAGGTGTTAGGAGAAAAAGGAAAAATGCATTTAGTTTTT 240
Db 181 CCAAACTTTGTGAACCTCATCGAGGTGTTAGGAGAAAAAGGAAAAATGCATTTAGTTTTT 240
Qy 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTCAT 300
Db 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTCAT 300
Qy 301 GGAGTGAATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAAATTTCTGTATATACAT 360
Db 301 GGAGTGAATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAAATTTCTGTATATACAT 360
Qy 361 AACTGTATTACAGAGATATAAAACCTGGAATAATTTCTAATACTAAGCAAGGAATAATC 420
Db 361 AACTGTATTACAGAGATATAAAACCTGGAATAATTTCTAATACTAAGCAAGGAATAATC 420
Qy 421 AAGATTTGTGACTTTCGGGTTTGCACAAATCTCGATTCAGGAGATGCTACACCGATTAT 480
Db 421 AAGATTTGTGACTTTCGGGTTTGCACAAATCTCGATTCAGGAGATGCTACACCGATTAT 480
Qy 481 GTAGCTACGAGATGGTACCGAGCTTCTGAACTTCTTGTGGGAGATATCTCAGTATGTTCT 540
Db 481 GTAGCTACGAGATGGTACCGAGCTTCTGAACTTCTTGTGGGAGATATCTCAGTATGTTCT 540
Qy 541 TCAGTCGATATATGGGCTATTTGGTTGTTTTCAGAGCTCTCTGACAGGCCAGCCACTG 600
Db 541 TCAGTCGATATATGGGCTATTTGGTTGTTTTCAGAGCTCTCTGACAGGCCAGCCACTG 600
Qy 601 TGGCTCGAAAAATCAGATGTGGACCAACTTTATCTGATAATCAACAACACTAGTAGAGAG 660
Db 601 TGGCTCGAAAAATCAGATGTGGACCAACTTTATCTGATAATCAACAACACTAGTAGAGAG 660
Qy 661 GGGTTTCGCCATGTTGACCAAGGCTGGTCTCGAACTCTTGAAGTCAAGTGATCCACCTGCC 720
Db 661 GGGTTTCGCCATGTTGACCAAGGCTGGTCTCGAACTCTTGAAGTCAAGTGATCCACCTGCC 720
Qy 721 GTAGCTCTCAAGTGTCTGGAAATTAAGGAAAAATTAATCCCAAGACATCAATCAATCTTT 780
Db 721 GTAGCTCTCAAGTGTCTGGAAATTAAGGAAAAATTAATCCCAAGACATCAATCAATCTTT 780
Qy 781 AAAAGTAAACGGGTTTTCATGCGATCAGTATACCTGAGCCAGAGACATGGAACCTCTT 840
Db 781 AAAAGTAAACGGGTTTTCATGCGATCAGTATACCTGAGCCAGAGACATGGAACCTCTT 840
Qy 841 GAGGAAAGTTCTCAGATGTTTCATCTGCTGGCTCTGAACTTTCATGAAGGGGTGCTGAAG 900
Db 841 GAGGAAAGTTCTCAGATGTTTCATCTGCTGGCTCTGAACTTTCATGAAGGGGTGCTGAAG 900
Qy 901 ATGAATCCAGATGACAGATTAACCTGTTCCCACTCTCTGAGAGCTCTCTACTTTGATTCT 960
Db 901 ATGAATCCAGATGACAGATTAACCTGTTCCCACTCTCTGAGAGCTCTCTACTTTGATTCT 960
Qy 961 TTTCAAGAGGCCCAAAATTAAGAAAGAACGACGTAATGAAGGAAGAAACAGAGACGCCAA 1020
Db 961 TTTCAAGAGGCCCAAAATTAAGAAAGAACGACGTAATGAAGGAAGAAACAGAGACGCCAA 1020
Qy 1021 CAGGTACTTCCGCTCAAAAGT 1041
Db 1021 CAGGTACTTCCGCTCAAAAGT 945

RESULT 4
US-10-766-691-5
; Sequence 5, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
```

; TITLE OF INVENTION: Novel Human Kinase Proteins and
 ; FILE OF INVENTION: Polynucleotides Encoding the Same
 ; FILE REFERENCE: LEX-0046-USA
 ; CURRENT APPLICATION NUMBER: US/10/766,691
 ; CURRENT FILING DATE: 2004-01-28
 ; PRIOR APPLICATION NUMBER: US/09/671,050
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: Fast-Seq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 972
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 ; US-10-766-691-5

Query Match 79.1%; Score 823; DB 19; Length 972;
 Best Local Similarity 90.6%; Pred. No. 5.4e-208;
 Matches 929; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

QY	1	ATCGAAAGTATGAAATTAAGTCTAGAGCTGGAGAGGCTCTTATGGGTTGTATTCAA	60
Db	1	ATCGAAAGTATGAAATTAAGTCTAGAGCTGGAGAGGCTCTTATGGGTTGTATTCAA	60
QY	61	TGCGAAACAAACCTCTGCAAGTAGTCTGTTAAATTTGCGAATCTGAAGAT	120
Db	61	TGCGAAACAAACCTCTGCAAGTAGTCTGTTAAATTTGCGAATCTGAAGAT	120
QY	121	GATCTGTTGTTAAGAAATAGCCTTAAGAGAAATACGTATGTTCAAGCAATTAACAT	180
Db	121	GATCTGTTGTTAAGAAATAGCCTTAAGAGAAATACGTATGTTCAAGCAATTAACAT	180
QY	181	CCAAATCTGTGAACCTCATGAGGTGTTAGGAGAAAGAAATGCAATTTAGTTTT	240
Db	181	CCAAATCTGTGAACCTCATGAGGTGTTAGGAGAAAGAAATGCAATTTAGTTTT	240
QY	241	GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATGAGTCTGAT	300
Db	241	GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATGAGTCTGAT	300
QY	301	GGAGTGATCAAAAGGTTATGTCGAAACACTTCAAGCTCTTAATTTCTGTCATATACAT	360
Db	301	GGAGTGATCAAAAGGTTATGTCGAAACACTTCAAGCTCTTAATTTCTGTCATATACAT	360
QY	361	AACCTGATTCACAGAGATATAAAACCTGAAATATCTTAATTAAGCAAGCAATATC	420
Db	361	AACCTGATTCACAGAGATATAAAACCTGAAATATCTTAATTAAGCAAGCAATATC	420
QY	421	AAGATTTGTGACTTCGGGTTTGCAAAATCTGATTCAGGAGATGCTACACCGATTAT	480
Db	421	AAGATTTGTGACTTCGGGTTTGCAAAATCTGATTCAGGAGATGCTACACCGATTAT	480
QY	481	GTAGCTACGAGATGTTACCGAGCTCTGAACTTTCTGTTGGAGATCTAGTATGTTCT	540
Db	481	GTAGCTACGAGATGTTACCGAGCTCTGAACTTTCTGTTGGAGATCTAGTATGTTCT	540
QY	541	TCAGTCGATATATGGCTATGTTGTTGTTTTCAGAGCTCTGACAGCCAGCCACTG	600
Db	541	TCAGTCGATATATGGCTATGTTGTTGTTTTCAGAGCTCTGACAGCCAGCCACTG	600
QY	601	TGCGCTGGAAATCAGATGTTGACCACTTTATCTGATTAATCAGAACACTAGAGAGC	660
Db	601	TGCGCTGGAAATCAGATGTTGACCACTTTATCTGATTAATCAGAACACTAGAGAGC	660
QY	661	GGGTTTCGCCATGTTGACCGAGGCTGCTCGAACTCTTGACGTCAAGTCACTCCCTGCC	720
Db	661	GGGTTTCGCCATGTTGACCGAGGCTGCTCGAACTCTTGACGTCAAGTCACTCCCTGCC	720
QY	721	GTAGCTCTCAAGTCTCTGGAATTAAGCAAAATTAATCCCAAGACATCAATCAATCTTT	780
Db	651	AGGAAATTAATCCCAAGACATCAATCAATCTTT	684

QY	781	AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGACATGGAACCTCTT	840
Db	685	AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGACATGGAACCTCTT	744
QY	841	GAGGAAAGTCTCAGATGTTTCATCTGTGGCTCTGAACTTTCATGAGGGGTGTTCAAG	900
Db	745	GAGGAAAGTCTCAGATGTTTCATCTGTGGCTCTGAACTTTCATGAGGGGTGTTCAAG	804
QY	901	ATGAATCCAGATGACAGATTAACCTGTTCCCACTCTGAACTTTCATGAGGGGTGTTCAAG	960
Db	805	ATGAATCCAGATGACAGATTAACCTGTTCCCACTCTGAACTTTCATGAGGGGTGTTCAAG	864
QY	961	TTTCAAGAGGCCCAATTTAAAGAAAGCAGCTGTAATGAAGGAAAGAAACAGAGCCCAA	1020
Db	865	TTTCAAGAGGCCCAATTTAAAGAAAGCAGCTGTAATGAAGGAAAGAAACAGAGCCCAA	924
QY	1021	CAGGT 1025	
Db	925	CAGGT 929	

RESULT 5
 US-10-333-314-30
 ; Sequence 30, Application US/10333314
 ; Publication No. US20030211093A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry
 ; APPLICANT: KHAN, Farrah A.; GURURAJAN, Rajagopal
 ; APPLICANT: HAFALIA, April J.A.; CHAWLA, Narinder K.
 ; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
 ; APPLICANT: GANDHI, Ameena R.; POLICKY, Jennifer L.
 ; APPLICANT: BAUGHN, Mariah R.; TRIBOLEY, Catherine M.
 ; APPLICANT: THORNTON, Michael B.; BANDMAN, Olga
 ; APPLICANT: NGUYEN, Daniel B.; LU, Yan
 ; APPLICANT: BURFORD, Neil; LAL, Preeti G.
 ; APPLICANT: DING, Li; YAO, Monique G.
 ; APPLICANT: ELLIOTT, Vicki S.; RECIPON, Shirley A.
 ; APPLICANT: KEARNEY, Liam; LU, Dzung Aina M.
 ; APPLICANT: GREENWALD, Sara R.; TANG, Y. Tom
 ; APPLICANT: XU, Yuming; WALSH, Roderick T.
 ; APPLICANT: GIEZEN, Kimberly J.; YANG, Junming
 ; APPLICANT: JACKSON, Jennifer L.
 ; TITLE OF INVENTION: HUMAN KINASES
 ; FILE REFERENCE: P1-0162 USN
 ; CURRENT APPLICATION NUMBER: US/10/333,314
 ; CURRENT FILING DATE: 2003-01-15
 ; PRIOR APPLICATION NUMBER: PCT/US01/23092
 ; PRIOR FILING DATE: 2001-07-20
 ; PRIOR APPLICATION NUMBER: US 60/220,038
 ; PRIOR FILING DATE: 2000-07-21
 ; PRIOR APPLICATION NUMBER: US 60/222,112
 ; PRIOR FILING DATE: 2000-07-28
 ; PRIOR APPLICATION NUMBER: US 60/222,831
 ; PRIOR FILING DATE: 2000-08-04
 ; PRIOR APPLICATION NUMBER: US 60/224,729
 ; PRIOR FILING DATE: 2000-08-11
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 30
 ; LENGTH: 1790
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No: 1698381CB1
 ; US-10-333-314-30

Query Match 78.9%; Score 821; DB 17; Length 1790;
 Best Local Similarity 90.6%; Pred. No. 2.5e-207;
 Matches 927; Conservative 0; Mismatches 0; Indels 96; Gaps 1;
 QY 1 ATCGAAAGTATGAAATTAAGTCTAGAGCTGGAGAGGCTCTTATGGGTTGTATTCAA 60

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Db 239 ATGGAAGAATGATAAATAGCTAAGCTGGAGAGGGCTTATGGGTTGTATTCAA 298
Qy 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTTAAAAAATTTGGAAATCTGAAGAT 120
Db 299 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTTAAAAAATTTGGAAATCTGAAGAT 358
Qy 121 GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACAT 180
Db 359 GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACAT 418
Qy 181 CCAATCTCTGTAACCTCATCGAGTCTTCAGAGAGAAAGAAAGAAATGCAATTTAGTTT 240
Db 419 CCAATCTCTGTAACCTCATCGAGTCTTCAGAGAGAAAGAAAGAAATGCAATTTAGTTT 478
Qy 241 GAATACCTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATGAGGTTGCTGAT 300
Db 479 GAATACCTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATGAGGTTGCTGAT 538
Qy 301 GGAGTGAATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTCTATACAT 360
Db 539 GGAGTGAATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTCTATACAT 598
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATATC 420
Db 599 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATATC 658
Qy 421 AAGATTGTTGACTTCGGGTTTGCAAAATCTGATTCAGAGAGTGCCTACACCGATTAT 480
Db 659 AAGATTGTTGACTTCGGGTTTGCAAAATCTGATTCAGAGAGTGCCTACACCGATTAT 718
Qy 481 GTAGCTACGAGATGGTACCGAGCTCTGAACTTCTGTGGAGATACCTAGTATGGTTCT 540
Db 719 GTAGCTACGAGATGGTACCGAGCTCTGAACTTCTGTGGAGATACCTAGTATGGTTCT 778
Qy 541 TCAGTGCATATATGGGCTATTGGTTGTTGTTTTCAGAGCTCTGAGAGCCAGCCACTG 600
Db 779 TCAGTGCATATATGGGCTATTGGTTGTTGTTTTCAGAGCTCTGAGAGCCAGCCACTG 838
Qy 601 TGGCCTGGAAATCAGATGTGGACCAACTTTATCTGATAATCAAGAACACTAGTAGAGAG 660
Db 839 TGGCCTGGAAATCAGATGTGGACCAACTTTATCTGATAATCAAGAACACT- 888
Qy 661 GGGTTTCGCCATGTTGACAGGGCTGGTCTCGAACTCTTGAGCTCAAGTGATCCACCTGCC 720
Db 889 ----- 888
Qy 721 GTAGCCTCTCAAAGTGTGGNAATTACAGGAATAATTATCCCAAGACATCAATCAATCTTT 780
Db 889 -----AGGAAATTAATCCCAAGACATCAATCAATCTTT 922
Qy 781 AAAAGTAAACGGGTTTTCATGGCATCAGTATACCTGAGCAGAGACATGGAACCTCTT 840
Db 923 AAAAGTAAACGGGTTTTCATGGCATCAGTATACCTGAGCAGAGACATGGAACCTCTT 982
Qy 841 GAGGAAAGTTCTCAGATGTTTCACTCTGGCTCTGAACTTCAATGAAGGGGTGTCTGAAG 900
Db 983 GAGGAAAGTTCTCAGATGTTTCACTCTGGCTCTGAACTTCAATGAAGGGGTGTCTGAAG 1042
Qy 901 ATGAATCCAGATGACAGATTAACTGTTCCCACTCTGAGAGAGCTCTACTTTGATCT 960
Db 1043 ATGAATCCAGATGACAGATTAACTGTTCCCACTCTGAGAGAGCTCTACTTTGATCT 1102
Qy 961 TTTCAAGAGGCCCAATTTAAAGAAAGAAAGACGTAATGAAGAAAGAAACAGAGAGCGCAA 1020
Db 1103 TTTCAAGAGGCCCAATTTAAAGAAAGAAAGACGTAATGAAGAAAGAAACAGAGAGCGCAA 1162
Qy 1021 CAG 1023
Db 1163 CAG 1165

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RESULT 6
US-10-250-889-6

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; Sequence 6, Application US/10250889
; Publication No. US20040115629A1
; GENERAL INFORMATION:
; APPLICANT: PANZER, Scott R; LINCOLN, Stephen E.;
; APPLICANT: ALTUS, Christina M.; DUFOUR, Gerard E.;
; APPLICANT: JACKSON, Jennifer L.; JONES, Anissa L.;
; APPLICANT: DAM, Tam C.; LIU, Tommy F.;
; APPLICANT: HARRIS, Bernard; FLORES, Vincent Z.;
; APPLICANT: DAFFO, Abel; MARWAHA, Rakesh;
; APPLICANT: CHEN, Alice J.; CHANG, Simon C.;
; APPLICANT: GERSTIN, Jr., Edward H.; PERALTA, Careyna H.;
; APPLICANT: DAVID, Marie H.; LEWIS, Samantha A.
; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PT-1195 USN
; CURRENT APPLICATION NUMBER: US/10/250,889
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: PCT/US02/01009
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/261,622
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,864
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/261,865
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/262,207
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,164
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,215
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/263,102
; PRIOR FILING DATE: 2001-01-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 1678
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: LI:058298.1:2001JAN12
; US-10-250-889-6

Query Match 73.3%; Score 762.8; DB 18; Length 1678;
Best Local Similarity 90.0%; Pred. No. 7.1e-192;
Matches 925; Conservative 0; Mismatches 2; Indels 101; Gaps 6;

Qy 1 ATGGAAGAATGATAAATAGCTAAGCTGGAGAGGGCTTATGGGTTGTATTCAA 60
Db 131 ATGGAAGAATGATAAATAGCTAAGCTGGAGAGGGCTTATGGGTTGTATTCAA 190
Qy 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTTAAAAAATTTGGAAATCTGAAG 119
Db 191 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTTAAAAAATTTGGAAATCTGAAG 250
Qy 120 TGATCCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTA-TGTTGAAGCAATTAAC 178
Db 251 TGATCCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTA-TGTTGAAGCAATTAAC 310
Qy 179 ATCCAAATCTTGAACCTCATCGAGTGTTCAGGAGAGAAAGAAATCAATTTAGTTT 238
Db 311 ATCCAAATCTTGAACCTCATCGAGTGTTCAGGAGAGAAAGAAATCAATTTAGTTT 370
Qy 239 TTGAATACCTGTGATCATACACTTTTAAATGAGCTGGAGAAAGAAACCCAAATGGAGTTGCTG 298
Db 371 TTGAATACCTGTGATCATACACTTTTAAATGAGCTGGAGAAAGAAACCCAAATGGAGTTGCTG 430
Qy 299 ATGGAAGTATCAAAAGCGTATTATGGAACACTTCAAGCTCTTAATTTCTGTCTATATAC 358

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Db 431 ATGGAGTGAACAAAGCGTATTATGCAACACCTTCAAGCTCTTAATTTCTGTCTATATAC 490
Qy 359 ATAACTGTATTCAGAGATATAAAACCTGAAATATCTTAATAACAAAGCAAGATATAA 418
Db 491 ATAACTGTATTCAGAGATATAAAACCTGAAATATCTTAATAACAAAGCAAGATATAA 550
Qy 419 TCAAGATTTGTGACTTCGGGTTTGCAAAATCTGATTCAGAGATGCTTACACGGATT 478
Db 551 TCAAGATTTGTGACTTCGGGTTTGCAAAATCTGATTCAGAGATGCTTACACGGATT 610
Qy 479 ATGTAGCTA-CGAGATGGTACCGAGCT-CCTGAACCTTCTGTGGGAGTACT-CAGTATG 535
Db 611 ATGTAGCTAGCAGATGGTACCGAGCTCCTGAACCTTCTGTGGGAGTACTCAGTATG 670
Qy 536 GTTCTTCAGTCGATATATCGGCTATTGGTGTGTTTTCAGAGCTCCTGACAGGCCAGC 595
Db 671 GTTCTTCAGTCGATATATCGGCTATTGGTGTGTTTTCAGAGCTCCTGACAGGCCAGC 730
Qy 596 CACTGTGGCCTGGAATAATCAGATGTGGACCAACTTTATCTGATATCAGAACACTAGTAG 655
Db 731 CACTGTGGCCTTGAATAATCAGATGTGGACCAACTTTATCTGATATCAGAACACT 785
Qy 656 AGACGGGGTTTCCGCATGTTGACCAAGGCTGTTCTGAACTCTTGACGTCAAGTGATCCAC 715
Db 786 ----- 785
Qy 716 CTGCCGTAGCCTCTCAAGTGTGGAATTAACAGGAAATTAATCCCAAGACATCAATCAA 775
Db 786 -----AGGAAATTAATCCCAAGACATCAATCAA 814
Qy 776 TCTTTAAAGTAAACGGGTTTTCATGTGCATCAGTATACCTGACCCAGAGACATGGAATA 835
Db 815 TCTTTAAAGTAAACGGGTTTTCATGTGCATCAGTATACCTGACCCAGAGACATGGAATA 874
Qy 836 CTCCTGAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTTCATGAAGGGGTGC 895
Db 875 CTCCTGAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTTCATGAAGGGGTGC 934
Qy 896 TGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTCTGGAGAGCTCCTACTTTG 955
Db 935 TGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTCTGGAGAGCTCCTACTTTG 994
Qy 956 ATTCTTTTCAAGAGGCCCAATTAAGAAAGACAGTANTGAAGGAAAGCAAGAC 1015
Db 995 ATTCTTTTCAAGAGGCCCAATTAAGAAAGACAGTANTGAAGGAAAGCAAGAC 1054
Qy 1016 GCCAACAG 1023
Db 1055 GCCAACAG 1062

```

RESULT 7
 US-10-766-691-13
 ; Sequence 13, Application US/10766691
 ; Publication No. US20050042626A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: Novel Human Kinase Proteins and
 ; FILE REFERENCE: Polynucleotides Encoding the Same
 ; CURRENT APPLICATION NUMBER: US/10/766,691
 ; PRIOR FILING DATE: 2004-01-28
 ; PRIOR APPLICATION NUMBER: US/09/671,050
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13

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; SOFTWARE: FastSeq for Windows Version 4.0.
; SEQ ID NO 13.
; LENGTH: 1819
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-13

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Query Match      68.1%; Score 709; DB 19; Length 1819;
Best Local Similarity 77.0%; Pred. No. 1.5e-177;
Matches 1025; Conservative 0; Mismatches 0; Indels 306; Gaps 1;

Qy 1 ATGGAAGATATGAAAAATTTAGCTAAGACTGGAAGAGGGTCTTATGGGGTTGATTCAAA 60
Db 138 ATGGAAGATATGAAAAATTTAGCTAAGACTGGAAGAGGGTCTTATGGGGTTGATTCAAA 197
Qy 61 TGCAGAAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTTGGNAATCTGAAGAT 120
Db 198 TGCAGAAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTTGGNAATCTGAAGAT 257
Qy 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAGAAAT 180
Db 258 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAGAAAT 317
Qy 181 CCAAAATCTTGTGAACCTCATCGAGGTGTTTCAAGAGAAAAGGAAATGCAATTTAGTTTTT 240
Db 318 CCAAAATCTTGTGAACCTCATCGAGGTGTTTCAAGAGAAAAGGAAATGCAATTTAGTTTTT 377
Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGGTGCTGAT 300
Db 378 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGGTGCTGAT 437
Qy 301 GGAGTCAATCAAAAGCGTATTTATGGCAACAATTCAAGCTCTTAAATTTCTGTCAATATACAT 360
Db 438 GGAGTCAATCAAAAGCGTATTTATGGCAACAATTCAAGCTCTTAAATTTCTGTCAATATACAT 497
Qy 361 AAATCTGATTTACAGAGATATAAAACCTGAAATATTTCTAAATACCTAAGCAAGGATATATC 420
Db 498 AAATCTGATTTACAGAGATATAAAACCTGAAATATTTCTAAATACCTAAGCAAGGATATATC 557
Qy 421 AAATCTGATTTACAGAGATATAAAACCTGAAATATTTCTAAATACCTAAGCAAGGATATATC 453
Db 558 AAATCTGATTTACAGAGATATAAAACCTGAAATATTTCTAAATACCTAAGCAAGGATATATC 617
Qy 454 ----- 453
Db 618 TCCTTTGATTGGCTTAATAGTGAACCTTCTGAAATCTTTTCTGCAATTCAGAGATTTT 677
Qy 454 ----- 453
Db 678 CTCTGGCTTGGATCCATTGCTGACACAGTGTGTTTCAACATGGGGCCAGGCTCATCTGA 737
Qy 454 ----- 453
Db 738 ACTTCTGGCTCAAGTGAATCCTTCCACCTCGGCTCCCAAGTCTGGATGCAAGTGTG 797
Qy 454 ----- 453
Db 798 AGCCACCGTGGCCAGCCAGAGATTTTTCACAAACAATACTACTGAGAGCTCACAAGATTTT 857
Qy 454 -----ATTCCAGAGATGCTTACACC 474
Db 858 TTAGTGGGAACACAATTTTCGAAACAATTTCTTGAGAACGCAATTCAGGAGATGCTTACACC 917
Qy 475 GATTATGTAGCTACGAGATGATGATCCGAGCTCCTGAACTCTTCTGTGGAGATATCTCAGTAT 534
Db 918 GATTATGTAGCTACGAGATGATGATCCGAGCTCCTGAACTCTTCTGTGGAGATATCTCAGTAT 977
Qy 535 GGTTCCTTCAGTCAATATATCGGCTATTTGGTGTGTTTTCAGAGCTCCTGACAGGCCAG 594
Db 978 GGTTCCTTCAGTCAATATATCGGCTATTTGGTGTGTTTTCAGAGCTCCTGACAGGCCAG 1037
Qy 595 CCACTGTGGCTCGAAAAATTCAGATGTGGACCAACTTTTATCTGATATCAGAACACTAGTA 654

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Db 1038 CCACTGTGGCTGGAAATCAGATGTGGACCACTTTATCTGATANTCAGAACACTAGTA 1097
Qy 655 GAGACGGGGTTTCGCCATGTTTGACACAGCTGGTCTCGAACTCTTGACGTCAGGTGATCCA 714
Db 1098 GAGACGGGGTTTCGCCATGTTTGACACAGCTGGTCTCGAACTCTTGACGTCAGGTGATCCA 1157
Qy 715 CCTGCCGTAGCCTCTCAAGAGCTGGAAATCAGAGAAATTAATCCCAAGACATCAATCA 774
Db 1158 CCTGCCGTAGCCTCTCAAGAGCTGGAAATCAGAGAAATTAATCCCAAGACATCAATCA 1217
Qy 775 ATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAA 834
Db 1218 ATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAA 1277
Qy 835 ACTCTTGAGGAAAGTTCTCAGATGTTTCATCCTGTGGCTCTGAACTTCATGAAGGGTGT 894
Db 1278 ACTCTTGAGGAAAGTTCTCAGATGTTTCATCCTGTGGCTCTGAACTTCATGAAGGGTGT 1337
Qy 895 CTGAGATGATCCAGATGACAGATTAACCTGTTCCCACTCTCTGGAGAGCTCTACTTTT 954
Db 1338 CTGAGATGATCCAGATGACAGATTAACCTGTTCCCACTCTCTGGAGAGCTCTACTTTT 1397
Qy 955 GATCTCTTTCAAGAGGCCCAATTTAAAGAAAGCACGTAATGAAGGAAGAAACAGAGA 1014
Db 1398 GATCTCTTTCAAGAGGCCCAATTTAAAGAAAGCACGTAATGAAGGAAGAAACAGAGA 1457
Qy 1015 CGCCACACAGGT 1025
Db 1458 CGCCACACAGGT 1468

RESULT 8
US-09-834-496A-3
; Sequence 3, Application US/09834496A
; Patent No. US20020090701A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann
; TITLE OF INVENTION: 14257 NOVEL PROTEIN KINASE MOLECULES AND
; FILE OF INVENTION: THEIR USES THEREFOR
; FILE REFERENCE: 381552000900
; CURRENT APPLICATION NUMBER: US/09/834,496A
; PRIOR FILING DATE: 2001-04-13
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-496A-3

Query Match 62.0%; Score 645.6; DB 9; Length 687;
Best Local Similarity 99.4%; Pred. No. 6.2e-161;
Matches 648; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ATGGAAGAATGATGAAAATAGCTAAGACTGGAGAGGGTCTTATGGGGTTGTATTCAAA 60
Db 1 ATGGAAGAATGATGAAAATAGCTAAGACTGGAGAGGGTCTTATGGGGTTGTATTCAAA 60
Qy 61 TGCAGAAACAAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 120
Db 61 TGCAGAAACAAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 120
Qy 121 GATCCTGTTGTAGAAATAGCACTAAGAAATAGTATGTTGAAGCAATTAACAT 180
Db 121 GATCCTGTTGTAGAAATAGCACTAAGAAATAGTATGTTGAAGCAATTAACAT 180
Qy 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAGAAATGCAATTTAGTTTTT 240
Db 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAGAAATGCAATTTAGTTTTT 240
Qy 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAGAAACCCCAATGGAGTTGCTGAT 300

Db 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAGAAACCCCAATGGAGTTGCTGAT 300
Qy 301 GGAGTGTATCAAAAGCGTATTTATGGCAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
Db 301 GGAGTGTATCAAAAGCGTATTTATGGCAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
Qy 361 AACTGTATTCACAGAGATATAAAACCTCGAAATATTTCTTAATACTAAGCAAGGAATATC 420
Db 361 AACTGTATTCACAGAGATATAAAACCTCGAAATATTTCTTAATACTAAGCAAGGAATATC 420
Qy 421 AAGATTTGTGACTTCGGGTTTGGCAAAATCTGATTCAGGAGATGCTACACCGATTAT 480
Db 421 AAGATTTGTGACTTCGGGTTTGGCAAAATCTGATTCAGGAGATGCTACACCGATTAT 480
Qy 481 GTAGCTACGAGATGGTACCGAGCTCTCGAACTCTTGTGGGAGATACCTCAGTATGGTTCT 540
Db 481 GTAGCTACGAGATGGTACCGAGCTCTCGAACTCTTGTGGGAGATACCTCAGTATGGTTCT 540
Qy 541 TCAGTGCATATATGGGCTATTTGGTTGTTTGTGTCAGAGCTCTCTGACAGGCCAGCCTG 600
Db 541 TCAGTGCATATATGGGCTATTTGGTTGTTTGTGTCAGAGCTCTCTGACAGGCCAGCCTG 600
Qy 601 TGGCTGGAAATCAGATGTGGACCACTTTATCTGATATCAAGCACTAG 652
Db 601 TGGCTGGAAATCAGATGTGGACCACTTTATCTGATATCAAGCACTAG 652

Query Match 62.0%; Score 645.6; DB 9; Length 882;
Best Local Similarity 99.4%; Pred. No. 7e-161;
Matches 648; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 ATGGAAGAATGATGAAAATAGCTAAGACTGGAGAGGGTCTTATGGGGTTGTATTCAAA 60
Db 129 ATGGAAGAATGATGAAAATAGCTAAGACTGGAGAGGGTCTTATGGGGTTGTATTCAAA 188
Qy 61 TGCAGAAACAAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 120
Db 189 TGCAGAAACAAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 248
Qy 121 GATCCTGTTGTAGAAATAGCACTAAGAAATAGTATGTTGAAGCAATTAACAT 180
Db 249 GATCCTGTTGTAGAAATAGCACTAAGAAATAGTATGTTGAAGCAATTAACAT 308
Qy 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAGAAATGCAATTTAGTTTTT 240
Db 309 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAGAAATGCAATTTAGTTTTT 368
Qy 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAGAAACCCCAATGGAGTTGCTGAT 300

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Db 369 GAATCTGTGATCATCTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTGTCTGAT 428
QY 301 GGAGTGTATCAAAAGCGTATATGGCAAAACACTTCAAGCTCTTAAATTTCTGTCTATATACAT 360
Db 429 GGAGTGTATCAAAAGCGTATATGGCAAAACACTTCAAGCTCTTAAATTTCTGTCTATATACAT 488
QY 361 AACTGTATTTCACAGAGATATAAACTGGAATATTTCTAAATTAACCTAAGCAAGGAATAATC 420
Db 489 AACTGTATTTCACAGAGATATAAACTGGAATATTTCTAAATTAACCTAAGCAAGGAATAATC 548
QY 421 AAGATTGTGCTTGGGTTTGCACAAATTTCTGATTTCCAGAGAGATGCTCTACACGATTAT 480
Db 549 AAGATTGTGCTTGGGTTTGCACAAATTTCTGATTTCCAGAGAGATGCTCTACACGATTAT 608
QY 481 GTAGCTACAGAGATGATCGGAGCTCTGAACTTCTGTTGGGAGATACCTAGTATGGTTCT 540
Db 609 GTAGCTACAGAGATGATCGGAGCTCTGAACTTCTGTTGGGAGATACCTAGTATGGTTCT 668
QY 541 TCAGTGTGATATATGGCTTATTTGTTGTTTTCAGAGAGCTCTGACAGGCGCCACTG 600
Db 669 TCAGTGTGATATATGGCTTATTTGTTGTTTTCAGAGAGCTCTGACAGGCGCCACTG 728
QY 601 TGGCTGTGAAATCATGATGTGGACCACTTTATCTGATTAATTCAGAACTAG 652
Db 729 TGGCTGTGAAATCATGATGTGGACCACTTTATCTGATTAATTCAGAACTAG 780

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RESULT 10

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US-10-766-691-1
; Sequence 1, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR FILING DATE: 2000-09-27
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 561
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-1

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Query Match 43.7%; Score 454.4; DB 19; Length 561;
Best Local Similarity 99.8%; Pred. No. 3.6e-110;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCAAAAGTATGAAAAATTTAGTAAAGCTGGAGAGAGGCTTTATGGGGTGTGTTTCAA 60
Db 1 ATGCAAAAGTATGAAAAATTTAGTAAAGCTGGAGAGAGGCTTTATGGGGTGTGTTTCAA 60
QY 61 TGCAGAAACAAACCTCTGGACAGTATGCTGTTTAAATAATTTGGAATCTGAAGAT 120
Db 61 TGCAGAAACAAACCTCTGGACAGTATGCTGTTTAAATAATTTGGAATCTGAAGAT 120
QY 121 GATCCTGTGTTTAAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACAT 180
Db 121 GATCCTGTGTTTAAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACAT 180
QY 181 CCAATCTTGTGTAACCTCTGGAAGTATGCTGTTTAAATAATTTGGAATCTGAAGAT 240
Db 181 CCAATCTTGTGTAACCTCTGGAAGTATGCTGTTTAAATAATTTGGAATCTGAAGAT 240
QY 241 GAATCTGTGATCATACATTTTAAATGAGCTGGAAGAAACCCAAATGGAGTGTCTGAT 300
Db 241 GAATCTGTGATCATACATTTTAAATGAGCTGGAAGAAACCCAAATGGAGTGTCTGAT 300
QY 301 GGAGTGTATCAAAAGCGTATATGGCAAAACACTTCAAGCTCTTAAATTTCTGTCTATATACAT 360

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Db 181 CCAATCTTGTGTAACCTCTGGAAGTATGCTGTTTAAATAATTTGGAATCTGAAGAT 240
QY 241 GAATCTGTGATCATACATTTTAAATGAGCTGGAAGAAACCCAAATGGAGTGTCTGAT 300
Db 241 GAATCTGTGATCATACATTTTAAATGAGCTGGAAGAAACCCAAATGGAGTGTCTGAT 300
QY 301 GGAGTGTATCAAAAGCGTATATGGCAAAACACTTCAAGCTCTTAAATTTCTGTCTATATACAT 360
Db 301 GGAGTGTATCAAAAGCGTATATGGCAAAACACTTCAAGCTCTTAAATTTCTGTCTATATACAT 360
QY 361 AACTGTATTTCACAGAGATATAAACTGGAATATTTCTGATTTCCAGAGAGATGCTCTACACGATTAT 420
Db 361 AACTGTATTTCACAGAGATATAAACTGGAATATTTCTGATTTCCAGAGAGATGCTCTACACGATTAT 420
QY 421 AAGATTGTGCTTGGGTTTGCACAAATTTCTGATTTCCAGAGAGATGCTCTACACGATTAT 456
Db 421 AAGATTGTGCTTGGGTTTGCACAAATTTCTGATTTCCAGAGAGATGCTCTACACGATTAT 456

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RESULT 11

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US-10-766-691-7
; Sequence 7, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR FILING DATE: 2000-09-27
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-7

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Query Match 43.7%; Score 454.4; DB 19; Length 594;
Best Local Similarity 99.8%; Pred. No. 3.7e-110;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGCAAAAGTATGAAAAATTTAGTAAAGCTGGAGAGAGGCTTTATGGGGTGTGTTTCAA 60
Db 1 ATGCAAAAGTATGAAAAATTTAGTAAAGCTGGAGAGAGGCTTTATGGGGTGTGTTTCAA 60
QY 61 TGCAGAAACAAACCTCTGGACAGTATGCTGTTTAAATAATTTGGAATCTGAAGAT 120
Db 61 TGCAGAAACAAACCTCTGGACAGTATGCTGTTTAAATAATTTGGAATCTGAAGAT 120
QY 121 GATCCTGTGTTTAAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACAT 180
Db 121 GATCCTGTGTTTAAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACAT 180
QY 181 CCAATCTTGTGTAACCTCTGGAAGTATGCTGTTTAAATAATTTGGAATCTGAAGAT 240
Db 181 CCAATCTTGTGTAACCTCTGGAAGTATGCTGTTTAAATAATTTGGAATCTGAAGAT 240
QY 241 GAATCTGTGATCATACATTTTAAATGAGCTGGAAGAAACCCAAATGGAGTGTCTGAT 300
Db 241 GAATCTGTGATCATACATTTTAAATGAGCTGGAAGAAACCCAAATGGAGTGTCTGAT 300
QY 301 GGAGTGTATCAAAAGCGTATATGGCAAAACACTTCAAGCTCTTAAATTTCTGTCTATATACAT 360

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Db 301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAGCTCTTAATTTCTGTCTATACAT 360
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATAATC 420
Db 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATAATC 420
Qy 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATT 456
Db 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATT 456

RESULT 12

US-09-960-706-1079
; Sequence 1079, Application US/09960706
; Publication No. US20030134280A1
; GENERAL INFORMATION:
; APPLICANT: Mungler, William E.
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960,706
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 09/873,319
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1079
; LENGTH: 1363
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 X66358
US-09-960-706-1079

Query Match 33.0%; Score 343.8; DB 10; Length 1363;
Best Local Similarity 71.2%; Pred. No. 1.4e-80;
Matches 469; Conservative 0; Mismatches 187; Indels 3; Gaps 1;
Qy 1 ATCGAAAGTATGAAATAGCTAGCTAGCTGAGAGGGTCTTATGGGTTGTTATTCAAA 60
Db 217 ATGGAGAGTATGAAATATGGGAAATTTGGGAAAGGATCCTATGAGTTGTTTCAA 276
Qy 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTTAAATAATTTGGGAATCTGAAGAT 120
Db 277 TGTAGAAACAGGNCACGGTCAAGTTGTGCCATCAAGAAGTTTCTGGATCAGAGAT 336
Qy 121 GATCCTGTTCTTAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAAT 180
Db 337 GACCTGTCTATAAGAAATTTGCCCTTCGGGAATCCGAATGCTCAAGCAACTCAAGCAT 396
Qy 181 CCAATCTGTGAACCTCATCGAGTGTTCAGGAGAAAGGAAATATGCAATTTAGTTTTT 240
Db 397 CCCAACCTTGTAACTCTCTGGAAGTCTTCAGGAGAAACGGAGGCTTCACCTGGTGT 456
Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAACCCAAATGAGTTGCTGAT 300
Db 457 GAATTTGTGACCAACAGTTCTCCATGAGTTGAGAGATACCAAGAGGGGTACCGAA 516
Qy 301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAGCTCTTAATTTCTGTCTATACAT 360
Db 517 CATCTCGTGAAGAGCATAACTTGGCAGACACTGCAAGCTGTAAATTTTTCCTATAAACAC 576
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATAATC 420
Db 577 AATTGTCATACATAGAGACGTGAAGCCAGAAATATCTCTATCAGAAACATTTCCGTGATT 636
Qy 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATT---CCAGAGATGCTTACACCGAT 477
Db 637 AAGCTTTGTGACTTTGGATTTCGCGCTTTTGACTGGACCGAGTACTACTATACAGAC 696

Qy 478 TATGTAGCTACGAGATGGTACCGAGCTCCTGAACCTTCTTCTGGGAGATACCTCAGTATGGT 537
Db 697 TACGTGGCTACCGAGTGGTATCCGCTCCCTCTGCTGGTGGGGACACGCGAGTACGGC 756
Qy 538 TCTTCAGTGCATATATGGGGCTATTGGTTGTGTTTTTGCAGAGCTCCTGACAGGCCAGCCA 597
Db 757 CCCCCTGGTGTGTTGGGCAATTTGGCTGTGTCTTTGCTGAGCTGTCTGTCTCAGGAGTGCCT 816
Qy 598 CTGTGCGCTGGAAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAAACACTAGTAGA 656
Db 817 CTGTGGCCAGAAAAATCGGATGTGGATCAGCTGTATCTGATTAGGAAGACCTTGGGGGA 875

RESULT 13

US-10-363-616-146
; Sequence 146, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 146
; LENGTH: 1612
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (463)..(1539)
US-10-363-616-146

Query Match 33.0%; Score 343.8; DB 17; Length 1612;
Best Local Similarity 71.2%; Pred. No. 1.5e-80;
Matches 469; Conservative 0; Mismatches 187; Indels 3; Gaps 1;
Qy 1 ATCGAAAGTATGAAATATAGCTAGCTGAGAGGGTCTTATGGGTTGTTATTCAAA 60
Db 466 ATGGAGAGTATGAAATATGGGAAATTTGGGAGAGGATCCTATGAGTTGTTTCAA 525
Qy 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTTAAATAATTTGGGAATCTGAAGAT 120
Db 526 TGTAGAAACAGGACACGGGTCAAGTTGTGCCATCAAGAAGTTTCTGGAAATCAGAAGAT 585
Qy 121 GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTATGTTGAGCAATTAACAAT 180
Db 586 GACCTGTCTATAAGAAATTTGCCCTTCGGGAATCCGAATGCTCAAGCAACTCAAGCAT 645
Qy 181 CCAATCTGTGAACCTCATCGAGTGTTCAGGAGAAAGGAAATATGCAATTTAGTTTTT 240
Db 646 CCCAACCTTGTAACTCTCTGGAAGTCTTCAGAGGAAACGGAGGCTTCACCTGGTGT 705
Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 300
Db 706 GAATTTGTGACCAACAGTTCTCCATGAGTTGGACAGATACCAAGAGGGGTACAGAA 765
Qy 301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAGCTCTTAATTTCTGTCTATACAT 360
Db 766 CATCTCGTGAAGAGCATAACTTGGCAGACACTCGAAGCTGTAAATTTTTCCTATAAACAC 825
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATAATC 420
Db 826 AATTGCATACATAGAGACGTGAAGCCAGAAATATCTCTATCAGAAACATTTCCGTGATT 885
Qy 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATT---CCAGAGATGCTTACACCGAT 477
Db 886 AAGCTTTGTGACTTTGGATTTCGCGCTTTTGACTGGACCGAGTACTACTATACAGAC 945
Qy 478 TATGTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACCTCAGTATGGT 537

Db 946 TAGTGGCTACCAAGTGGTACCGCTCCCTGAGCTGCTGGGGGACACGAGTACGGC 1005
 QY 538 TCTTCAGTCGATATATGGCTATTTGGTTGGTTTGGAGAGCTCTGACAGCCAGCCA 597
 Db 1006 CCCCCTGGTGGATGTTGGGCAATGGCTGTGCTTTGGTGGAGCTGCTGACAGGTGCT 1065
 QY 598 CTGTGGCTTGGAAATCAGATGGACCAACTTTATCTGATATCAGAACTAGTAGA 656
 Db 1066 CTGTGGCCAGGAAATCGATGCTGATCAGCTGATCTGATTTAGGAAGACCTTGGGGA 1124

RESULT 14
 US-10-357-930-24573
 ; Sequence 24573, Application US/10357930
 ; Publication No. US20040259086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Endege, Wilson
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 ; TITLE OF INVENTION: HUMAN PROSTATE CANCER
 ; FILE REFERENCE: MRI-007BCN
 ; CURRENT APPLICATION NUMBER: US/10/357,930
 ; CURRENT FILING DATE: 2003-02-04
 ; PRIOR APPLICATION NUMBER: 09/785,276
 ; PRIOR FILING DATE: 2003-02-16
 ; PRIOR APPLICATION NUMBER: 60/183,319
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 60/189,862
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/207,454
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/211,314
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: 60/219,007
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 60/255,281
 ; PRIOR FILING DATE: 2000-12-13
 ; NUMBER OF SEQ ID NOS: 62232
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 24573
 ; LENGTH: 2944
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 1, 2, 3, 2940, 2941, 2942, 2943, 2944
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-357-930-24573

Query Match 33.0%; Score 343.8; DB 18; Length 2944;
 Best Local Similarity 71.2%; Pred. No. 2.1e-80;
 Matches 469; Conservative 0; Mismatches 187; Indels 3; Gaps 1;
 QY 1 ATGCAAAAGTATCAAAAATAGCTAGACTGCGAGAGGCTCTATGGGTTGTTATTCAAA 60
 Db 829 ATGCAAGATGATGAAAAATTTGGAAAAATGGAGAAATGCGAGAGGATCTATGGAGTTGTTTCAA 888
 QY 61 TGCAGAAACAAACCTCTCGCAAGTAGTAGCTGTTTAAAAAATTTGTGGAATCTGAAGAT 120
 Db 889 TGTAGAAACAGGACACGGTCTAGATGTGGCCATCAGAGATTTCTGGAATCAGAGAT 948
 QY 121 GATCCTGTTTAAAGAAATAGCACTAAGAAATACTGATTTGAAGCAATTAAGACAT 180
 Db 949 GACCTGTCTAAGAAAAATTTGCCCTTCGGGAAATCCGAATCTCAAGCACTCAAGCAT 1008
 QY 181 CCAAAATCTGTGAACCTCATCAGGTTTTCAGGAGAAAGGAAATGCAATTTAGTTTTT 240
 Db 1009 CCAACCTTGTAACTCTCGAGTCTTCAGAGAAACGAGGCTTCACCTGGTGT 1068
 QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300

Db 1069 GAATATTGTGACACACAGTTCTCCATGAGTTGGACAGATACCAAGAGGGGTACCAGAA 1128
 QY 301 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
 Db 1129 CATCTCGTGAAGACATTAACCTGGACACACTGCAAGCTGTAAATTTTGGCCATAAACAC 1188
 QY 361 AACTGTATTACAGAGATATAAAACCTGAAAAATTTCTAATAACTAAGCAAGGAATAATC 420
 Db 1189 AATTGCATACATAGAGACGTGAAGCCAGAAAAATATCTCATCAGAAACATTCGGTGATT 1248
 QY 421 AAGATTGTGACTTCGGTTTGCACAAATTTCTGATT---CCAGGAGATGCTTACACCGAT 477
 Db 1249 AAGCTTTGTGACTTTGGATTGTCTCGGCTTTTGCATGGACCGAGTACTACTATACAGAC 1308
 QY 478 TATGTAGCTACGAGATGGTACCGAGCTCTCGAACTTCTTGTGGGAGATACCTCAGTATGGT 537
 Db 1309 TACGTGGCTACCAAGTGGTACCGCTCCCTGAGCTGCTGGTGGGGACACGCAAGTACGGC 1368
 QY 538 TCTTCAGTCGATATATGGGCTATTTGGTTGTTTTTGCAGAGCTCTCGACAGCCAGCCA 597
 Db 1369 CCCCCTGGTGGATGTTTGGGCAATTTGGCTGTGCTTGTCTGAGCTGCTGTCAGGAGTGCCT 1428
 QY 598 CTGTGGCTTGGAAATCAGATGGACCAACTTTATCTGATATCAGAACTAGTAGA 656
 Db 1429 CTGTGGCCAGGAAATCGGATGGATCAGCTGATCTGATTAGGAAGACCTTTGGGGGA 1487

RESULT 15
 US-10-174-794-5
 ; Sequence 5, Application US/10174794
 ; Publication No. US20030166220A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Southern California
 ; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
 ; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
 ; FILE REFERENCE: 13761-707
 ; CURRENT APPLICATION NUMBER: US/10/174,794
 ; CURRENT FILING DATE: 2002-06-18
 ; PRIOR APPLICATION NUMBER: US/09/411,628
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: US 60/102,906
 ; PRIOR FILING DATE: 1998-10-02
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 1701
 ; TYPE: DNA
 ; ORGANISM: Orcyctolagus cuniculus
 US-10-174-794-5

Query Match 24.2%; Score 251.8; DB 16; Length 1701;
 Best Local Similarity 62.9%; Pred. No. 4.4e-56;
 Matches 407; Conservative 0; Mismatches 237; Indels 3; Gaps 1;
 QY 1 ATGAAAAAGTATGAAAAATTAGCTAAGACTGGAAGAGGCTCTATGGGTTGTTATTCAAA 60
 Db 1 ATGAAAAAATATGAAACCTTTGGATTGTTGAGAGAGGAGCTTATGGAATGCTGATGAAG 60
 QY 61 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTGTTTAAAAAATTTGTGGAATCTGAAGAT 120
 Db 61 TGTAGGAATAAAGATAGTGGGAAGAAATTTGGCCATCAAGAAAGTTCTTAGAAGTGAATGAT 120
 QY 121 GATCCTGTTTAAAGAAAAATAGCACTAAGAAAAATACGTATGTTGGAACCAATTAAGACAT 180
 Db 121 GACAAATGGTTTAAAAAATGCTATCGGAAATCAAGTTACTAAGACCACTGAGGCAT 180
 QY 181 CCAAACTTGTGAACCTCATCGAGGTGTTCAAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
 Db 181 GAAAAATTTGGTGAATCTGTTGGAGGTGTGTAAAAAAGAAAAAAGCAATGCTACCTAGTCTTT 240
 QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300
 Db 241 GAATTTGTTGACCAACAGATCTTTGATGACTTGGAACTCTTTCCAAATGAGTAGATGAC 300

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OM nucleic - nucleic search, using sw model

Run on: April 21, 2005, 20:27:40 ; Search time 197.088 Seconds
(without alignments)
8642.674 Million cell updates/sec

Title: US-10-766-691-9
Perfect score: 1041
Sequence: 1 atggaaagtatgaaaatt.....aggtacttcgctcaaaagt 1041

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1025	98.5	1068	4	US-09-671-050-3
3	839	80.6	945	4	US-09-671-050-11
4	823	79.1	972	4	US-09-671-050-5
5	709	68.1	1819	4	US-09-671-050-13
6	454.4	43.7	561	4	US-09-671-050-1
7	454.4	43.7	594	4	US-09-671-050-7
8	343.8	33.0	1177	4	US-09-949-016-1681
9	251.8	24.2	1701	3	US-09-411-628-5
10	251.8	24.2	1701	4	US-10-174-794-5
11	251.8	24.2	3080	3	US-09-411-628-3
12	251.8	24.2	3080	4	US-10-174-794-3
13	241.2	23.2	1794	4	US-09-949-016-2083
14	163.8	15.7	903	2	US-08-874-347-9
15	163.8	15.7	903	3	US-09-093-522-9
16	162	15.6	1476	6	US-09-969-106-1
17	162	15.6	1476	4	US-09-338-125-1
18	162	15.6	1476	4	US-09-266-225D-13
19	162	15.6	1635	4	US-09-417-197-112
20	162	15.6	1635	4	US-09-417-197-114
21	160.4	15.4	1296	4	US-09-949-016-2154
22	160.4	15.4	2213	4	US-09-023-655-1037
23	154.2	14.8	1050	4	US-09-220-132-3
24	154.2	14.8	1825	4	US-09-949-039-115
25	151	14.5	1042	4	US-09-949-016-4802
26	145.8	14.0	3823	4	US-09-949-016-4276
27	134.8	12.9	1158	4	US-09-949-016-4906

28	134.8	12.9	1161	4	US-09-023-655-1373	Sequence 1373, Ap
29	134.8	12.9	1161	4	US-09-949-016-181	Sequence 181, App
30	134.8	12.9	1825	4	US-09-620-312B-313	Sequence 313, App
31	133.2	12.8	987	4	US-09-949-016-5854	Sequence 5854, Ap
32	133.2	12.8	1089	1	US-08-154-915-1	Sequence 1, Appli
33	133.2	12.8	1089	2	US-08-464-517-37	Sequence 37, Appl
34	133.2	12.8	1089	2	US-08-246-361A-37	Sequence 37, Appl
35	133.2	12.8	1089	3	US-08-463-772-37	Sequence 37, Appl
36	133.2	12.8	1089	5	PCT-US93-09945-1	Sequence 1, Appli
37	128	12.3	993	4	US-09-248-796A-4323	Sequence 4323, Ap
38	128	12.3	1002	1	US-08-463-090B-3	Sequence 3, Appli
39	119.2	11.5	1044	4	US-09-248-796A-4325	Sequence 4325, Ap
40	116	11.1	1070	1	US-08-463-090B-5	Sequence 5, Appli
41	113.2	10.9	69909	4	US-09-949-016-13423	Sequence 13423, A
42	112	10.8	1308	4	US-09-801-861-4	Sequence 4, Appli
43	112	10.8	1308	4	US-10-224-562-4	Sequence 4, Appli
44	112	10.8	2203	4	US-09-801-861-1	Sequence 1, Appli
45	112	10.8	2203	4	US-10-224-562-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-671-050-9

; Sequence 9, Application US/09671050

; Patent No. 6716616

; GENERAL INFORMATION:

; APPLICANT: Donoho, Gregory

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Nehls, Michael

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and

; FILE REFERENCE: Polynucleotides Encoding the Same

; CURRENT APPLICATION NUMBER: US/09/671,050

; PRIOR FILING DATE: 2001-06-11

; PRIOR APPLICATION NUMBER: US 60/156,511

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 1041

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-671-050-9

Query Match 100.0%; Score 1041; DB 4; Length 1041;

Best Local Similarity 100.0%; Pred. No. 1.7e-285;

Matches 1041; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAAAGTATGAAAAATAGCTAGACCTGGAGAGGGTCTTATGGGTTGTTATTCAAA 60

Db 1 ATGAAAAGTATGAAAAATAGCTAGACCTGGAGAGGGTCTTATGGGTTGTTATTCAAA 60

Qy 61 TCAGAAACAAAACCTCTGACAAAGTAGTAGCTTTAAAAAATTTGTGGAATCTGAAGAT 120

Db 61 TCAGAAACAAAACCTCTGACAAAGTAGTAGCTTTAAAAAATTTGTGGAATCTGAAGAT 120

Qy 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAAGCAATTAACAT 180

Db 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAAGCAATTAACAT 180

Qy 181 CCAAACTTTGTAACCTCATCGAGGTGTTTCAGAGAAAAAGAAAAATGCAATTTAGTTTT 240

Db 181 CCAAACTTTGTAACCTCATCGAGGTGTTTCAGAGAAAAAGAAAAATGCAATTTAGTTTT 240

Qy 241 GAATACCTGTCATACACATTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 300

Db 241 GAATACCTGTCATACACATTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 300

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Qy 301 GGAGTGATCAAAACGGTATTATGTCACAAACACTTCAAGCTCTTAATTTCTGTCAATATACAT 360
Db 301 GGAGTGATCAAAACGGTATTATGTCACAAACACTTCAAGCTCTTAATTTCTGTCAATATACAT 360
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATCTTAATTAACCTAAGCAAGGAATATC 420
Db 361 AACTGTATTACAGAGATATAAAACCTGAAATATCTTAATTAACCTAAGCAAGGAATATC 420
Qy 421 AAGATTGTGACTTCGGGTTTGCAAAATCTGATTCAGAGATGCTTACACCGATTAT 480
Db 421 AAGATTGTGACTTCGGGTTTGCAAAATCTGATTCAGAGATGCTTACACCGATTAT 480
Qy 481 GTAGTACGAGATGGTACCGAGCTCTGAACTCTTCTGTGGAGATACCTCAGTATGTTCT 540
Db 481 GTAGTACGAGATGGTACCGAGCTCTGAACTCTTCTGTGGAGATACCTCAGTATGTTCT 540
Qy 541 TCAGTCCATATATGGGCTATTGTTGTTTTCAGAGCTCTTCAGAGCCAGCCACTG 600
Db 541 TCAGTCCATATATGGGCTATTGTTGTTTTCAGAGCTCTTCAGAGCCAGCCACTG 600
Qy 601 TGGCTCGAAATCAGATGTGGACCAACTTATCTGATATCAGAACACTAGTAGAGACG 660
Db 601 TGGCTCGAAATCAGATGTGGACCAACTTATCTGATATCAGAACACTAGTAGAGACG 660
Qy 661 GGGTTTCGCCATGTGACAGGCTGGTCTCGAACTCTTGACGTCAAGTGATCCACCTGCC 720
Db 661 GGGTTTCGCCATGTGACAGGCTGGTCTCGAACTCTTGACGTCAAGTGATCCACCTGCC 720
Qy 721 GTAGCCTCTCAAGTGTGGAATTTACAGGAATTAATCCAGACATCAATCAATCTTT 780
Db 721 GTAGCCTCTCAAGTGTGGAATTTACAGGAATTAATCCAGACATCAATCAATCTTT 780
Qy 781 AAAAGTAACGGGTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAACCTCTT 840
Db 781 AAAAGTAACGGGTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAACCTCTT 840
Qy 841 GAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTCTGAAAGGGGTGTCTGAAG 900
Db 841 GAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTCTGAAAGGGGTGTCTGAAG 900
Qy 901 ATGATCCAGATGACAGATTAACCTGTTCGCACTCTGAGAGCTCTTACTTTGATTCT 960
Db 901 ATGATCCAGATGACAGATTAACCTGTTCGCACTCTGAGAGCTCTTACTTTGATTCT 960
Qy 961 TTTCAAGAGCCCAAATTAAGAAAGACAGCTAAATGAAGGAAAGACAGAGACGCCAA 1020
Db 961 TTTCAAGAGCCCAAATTAAGAAAGACAGCTAAATGAAGGAAAGACAGAGACGCCAA 1020
Qy 1021 CAGGTACTTCCGCTCAAAAGT 1041
Db 1021 CAGGTACTTCCGCTCAAAAGT 1041

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RESULT 2

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US-09-671-050-3
; Sequence 3, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT FILING DATE: 2001-06-11
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 3
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-671-050-3

Query Match      98.5%; Score 1025; DB 4; Length 1068;
Best Local Similarity 100.0%; Pred. No. 5.9e-281;
Matches 1025; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAAGAATGATGAAAAATAGCTAGACCTGGAGAGGGCTTTATGGGGTGTGATTCAAA 60
Db 1 ATGGAAGAATGATGAAAAATAGCTAGACCTGGAGAGGGCTTTATGGGGTGTGATTCAAA 60
Qy 61 TGCAGAAAAACCAACCTCTGCACCAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
Db 61 TGCAGAAAAACCAACCTCTGCACCAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
Qy 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAATAACAT 180
Db 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAATAACAT 180
Qy 181 CCAATCTTGTGAACCTCATCGAGGTGTTTCAGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
Db 181 CCAATCTTGTGAACCTCATCGAGGTGTTTCAGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGCGATGCTGTGAT 300
Db 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGCGATGCTGTGAT 300
Qy 301 GGAGTGATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAATTTCTGTCAATATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAATTTCTGTCAATATACAT 360
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAAAATTTCTTAATACTAAGCAAGGAATATC 420
Db 361 AACTGTATTACAGAGATATAAAACCTGAAAAATTTCTTAATACTAAGCAAGGAATATC 420
Qy 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATTCAGAGATGCTTACACCGATTAT 480
Db 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATTCAGAGATGCTTACACCGATTAT 480
Qy 481 GTAGTACGAGATGTAACCGAGCTCTGAACTCTTGTGGGAGATACCTCAGTATGTTCT 540
Db 481 GTAGTACGAGATGTAACCGAGCTCTGAACTCTTGTGGGAGATACCTCAGTATGTTCT 540
Qy 541 TCAGTCCATATATGGGCTATTGTTGTTTTCAGAGCTCTTCAGAGCCAGCCACTG 600
Db 541 TCAGTCCATATATGGGCTATTGTTGTTTTCAGAGCTCTTCAGAGCCAGCCACTG 600
Qy 601 TGGCCTCGAAAAATCAGATGTGGACCAACTTATCTGATATCAGAACACTAGTAGAGACG 660
Db 601 TGGCCTCGAAAAATCAGATGTGGACCAACTTATCTGATATCAGAACACTAGTAGAGACG 660
Qy 661 GGGTTTCGCCATGTTCAGCCAGGCTGGTCTCGAACTCTTGTGAGCTCAAGTGTACCACTGCC 720
Db 661 GGGTTTCGCCATGTTCAGCCAGGCTGGTCTCGAACTCTTGTGAGCTCAAGTGTACCACTGCC 720
Qy 721 GTAGCCTCTCAAAAGTGTGGAATTTACAGGAATTAATCCAGACATCAATCAATCTTT 780
Db 721 GTAGCCTCTCAAAAGTGTGGAATTTACAGGAATTAATCCAGACATCAATCAATCTTT 780
Qy 781 AAAAGTAACGGGTTTTTTCATGGCATCAGTATACCTGAGCCAGAGACATGGAACCTCTT 840
Db 781 AAAAGTAACGGGTTTTTTCATGGCATCAGTATACCTGAGCCAGAGACATGGAACCTCTT 840
Qy 841 GAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTCTGAAAGGGGTGTCTGAAG 900
Db 841 GAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTCTGAAAGGGGTGTCTGAAG 900
Qy 901 ATGAATCCAGATGACAGATTAACCTGTTCGCACTCTGAGAGCTCTTACTTTGATTCT 960
Db 901 ATGAATCCAGATGACAGATTAACCTGTTCGCACTCTGAGAGCTCTTACTTTGATTCT 960

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Qy 961 TTTTCAAGAGGCCCAAAATTTAAAGAAAAAGCACGTTAATGAAGAGAAACAGAGACGCCAA 1020
Db 961 TTTTCAAGAGGCCCAAAATTTAAAGAAAAAGCACGTTAATGAAGAGAAACAGAGACGCCAA 1020

Qy 1021 CAGGT 1025
Db 1021 CAGGT 1025

RESULT 3
US-09-671-050-11
; Sequence 11, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur I.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671,050
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 945
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-671-050-11

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Query Match	80.6%;	Score 839;	DB 4;	Length 945;
Best Local Similarity	90.8%;	Pred. No. 3.5e-228;		
Matches 945;	Conservative 0;	Mismatches 0;	Indels 96;	Gaps 1;
Qy	1	ATGGAAGAAGTATGAAAAATTAGCTTAAGACTCGAGAGGGTCTTATGGGGTTGTATTCAA	60	
Db	1	ATGGAAGAAGTATGAAAAATTAGCTTAAGACTCGAGAGGGTCTTATGGGGTTGTATTCAA	60	
Qy	61	TGCAGAACCAAAACCTCTGGCAACAAGTAGTAGCTGTAAAAAATTTGTGGAATCTGAAGAT	120	
Db	61	TGCAGAACCAAAACCTCTGGCAACAAGTAGTAGCTGTAAAAAATTTGTGGAATCTGAAGAT	120	
Qy	121	GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTTAAAAACAT	180	
Db	121	GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTTAAAAACAT	180	
Qy	181	CCAAATCTTGCGAACCTCATCGAGGTGTTCAGGAGAAAAAGGAAAAATGCATTAGTTT	240	
Db	181	CCAAATCTTGCGAACCTCATCGAGGTGTTCAGGAGAAAAAGGAAAAATGCATTAGTTT	240	
Qy	241	GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAAAAACCACCAATGGAAGTTGCTGAT	300	
Db	241	GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAAAAACCACCAATGGAAGTTGCTGAT	300	
Qy	301	GGAGTGATCAAAAGCGTATTATGCAACAACATTCAAGCTCTTAATTTCTGTCAATACAT	360	
Db	301	GGAGTGATCAAAAGCGTATTATGCAACAACATTCAAGCTCTTAATTTCTGTCAATACAT	360	
Qy	361	AACGTGATTCACAGAGATATAAAACCTGAAAAATATTCTAAATACTNAGCAGGAATAATC	420	
Db	361	AACGTGATTCACAGAGATATAAAACCTGAAAAATATTCTAAATACTNAGCAGGAATAATC	420	
Qy	421	AAGATTTTGTGACTTCGGGTTTGGCAAAATCTCGATTTCCAGAGAGATGCCCTACACCGATTAT	480	
Db	421	AAGATTTTGTGACTTCGGGTTTGGCAAAATCTCGATTTCCAGAGAGATGCCCTACACCGATTAT	480	
Qy	481	GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACCTCAGTATGGTTCT	540	

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481 Db GTAGCTACGAGATGGTACCAGGCTCCTGAACTCTTGTGGGAGATACTCAGTATGGTTCT 540
541 QY TCAGTCGATATATGGGCTATTGGTTGTGTTTTTGCAGAGCTCCTGCACAGGCCAGCCACTG 600
541 Db TCAGTCGATATATGGGCTATTGGTTGTGTTTTTGCAGAGCTCCTGCACAGGCCAGCCACTG 600
601 QY TGGCCTGGAAAAATCAGATGTGGACCAACTTTTATCTGATTAATTCAGAACACTAGTAGAGACG 660
601 Db TGGCCTGGAAAAATCAGATGTGGACCAACTTTTATCTGATTAATTCAGAACACTAGTAGAGACG 660
661 QY GGGTTTCGCCCATGTGTGACACAGGCTGCTCGAACTCTTGAAGTCAAGTGATCCACCTGCC 720
661 Db ----- 650
721 QY GTAGCCTCTCAAAGTGTCTGGAATTACAGGAAAAATTAATCCCAAGACATCAATCAATCTTT 780
721 Db -----AGGAAAAATTAATCCCAAGACATCAATCAATCTTT 680
781 QY AAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAAAACTCTT 840
781 Db AAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAAAACTCTT 740
841 QY GAGGAAAAAGTCTCAGATGTTCATCTCTGGCTCTGAACTTCATGAAGGGGTGCTGAAG 900
841 Db GAGGAAAAAGTCTCAGATGTTCATCTCTGGCTCTGAACTTCATGAAGGGGTGCTGAAG 800
901 QY ATGAATCCAGATGACAGATTAACTGTGTTCCCAACTCTCTGGAGAGCTCCTACTTTGATTCT 960
901 Db ATGAATCCAGATGACAGATTAACTGTGTTCCCAACTCTCTGGAGAGCTCCTACTTTGATTCT 860
961 QY TTTCAAGAGAGCCCAAATTTAAAGAAAAAGCAGTGTAATGAAGGAAAGAAAACAGAAAGCGCAA 1020
961 Db TTTCAAGAGAGCCCAAATTTAAAGAAAAAGCAGTGTAATGAAGGAAAGAAACAGAAAGCGCAA 920
1021 QY CAGGTACTTCCGCTCAAAAGT 1041
1021 Db CAGGTACTTCCGCTCAAAAGT 945

RESULT 4
US-09-671-050-5
; Sequence 5, Application US/09671050
; Patent No. 671616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 671616el Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671,050
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 972
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-671-050-5

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Query Match	79.1%	Score 823;	DB 4;	Length 972;
Best Local Similarity	90.6%;	Pred. No. 1.2e-233;		
Matches 929;	Conservative	0;	Mismatches 0;	Indels 96; Gaps 1

Qy	1	ATGGAAGAAGTATGAAAAATTAGCTTAAGCATGGAAGGGCTTTATGGGGTTGTATTCAAA	60
Db	1	ATGGAAGAAGTATGAAAAATTAGCTTAAGCATGGAAGGGCTTTATGGGGTTGTATTCAAA	60


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QY 61 TGCAGAAACAAACCTCTCGACAGTAGTAGCTGTATAAAATTTGTGGAATCTGAAGAT 120
Db 61 TGCAGAAACAAACCTCTCGACAGTAGTAGCTGTATAAAATTTGTGGAATCTGAAGAT 120
QY 121 GATCCTGTTGTTAAGAAATAGCCTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
Db 121 GATCCTGTTGTTAAGAAATAGCCTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
QY 181 CCAATCTTGTCGAACCTCATCGAGGTGTCAGGAGAAAGAAATGCAATTTAGTTTTT 240
Db 181 CCAATCTTGTCGAACCTCATCGAGGTGTCAGGAGAAAGAAATGCAATTTAGTTTTT 240
QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGCAATTTAGTTTTT 300
Db 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGCAATTTAGTTTTT 300
QY 301 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
QY 361 AACTGTATTCACAGATATAAAACCTGAAATATTTCTAATTAAGCAAGCAATTAATC 420
Db 361 AACTGTATTCACAGATATAAAACCTGAAATATTTCTAATTAAGCAAGCAATTAATC 420
QY 421 AAGATTTGTCACCTCGGTTTGCACAAATTTCTGATTCAGGAGATGCCCTACACCATAT 480
Db 421 AAGATTTGTCACCTCGGTTTGCACAAATTTCTGATTCAGGAGATGCCCTACACCATAT 480
QY 481 GTAGTACGAGATGGTACCGAGCTCTGAACTTTCTGTTGGGAGATCACTAGTGGTCT 540
Db 481 GTAGTACGAGATGGTACCGAGCTCTGAACTTTCTGTTGGGAGATCACTAGTGGTCT 540
QY 541 TCAGTGCATATATGGCTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 600
Db 541 TCAGTGCATATATGGCTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 600
QY 601 TGCCCTGGAATATCAGATGTGACCAACTTTATCTGATTAATCAGAACACTAGTAGAGAG 660
Db 601 TGCCCTGGAATATCAGATGTGACCAACTTTATCTGATTAATCAGAACACTAGTAGAGAG 660
QY 661 GGGTTTCGCCATGTTGACAGAGCTGGTCTCGAACTCTTGACGTCAAGTGATCCACCTGCC 720
Db 661 GGGTTTCGCCATGTTGACAGAGCTGGTCTCGAACTCTTGACGTCAAGTGATCCACCTGCC 720
QY 721 GTAGCCTCTCAAAGTGTGGAATTACAGGAAATTAATCCCAAGACATCAATCAATCTTT 780
Db 721 GTAGCCTCTCAAAGTGTGGAATTACAGGAAATTAATCCCAAGACATCAATCAATCTTT 780
QY 781 AAAAGTAACGGGTTTTTCATGGCATCAGTATACCTGAGCCAGAGACATGGAACCTCTT 840
Db 781 AAAAGTAACGGGTTTTTCATGGCATCAGTATACCTGAGCCAGAGACATGGAACCTCTT 840
QY 841 GAGGAAAGTTCTCAGATGTTCACTCTGCTGCTGAACTTCAATGAAGGGGTGCTGGAAG 900
Db 841 GAGGAAAGTTCTCAGATGTTCACTCTGCTGCTGAACTTCAATGAAGGGGTGCTGGAAG 900
QY 901 ATGAATCCAGATGACAGATTAACCTGTTCCCAACTCTCGAGAGCTCTACTTTGATCT 960
Db 901 ATGAATCCAGATGACAGATTAACCTGTTCCCAACTCTCGAGAGCTCTACTTTGATCT 960
QY 961 TTTCAAGAGGCCCAATTAAGAAAGCAAGCAAGCTTAATGAAGGAGAAACAGAGAGCCAA 1020
Db 961 TTTCAAGAGGCCCAATTAAGAAAGCAAGCAAGCTTAATGAAGGAGAAACAGAGAGCCAA 1020
QY 1021 CAGGT 1025
Db 925 CAGGT 929

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RESULT 5
US-09-671-050-13
Sequence 13, Application US/09671050

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; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671.050
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1819
; TYPE: DNA
; ORGANISM: homo sapiens
; US-09-671-050-13

Query Match
Best Local Similarity 68.1%; Score 709; DB 4; Length 1819;
Matches 1025; Conservative 0; Mismatches 0; Indels 306; Gaps 1;

QY 1 ATGGAAGATGATGAAATTTAGCTAAGACTGGAGAGGGTCTTATGGGGTGTATTCAAA 60
Db 138 ATGGAAGATGATGAAATTTAGCTAAGACTGGAGAGGGTCTTATGGGGTGTATTCAAA 197
QY 61 TGCAGAAACAAACCTCTCGACAGTAGTAGCTGTATAAAATTTGTGGAATCTGAAGAT 120
Db 198 TGCAGAAACAAACCTCTCGACAGTAGTAGCTGTATAAAATTTGTGGAATCTGAAGAT 257
QY 121 GATCCTGTTGTTAAGAAATAGCCTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
Db 258 GATCCTGTTGTTAAGAAATAGCCTAAGAGAAATACGTATGTTGAAGCAATTAACAT 317
QY 181 CCAATCTTGTCGAACCTCATCGAGGTGTTCAAGAGAAAGAAAGCAATTTAGTTTTT 240
Db 318 CCAATCTTGTCGAACCTCATCGAGGTGTTCAAGAGAAAGAAAGCAATTTAGTTTTT 377
QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 300
Db 378 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 437
QY 301 GGAGTGATCAAAAGCGTATTATGGAACACCTTCAAGCTCTTAATTTCTGTCATATACAT 360
Db 438 GGAGTGATCAAAAGCGTATTATGGAACACCTTCAAGCTCTTAATTTCTGTCATATACAT 497
QY 361 AACTGTATTCACAGATATAAAACCTGGAATAATTTCTAATACTAAGCAAGGAATAATC 420
Db 498 AACTGTATTCACAGATATAAAACCTGGAATAATTTCTAATACTAAGCAAGGAATAATC 557
QY 421 AAGATTTGTCACCTCGGTTTGCACAAATTTCTG----- 453
Db 558 AAGATTTGTCACCTCGGTTTGCACAAATTTCTGAGTTGAGCTTCATCTTCTGCTGCTGCC 617
QY 454 ----- 453
Db 618 TCCTTGATTTGGCTTAATAGTTGACCTTTCTGAATTTCTTTCTGCCAATTCAGAGATTTTT 677
QY 454 ----- 453
Db 678 CTCTCGCTTGGATCCATTTGCTGACACAGTGTTCACCATGGGGGCCAGGCTCATCTCGA 737
QY 454 ----- 453
Db 738 ACTTCTGGCTCAAGTGTATCTTCCACCTCGGCCCTCCCAAGTGTGATTCAGTGTG 797
QY 454 ----- 453

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Db 798 AGCCACCGTGCCAGCCAGATTTTCAACAATACTACTGAGAGCTCAACAAGTTGTTT 857
Qy 454 -----ATTCCAGGAGATGCTACACC 474
Db 858 TTAGTGGGAACAACAATTCGAACAAATTCCTTGAGAACGCATTCAGGAGATGCTACACC 917
Qy 475 GATTATGTACTAGCAGATGGTACCGAGCTCTGAGCTCTCTGCGGAGATATCTCAGTAT 534
Db 918 GATTATGTACTAGCAGATGGTACCGAGCTCTGAGCTCTCTGCGGAGATATCTCAGTAT 977
Qy 535 GGTTCCTCAGTCGATATATGGGCTATTGGTGTGTTTTTTCGAGAGCTCTCTGACAGGCCAG 594
Db 978 GGTTCCTCAGTCGATATATGGGCTATTGGTGTGTTTTTTCGAGAGCTCTCTGACAGGCCAG 1037
Qy 595 CCACCTGTGGCTGGAAATCAGATGTGGACCAACTTTTATCTGATAATCAAGACATCAATCA 654
Db 1038 CCACCTGTGGCTGGAAATCAGATGTGGACCAACTTTTATCTGATAATCAAGACATCAATCA 1097
Qy 655 GAGACGGGTTTCGCCATGTTGACCGAGCTGCTCGAACTCTTGAGCTCAAGTGATCCA 714
Db 1098 GAGACGGGTTTCGCCATGTTGACCGAGCTGCTCGAACTCTTGAGCTCAAGTGATCCA 1157
Qy 715 CCTGCCGTAGCCTCTCAAGCTGTGGAATTAACAGGAAATTAATCCCAAGACATCAATCA 774
Db 1158 CCTGCCGTAGCCTCTCAAGCTGTGGAATTAACAGGAAATTAATCCCAAGACATCAATCA 1217
Qy 775 ATCTTTAAAGTAACCGGTTTTTCCATGGCATCAGTATACCTGAGCAGAGACATGGAA 834
Db 1218 ATCTTTAAAGTAACCGGTTTTTCCATGGCATCAGTATACCTGAGCAGAGACATGGAA 1277
Qy 835 ACTCTTGAGAAAGTTCTCAGATGTTTCATCTGTGCTCTGAGCTCTGAACTTCATGAAGGGTGT 894
Db 1278 ACTCTTGAGAAAGTTCTCAGATGTTTCATCTGTGCTCTGAGCTCTGAACTTCATGAAGGGTGT 1337
Qy 895 CTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCACTCTCTGAGAGCTCTCTACTTT 954
Db 1338 CTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCACTCTCTGAGAGCTCTCTACTTT 1397
Qy 955 GATTCTTTTCAAGAGGCCCAATTTAAAGAAAGACAGTAAATGAAGGAAGAAACAGAGA 1014
Db 1398 GATTCTTTTCAAGAGGCCCAATTTAAAGAAAGACAGTAAATGAAGGAAGAAACAGAGA 1457
Qy 1015 CGCCACAGGT 1025
Db 1458 CGCCACAGGT 1468

RESULT 6
US-09-671-050-1
; Sequence 1, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US/09/671.050
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 561
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-671-050-1

Query Match 43.7%; Score 454.4; DB 4; Length 561;
Best Local Similarity 99.8%; Pred. No. 4.1e-119;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGCAAAAGTATGAAAAATTTAGCTAAGACTGGAGAGGGTCTTTATGGGTTGTATTCAAA 60
Db 1 ATGCAAAAGTATGAAAAATTTAGCTAAGACTGGAGAGGGTCTTTATGGGTTGTATTCAAA 60
Qy 61 TGCAAGAAACAAACCTCTCGACAAAGTAGTAGTGTGTTAAAAAATTTGTGGAATCTGAAGAT 120
Db 61 TGCAAGAAACAAACCTCTCGACAAAGTAGTAGTGTGTTAAAAAATTTGTGGAATCTGAAGAT 120
Qy 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAGCAATTTAAACAT 180
Db 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAGCAATTTAAACAT 180
Qy 181 CCAAACTCTTGTAACCTCATCGAGGTGTTTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
Db 181 CCAAACTCTTGTAACCTCATCGAGGTGTTTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
Qy 241 GAATACGTGATCATACACTTTTAAATGAGCTCGAAAGAAACCCAAATGAGGTGCTGAT 300
Db 241 GAATACGTGATCATACACTTTTAAATGAGCTCGAAAGAAACCCAAATGAGGTGCTGAT 300
Qy 301 GAGTGTATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
Db 301 GAGTGTATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTCTAATAACTAAGCAAGGAATATC 420
Db 361 AACTGTATTACAGAGATATAAAACCTGAAATATTCTAATAACTAAGCAAGGAATATC 420
Qy 421 AAGATTGTGACTTCGGGTTTGACAAATTTCTGATT 456
Db 421 AAGATTGTGACTTCGGGTTTGACAAATTTCTGATT 456
RESULT 7
US-09-671-050-7
; Sequence 7, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US/09/671.050
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-671-050-7
Query Match 43.7%; Score 454.4; DB 4; Length 594;
Best Local Similarity 99.8%; Pred. No. 4.2e-119;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGCAAAAGTATGAAAAATTTAGCTAAGACTGGAGAGGGTCTTTATGGGTTGTATTCAAA 60
Db 1 ATGCAAAAGTATGAAAAATTTAGCTAAGACTGGAGAGGGTCTTTATGGGTTGTATTCAAA 60
Qy 61 TGCAAGAAACAAACCTCTCGACAAAGTAGTAGTGTGTTAAAAAATTTGTGGAATCTGAAGAT 120
Db 61 TGCAAGAAACAAACCTCTCGACAAAGTAGTAGTGTGTTAAAAAATTTGTGGAATCTGAAGAT 120

Db 61 TGCAGAAACAAACCTCTGGACAGTAGTAGCTGTTAAAAAATTGTGGAAATCTGAAGAT 120
QY 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
Db 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
QY 181 CCAATCTGTGTAACCTCATCGAGGTGTTCCAGAGAAAGGAAATGCAATTAAGTTT 240
Db 181 CCAATCTGTGTAACCTCATCGAGGTGTTCCAGAGAAAGGAAATGCAATTAAGTTT 240
QY 241 GATACCTGTGATCATACACTTTTAAATAGCTGGAAGAAACCAATCGAGTCTGAT 300
Db 241 GATACCTGTGATCATACACTTTTAAATAGCTGGAAGAAACCAATCGAGTCTGAT 300
QY 301 GGAGTGATCAAAAGCGTATATGCGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
Db 301 GGAGTGATCAAAAGCGTATATGCGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
QY 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATAACTAAGCAAGGAAATATC 420
Db 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATAACTAAGCAAGGAAATATC 420
QY 421 AAGATTGTGACTTCGGTTCGCAAAATCTGATT 456
Db 421 AAGATTGTGACTTCGGTTCGCAAAATCTGATT 456

RESULT 8

US-09-949-016-1681
; Sequence 1681, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1681
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1681

Query Match 33.0%; Score 343.8; DB 4; Length 1177;
Best Local Similarity 71.2%; Pred. No. 1.5e-87;
Matches 469; Conservative 0; Mismatches 187; Indels 3; Gaps 1;
QY 1 ATGGAAGAATGATGAAAAATTTAGCTAAGACTGGAGAGGCTCTATGGGGTTGTTTCAA 60
Db 32 ATGGAAGAATGATGAAAAATTTAGCTAAGACTGGAGAGGCTCTATGGGGTTGTTTCAA 91
QY 61 TGCAGAAACAAACCTCTCGACAGTAGTAGCTGTTAAAAAATTGTGGAATCTGAAGAT 120
Db 92 TGTAGAAACAGGACACCGGCTCAGATTGTGGCCATCAAGAAGTTCTGGAATCAGAAT 151
QY 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
Db 152 GACCCCTGTATAGAAATTTGCCCTTCGGAAATCCGAATGCTCAAGCAACTCAAGCAT 211
QY 181 CCAATCTGTGAACTCATCGAGGTGTTCCAGAGAAAGGAAATGCAATTAAGTTT 240
Db 212 CCAACCTTGTGTAACCTCTCGAAGTCTTCAGAGAAACGAGGCTTCACCTGTT 271
QY 241 GAATACCTGTGATCATACACTTTTAAATAGCTGGAAGAAACCAATGAGGTGCTGAT 300

Db 272 GAATATTGTGACCAACAGTTCTCCATGAGTTGGACAGATACCAAGAGGGTACCAGAA 331
QY 301 GGAGTGATCAAAAGCGTATATGCGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
Db 332 CATCTCGTGAAGACATAAATGTCACACACTGCAAGCTGTAATTTTCCCAATAACAC 391
QY 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATAACTAAGCAAGAAATATC 420
Db 392 AATTCATATAGAGACGTGAAGCCAGAAATATCTCATACAGAAACATTCGTTGATT 451
QY 421 AAGATTGTGACTTCGGGTTTGCACAAATCTGATT---CCAGAGATGCTTACACCGAT 477
Db 452 AAGCTTTGACCTTTGGAATTTGCTCGGCTTTTACTGGACCGAGTGAATATACAGAC 511
QY 478 TATGTAGTACAGAGATGTTACCGAGTCTCTGAACTTCTTGTGGAGATACTCAGTATGTT 537
Db 512 TAGCTGGCTACCAAGTGTACCGCTCCCTGAGTCTGTTGGGGACAGCAGTAGTACG 571
QY 538 TCTTCACTGATATATGGGCTATTTGTTGTTTGTGAGAGTCTCTGACAGCCAGCCA 597
Db 572 CCCCCGTTGAAGTTTGGGCAATTTGGCTGTCTTTTGTGAGTCTGTTGAGAGTGCCT 631
QY 598 CTGTGCTGGAATAATCAGATGTGGAACCAACTTTATCTGATAATCAGAACTACTAGTA 656
Db 632 CTGTGCGCAGGAAATCGGATGTGGATCAGCTGATCTGATTAGGAAGACCTTGGGGA 690

RESULT 9

US-09-411-628-5
; Sequence 5, Application US/09411628
; Patent No. 6428994
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; FILE REFERENCE: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/09/411,628
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: US 60/102,906
; EARLIER FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Orcytolagus cuniculus
US-09-411-628-5

Query Match 24.2%; Score 251.8; DB 3; Length 1701;
Best Local Similarity 62.9%; Pred. No. 2.4e-61;
Matches 407; Conservative 0; Mismatches 237; Indels 3; Gaps 1;
QY 1 ATGGAAGAATGATGAAAAATTTAGCTAAGACTGGAGAGGCTCTATGGGGTTGTTTCAA 60
Db 1 ATGGAAGAATGATGAAAAATTTAGCTAAGACTGGAGAGGCTCTATGGGGTTGTTTCAA 60
QY 61 TGCAGAAACAAACCTCTCGACAGTAGTAGCTGTTAAAAAATTGTGGAATCTGAAGAT 120
Db 61 TGTAGGAATAAGATAGTGGAGAAATTTGGGCCATCAAGAAGTTCTAGAAAGTATGAT 120
QY 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
Db 121 GACAAAAATGTTAAAAAATTTGCTATGCGGAATCAAGTTACTAAGCAACTGAGGCAT 180
QY 181 CCAATCTTGTGAACTCATCGAGGTGTTCCAGAGAAAGGAAATGCAATTAAGTTT 240
Db 181 GAAAAATTTGTTGAACTCTGTTGGAGTGTGTAATAAAAAAAGGAAATGCTTCTT 240
QY 241 GAATACCTGTGATCATACACTTTTAAATAGCTGGAAGAAACCAATGAGGTGCTGAT 300
Db 241 GAATTTGTTGACCAACGATTTCTGATGACTTGGAACTCTTTTCCAAATGGACTAGATGAC 300

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Qy 301 GGAGTGATCAAAAGCGTATTATGCAACACCTTCAAGCTCTTAATTTCTGTCTATACAT 360
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
301 CAAGTAGTTCAAAAGTATTGTTTTCAGATTAATTAATGAAATGGATTTGTGCACAGTCAC 360
Qy 361 AACTGTATTCCAGAGATATAAAACCTGAAAATATCTTAATAAATAAGCAAGGAATAATC 420
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
361 AATATCATACATAGAGATATAAAGCCAGAGATATATTTGGTCTCCAGTCTGGCGTTGTC 420
Qy 421 AAGATTGTGACTTCGGGTTTGCACAAATTCG---ATTCCAGAGATGCGCTACACCGAT 477
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
421 AAGTTATGTGATTTTGGATTTCACCGACACTGCGCAGCTCCCGAGAGGTTTACACTGAT 480
Qy 478 TATGTAGTACAGATGTCACCGAGCTCTGAACCTTCTTGTGGAGATACACTCAGTATGGT 537
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
481 TATGTGCAACTCGATGTCAGAGCTCCAGAACTACTGTTGGTGTGATGTCGAATATGGC 540
Qy 538 TCTTCAGTTCGATATATGGGCTATTGGTTGTTGTTTTCAGAGCTCCTGACAGGCCAGCCA 597
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
541 AAAGCTGTGGATGTGGGCCATTGGTTGCTGTGTAACCTGAATGCTCATGGGGGAACCC 600
Qy 598 CTGTGGCTGGAATAATCAGATGTGGACCAACTTTATCTGATAATCAG 644
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
601 CTGTTCTCGAGACTCTGATATTGATCAGCTTTATCTTATTATGAG 647

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RESULT 10

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US-10-174-794-5
; Sequence 5, Application US/10174794
; Patent No. 6664086
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10174,794
; PRIOR FILING DATE: 2002-06-18
; PRIOR FILING DATE: 1999-10-01
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Orcytolagus cuniculus
US-10-174-794-5

```

Query Match 24.2%; Score 251.8; DB 4; Length 1701;
 Best Local Similarity 62.9%; Pred. No. 2.4e-61;
 Matches 407; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

```

Qy 1 ATGGAAGAAGTATGAAAATTTAGCTTAAGACTGAGAGGGCTTATGGGTTGTATTCAA 60
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 ATGGAANAATATGAAACCTTGGATTGTTGGAGAGGGAGTTATGGAATGGTATGAG 60
Qy 61 TGCAGAAACAAAACCTCTGGAACAAGTAGTAGCTGTTAAAAAATTTTGGAAATCTGAAGAT 120
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
61 TGTAGGAATAAAGATAGTGGAGAAATTTGTGCCATCAAGAAGTTCTTAGAAAGTGATGAT 120
Qy 121 GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACACAT 180
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
121 GACAAAATGGTTAAAAAATTTGCTATGCGAGAAATCAAGTTACTTAAAGCAACTGAGGCAT 180
Qy 181 CCAAACTCTGTGAACCTCATCGAGTGTTCAGGAGAAAAGGAAAATGCAATTTAGTTT 240
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
181 GAAAATTTGGTGAATCTGTTGGAGGTGTGTAAAAAATAAACAATGCTACCTAGTCTTT 240
Qy 241 GAATFACTGTGATCATACACTTTTAAATGAGCTGGAAGAAAACCCAAATGGAGTTGCTGAT 300
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
241 GAAATTTGTGACACACAGATTTCTTGATGACTTGGAACTCTTTCCAAATGGACTAGATGAC 300
Qy 301 GGAGTGATCAAAAGCGTATTATGCAACACCTTCAAGCTCTTAATTTCTGTCTATACAT 360

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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
301 CAAGTAGTTCAAAAGTATTGTTTTCAGATTAATTAATGAAATGGATTTGTGCACAGTCAC 360
Qy 361 AACTGTATTCCAGAGATATAAAACCTGAAAATATCTTAATAAATAAGCAAGGAATAATC 420
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
361 AATATCATACATAGAGATATAAAGCCAGAGATATATTTGGTCTCCAGTCTGGCGTTGTC 420
Qy 421 AAGATTGTGACTTCGGGTTTGCACAAATTCG---ATTCCAGAGATGCGCTACACCGAT 477
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
421 AAGTTATGTGATTTTGGATTTCACCGACACTGCGCAGCTCCCGAGAGGTTTACACTGAT 480
Qy 478 TATGTAGTACAGATGTCACCGAGCTCTGAACCTTCTTGTGGAGATACACTCAGTATGGT 537
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
481 TATGTGCAACTCGATGTCAGAGCTCCAGAACTACTGTTGGTGTGATGTCGAATATGGC 540
Qy 538 TCTTCAGTTCGATATATGGGCTATTGGTTGTTGTTTTCAGAGCTCCTGACAGGCCAGCCA 597
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
541 AAAGCTGTGGATGTGGGCCATTGGTTGCTGTGTAACCTGAATGCTCATGGGGGAACCC 600
Qy 598 CTGTGGCTGGAATAATCAGATGTGGACCAACTTTATCTGATAATCAG 644
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
601 CTGTTCTCGAGACTCTGATATTGATCAGCTTTATCTTATTATGAG 647

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RESULT 11

```

US-09-411-628-3
; Sequence 3, Application US/09411628
; Patent No. 6428994
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/09/411,628
; CURRENT FILING DATE: 1999-10-01
; EARLIER APPLICATION NUMBER: US 60/102,906
; EARLIER FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3080
; TYPE: DNA
; ORGANISM: Orcytolagus cuniculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (249)...(1949)
US-09-411-628-3

```

Query Match 24.2%; Score 251.8; DB 3; Length 3080;
 Best Local Similarity 62.9%; Pred. No. 3.2e-61;
 Matches 407; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

```

Qy 1 ATGGAAGAAGTATGAAAATTTAGCTTAAGACTGAGAGGGCTTATGGGTTGTATTCAA 60
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
249 ATGGAANAATATGAAACCTTGGATTGTTGGAGAGGGAGTTATGGAATGGTATGAG 308
Qy 61 TGCAGAAACAAAACCTCTGGAACAAGTAGTAGCTGTTAAAAAATTTTGGAAATCTGAAGAT 120
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
309 TGTAGGAATAAAGATAGTGGAGAAATTTGTGCCATCAAGAAGTTCTTAGAAAGTGATGAT 368
Qy 121 GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACACAT 180
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
369 GACAAAATGGTTAAAAAATTTGCTATGCGAGAAATCAAGTTACTTAAAGCAACTGAGGCAT 428
Qy 181 CCAAACTCTGTGAACCTCATCGAGTGTTCAGGAGAAAAGGAAAATGCAATTTAGTTT 240
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
429 GAAAATTTGGTGAATCTGTTGGAGGTGTGTAAAAAATAAACAATGCTACCTAGTCTTT 488
Qy 241 GAATFACTGTGATCATACACTTTTAAATGAGCTGGAAGAAAACCCAAATGGAGTTGCTGAT 300
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
489 GAAATTTGTGACACACAGATTTCTTGATGACTTGGAACTCTTTCCAAATGGACTAGATGAC 548
Qy 301 GGAGTGATCAAAAGCGTATTATGCAACACCTTCAAGCTCTTAATTTCTGTCTATACAT 360

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Db 549 CAAGTAGTCAAAAGATATTGTTTCAGATTATTAAGGAATTGGATTGTGCAGTCAC 608
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATAAGCAAGGAATAATC 420
Db 609 AATATCATACATAGAGATATAAAGCCAGAGAAATATATGTTCTCCCAAGTCTGGCGTTGC 668
Qy 421 AAGATTGTGACTTCGGGTTTGACAAATTTCTG---ATTCCAGGAGATCCCTACACCGAT 477
Db 669 AAGTTATGTGATTGGAATTGACCGGACACTGGGAGCTCCCGGAGAGGTTTACACTGAT 728
Qy 478 TATGTAGCTACAGATAGTACCGAGCTCCTGAACTTTCTTGTGGGAGATCTCAGTATGCT 537
Db 729 TATGTGGCAACTCGATGGTACAGACTCCAGAACTACTGTTTGGTGAATGCTCAAGTATGCG 788
Qy 538 TCTTCAGTCGATATATGGGCTATTGTTGTTTTCAGAGCTCCTGCAGGCCAGCCA 597
Db 789 AAAGCTGTGATGTTGGGCCATTGTTCTGGTAACTGAAATGCTCATGGGGGAACCC 848
Qy 598 CTGTGGCCTGGAAATCAGATGTCAGCAACTTTATCTGATAATCAG 644
Db 849 CTGTTTCTGGAGACTCTGATATTCATCAGCTTTTATTTATGAG 895

```

RESULT 12

US-10-174-794-3

; Sequence 3, Application US/10174794

; Patent No. 6664086

; GENERAL INFORMATION:

; APPLICANT: University of Southern California

; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN

; FILE REFERENCE: SEQUENCES OF LEARNING-INDUCED KINASES

; CURRENT APPLICATION NUMBER: US/10/174,794

; CURRENT FILING DATE: 2002-06-18

; PRIOR APPLICATION NUMBER: US/09/411,628

; PRIOR FILING DATE: 1999-10-01

; PRIOR APPLICATION NUMBER: US 60/102,906

; PRIOR FILING DATE: 1998-10-02

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 3080

; TYPE: DNA

; ORGANISM: Orcytolagus cuniculus

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (249)....(1949)

; US-10-174-794-3

Query Match

Best Local Similarity 24.2%; Score 251.8; DB 4; Length 3080;

Matches 407; Conservative 0; Mismatches 237; Indels 3; Gaps 1;

```

Qy 1 ATGGAAGAAGTATGAAAATTTAGCTAGACTGGAGAAAGGCTTTATGGGTTGTTATTCAAA 60
Db 249 ATGGAAGAAGTATGAAAATTTAGCTAGACTGGAGAAAGGCTTTATGGGTTGTTATTCAAA 308
Qy 61 TGCAGAAAACAAACCTCTGGCAAGTAGTAGCTGTTTAAATAATTTGTGGAATCTGAAGAT 120
Db 309 TGTAGGAATAAAGATAGTGGAGAATTTGGGCCATCAAGAAGTCTCTAGAAAGTGTATGAT 368
Qy 121 GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAAATACGTTATCTTGAAGCAATTTAAACAT 180
Db 369 GACAAAATGGTTTAAATAATTTGCTATGCGAGAAAATCAAGTTACTAAGCAACTGAGGAT 428
Qy 181 CCAAAATCTTGTGAACCTCATCGAGGTTCAGAGAAAAGAAAATGCATTTAGTTTTT 240
Db 429 GAAAATTTGGTGAATCTGTTGAGGTGTGTAATAAATAAATAAACAACGATGTAGTCTTT 488
Qy 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAGAAAACCCAAATGGAGTTGCTGAT 300
Db 489 GAAATTTGTTGACACACGATCTTGTATGACTTGGAACTCTTCCAAATGGACTAGATGAC 548

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Qy 301 GGAGTGATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTCTATACAT 360
Db 549 CAAGTAGTCAAAAGATATTGTTTCAGATTATTAAGGAATTGGATTGTGCAGTCAC 608
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATAAGCAAGGAATAATC 420
Db 609 AATATCATACATAGAGATATAAAGCCAGAGAAATATATGTTCTCCCAAGTCTGGCGTTGC 668
Qy 421 AAGATTGTGACTTCGGGTTTGACAAATTTCTG---ATTCCAGGAGATCCCTACACCGAT 477
Db 669 AAGTTATGTGATTGGAATTGACCGGACACTGGGAGCTCCCGGAGAGGTTTACACTGAT 728
Qy 478 TATGTAGCTACAGATAGTACCGAGCTCCTGAACTTTCTTGTGGGAGATCTCAGTATGCT 537
Db 729 TATGTGGCAACTCGATGGTACAGACTCCAGAACTACTGTTTGGTGAATGCTCAAGTATGCG 788
Qy 538 TCTTCAGTCGATATATGGGCTATTGTTGTTTTCAGAGCTCCTGCAGGCCAGCCA 597
Db 789 AAAGCTGTGATGTTGGGCCATTGTTCTGGTAACTGAAATGCTCATGGGGGAACCC 848
Qy 598 CTGTGGCCTGGAAATCAGATGTCAGCAACTTTATCTGATAATCAG 644
Db 849 CTGTTTCTGGAGACTCTGATATTCATCAGCTTTTATTTATGAG 895

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RESULT 13

US-09-949-016-2083

; Sequence 2083, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2083

; LENGTH: 1794

; TYPE: DNA

; ORGANISM: Human

; US-09-949-016-2083

Query Match

Best Local Similarity 23.2%; Score 241.2; DB 4; Length 1794;

Matches 400; Conservative 0; Mismatches 243; Indels 3; Gaps 1;

```

Qy 1 ATGGAAGAAGTATGAAAATTTAGCTAGACTGGAGAAAGGCTTTATGGGTTGTTATTCAAA 60
Db 376 ATGGAAGAAGTATGAAAATTTAGCTAGACTGGAGAAAGGCTTTATGGGTTGTTATTCAAA 435
Qy 61 TGCAGAAAACAAACCTCTGGCAAGTAGTAGCTGTTTAAATAATTTGTGGAATCTGAAGAT 120
Db 436 TGTAGGAATAAAGATAGTGGAGAATTTGGGCCATTAAGAAGTCTTTAGAAAGTGCAGAT 495
Qy 121 GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAAATACGTTATGTTGAAGCAATTTAAACAT 180
Db 496 GACAAAATGGTTTAAATAATTTGCAATGCGAGAAAATCAAGTTACTAAGCAACTTAGGCAT 555
Qy 181 CCAAAATCTTGTGAACCTCATCGAGGTTCAGAGAAAAGAAAATGCATTTAGTTTTT 240
Db 556 GAAAATCTTGTGGAATCTCTTGGAGGTGTGTAAGAAAATAAACAACGATGTAGTCTTT 615
Qy 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAGAAAACCCAAATGGAGTTGCTGAT 300

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Db 616 GAATTTGTTGACACACAAATCTTGTGACCTTGGAGCTCTTCCAAATGGACTAGACTAC 675
Qy 301 GGAGTATCAAAAGCGTATTATGACCAACACTTCAAGCTCTTAATTTCTGTATATACAT 360
Db 676 CAAGTAGTTCAAAAGTATTTGTTTTCAGATTAATTAATGGAATTTGTTGTCACAGTCAC 735
Qy 361 AACTGTATTACAGAGATATAAACCCTGAAATATTTCTTAATACTAAGCAAGGATATAC 420
Db 736 AATATACACAGAGATATAAAGCCAGAGAAATATATTAGTCTCCAGTCTGGCGTTGTC 795
Qy 421 AAGATTGTTGACTTTCGGGTTTGGCAAAATCTG---ATTCCAGGAGATGCTTACACCGAT 477
Db 796 AAGCTATGCGATTTTGGATTTGCGGACATTTGGCAGCTCTCGGGAGTTTATACATGAT 855
Qy 478 TATGTAGTACGAGATGGTACCGAGCTCTGAACTTCTTGTGGGAGATACCTAGTATGGT 537
Db 856 TATGTGCAACCCGATGGTACAGAGCTCCAGAACTATTGGTTGGTGATGTCACAGTATGGC 915
Qy 538 TCTTCAGTGCATATATGGGCTATTGGTTGGTTGTTTGGCAGAGCTCTGACAGGCCAGCCA 597
Db 916 AAGGCTGTTGATGTGGGCCATTTGGTTGTTCTGTGTAATCTGAAATGTTTCATGGGGGAACCC 975
Qy 598 CTGTGGCCTGGAATCAGATGTGGCAACACTTTATCTGATAATCA 643
Db 976 CTATTTCTGGAGATCTGTATATTGATCAGCTATATATATGA 1021

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RESULT 14
US-08-874-347-9
; Sequence 9, Application US/08874347
; Patent No. 5863741
; GENERAL INFORMATION:
; APPLICANT: Limper, Andrew H.
; APPLICANT: Leof, Edward B.
; APPLICANT: Thomas, Charles F.
; APPLICANT: Gustafson, Michael P.
; TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
; NUMBER OF INVENTIONS: CARINII
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C., P.A.
; STREET: 60 South Sixth Street, Suite 3300
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/874,347
; FILING DATE: 13-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellinger, Mark S.
; REGISTRATION NUMBER: 34,812
; REFERENCE/DOCKET NUMBER: 07039/055001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-335-5070
; TELEFAX: 612-288-9696
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 903 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...900

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; OTHER INFORMATION:
US-08-874-347-9
Query Match 15.7%; Score 163.8; DB 2; Length 903;
Best Local Similarity 55.2%; Pred. No. 1.6e-36;
Matches 365; Conservative 0; Mismatches 287; Indels 9; Gaps 2;
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Db 1 ATGGAGCAATATCAGAGGTTAGAGAAAGATTGGAGAGAACTTATGGAGTTGTTTATAAA 60
Qy 61 TGCAGAAACAAACCTCTCGACAAAGTAGTAGCTGTTAAATAAATTTTGGGAATCTGAAGAT 120
Db 61 GCAAGGATCTTGAAGTGGTACAAATTTAGTCTCTTAAGAAATCCGATTTAGAGAGAA 120
Qy 121 GATCCTCTGTTTGAAGAAATAGCACTAAGAGAAATAGTATGTTTGAAGCAATTTAAAAACAT 180
Db 121 GATCAGGAGTCTCTAGTACAGCAATTTCTGTGAGATATCACTTTTGAAGAGATGCACAAT 180
Qy 181 CCAAACTTTGTGAACCTCATCGAGGTTTCAGGAGAAAGAAAGAAATATGCAATTTATGTTTTT 240
Db 181 GATAATGTTTGAAGACTTTTGAATATAAATTCATCAAGAGTCACTTTTATATATCTTTGTTTTT 240
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Qy 355 ATACATAACTGTATTTCACAGAGATATAAAACCTGAAATAATTTCTAATACTAAGCAAGGA 414
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Qy 415 ATAATCAGATTTTGTGACTTCGGGTTTGGCAAAA---TTCTGATTCAGGAGATGCGCTAC 471
Db 421 AATCTTAAATTTAGCAGATTTTGGGCTTTGCAAGGCGTTTGGTGTCTCATTCGCGGTTAT 480
Qy 472 ACCGATTATGTAGTACGAGATGTCACCGAGCTCCTGAACCTTCTTGTGGGAGATACCTCAG 531
Db 481 ACTCATGAGTTGTTTACACTTTGTTATCGTCTCCAGAAAGTTCTTTTAGTGGTTCGACAA 540
Qy 532 TATGGTTCTTTCAGTCGATATATGGGCTATTGGTTGTTGTTTTCAGAGCTCTTCGACAGGC 591
Db 541 TATGCAACAGCGCTTGATATATGAGCATTTGGATGTTATTTTTCAGAAAATGGCTACAAA 600
Qy 592 CAGCCACTGGGCTGGAATAATCAGATGTCGACCACTTTATCTGATAATCAGACACTA 651
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Db 661 G 661

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RESULT 15
US-09-093-522-9
; Sequence 9, Application US/09093522
; Patent No. 6015700
; GENERAL INFORMATION:
; APPLICANT: Limper, Andrew H.
; APPLICANT: Leof, Edward B.
; APPLICANT: Thomas, Charles F.
; APPLICANT: Gustafson, Michael P.
; TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
; NUMBER OF INVENTIONS: CARINII
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C., P.A.
; STREET: 60 South Sixth Street, Suite 3300
; CITY: Minneapolis
; STATE: MN

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:/ COUNTRY: USA
:/ ZIP: 55402
:/ COMPUTER READABLE FORM:
:/ MEDIUM TYPE: Diskette
:/ COMPUTER: IBM Compatible
:/ OPERATING SYSTEM: DOS
:/ SOFTWARE: FastSeq for Windows Version 2.0
:/ CURRENT APPLICATION DATA:
:/ APPLICATION NUMBER: US/09/093,522
:/ FILING DATE: 08-JUN-1998
:/ CLASSIFICATION:
:/ PRIOR APPLICATION DATA:
:/ APPLICATION NUMBER: 08/874,347
:/ FILING DATE: 13-JUN-1997
:/ ATTORNEY/AGENT INFORMATION:
:/ NAME: Ellinger, Mark S.
:/ REGISTRATION NUMBER: 34,812
:/ REFERENCE/DOCKET NUMBER: 07039/055002
:/ TELECOMMUNICATION INFORMATION:
:/ TELEPHONE: 612-335-5070
:/ TELEFAX: 612-288-9696
:/ TELEX:
:/ INFORMATION FOR SEQ ID NO: 9:
:/ SEQUENCE CHARACTERISTICS:
:/ LENGTH: 903 base pairs
:/ TYPE: nucleic acid
:/ STRANDEDNESS: single
:/ TOPOLOGY: linear
:/ MOLECULE TYPE: cDNA
:/ FEATURE:
:/ NAME/KEY: Coding Sequence
:/ LOCATION: 1...900
:/ OTHER INFORMATION:
:/ US-09-093-522-9

Query Match 15.7%; Score 163.8; DB 3; Length 903;

Best Local Similarity 55.2%; Pred.No. 1.6e-36;

Matches 365; Conservative 0; Mismatches 287; Indels 9; Gaps 2;

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Db	121	GATGAGGAGTTCCTAGTACAGCAATTCGTGAGATATCACTTTTGAAGAGATGCACAAT	180
QY	181	CCAAATCTTTGTAACCTCATCGAGGTGTTCCAGGAGAAAAGGAAATGCAATTTAGTTTTT	240
Db	181	GATAATGTTGTAAGACTTTTGAATAAATTCATCAGAGTCAGCTTTATCTTGTTTTT	240
QY	241	GAATCTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATG-----GAGTT	294
Db	241	GAATTTCTTGATCTTGATTTAAATAAGTATATGAATAGTATTCCAAAGGACATGATGCTT	300
QY	295	GCTGATGGAGTATCAAAACGCTATTATGCAACACTTCAAGCTTTAATTTCTGTCAT	354
Db	301	GGTGCAAGAAATGATTAAGAATTTATGTCACAACTTGATCAGGTGTTAAATTTGTCAT	360
QY	355	ATACATACTGTATTCCAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGA	414
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QY	592	CAGCACTGTGGCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACTA	651
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QY	652	G 652	
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Job time : 202.088 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	821	78.9	1790	6 AAD30557	Aad30557 Human kin
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16	454.4	43.7	594	4 AAD03815	Aad03815 Human kin
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26	242.2	23.3	1179	4 ABL12603	Abi12603 Drosophil
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36	177.4	17.0	1158	5 AAS70329	Aas70329 DNA encod
37	175.2	16.8	1866	4 AAF44672	Aaf44672 Novel pro
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43	161.6	15.5	1024	10 ABZ83372	Abz83372 Toxicolog
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45	161.6	15.5	1297	10 ADD21391	Add21391 Human cyc

ALIGNMENTS

RESULT 1
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ID AAD03816 standard; cDNA; 1041 BP.
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AC AAD03816;
XX
DT 19-JUN-2001 (first entry)
XX
DE Human kinase cDNA #5.
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KW Human; kinase; gene therapy; bioreactor; mental disorder;
KW biological disorder; ss.
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OS Homo sapiens.
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FH Key Location/Qualifiers
CDS 1..1041
FT /*tag= a
FT /product= "Human kinase #5"
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XX
PN WO200123579-A1.
XX
PD 05-APR-2001.
XX
PF 27-SEP-2000; 2000WO-US026621.
XX
PR 28-SEP-1999; 99US-0156511P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
PI Sands AT;
XX
DR WPI; 2001-266166/27.
DR P-PSDE; AAE00494.
XX
PT New isolated human kinase polynucleotide useful for generating
PT antibodies, as reagents in diagnostic assays and for screening for
PT compounds useful for treating mental, biological or medical diseases.
XX
PS Claim 1; Page 31-32; 38pp; English.

XX The present sequence is a cDNA encoding novel human protein (NHP) known
 CC as human kinase. The human kinases share structural similarity with
 CC animal kinases, more particularly serine or threonine protein kinases.
 CC Human kinase cDNA is useful for the detection of mutant human kinase for
 CC the diagnosis of disease, and also as a therapeutic. It is useful for
 CC screening drugs effective in the treatment of symptomatic or phenotypic
 CC manifestations perturbing the normal function of NHP in the body. The NHP
 CC nucleotide sequences are useful for generation of antibodies, as reagents
 CC in diagnostic assays, for the identification of other cellular gene
 CC products related to human kinases, and as reagents in assays for
 CC screening compounds that are useful for treating mental, biological or
 CC medical disorders. NHP oligonucleotides are used as probes. The labelled
 CC NHP probes are useful for screening human genomic library for identifying
 CC polymorphisms and as primers in amplification assays to detect mutations
 CC within the exons, introns and splice sites that can be used in
 CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP
 CC products are used to genetically engineer cells in vivo that functions as
 CC bioreactors in the body delivering a continuous supply of NHP to the
 CC body. Nucleotide constructs encoding functional NHPs are used in gene
 CC therapy for the modulation of NHP expression
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Query Match 100.0%; Score 1041; DB 4; Length 1041;
 Best Local Similarity 100.0%; Pred. No. 9.9e-268;
 Matches 1041; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 61 TGCAGAACAAACCTCTGCAAGTAGTAGCTGTTAAAAAATTTGGAACTGGAAGAT 120
 QY 121 GATCCTCTGTTAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACAAT 180
 DB 121 GATCCTCTGTTAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACAAT 180
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 QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 300
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 DB 481 GTAGCTACGAGATGGTACCGAGCTCTGAACTCTTGTGGAGATACCTAGTATGTTCTT 540
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 QY 781 AARAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCAGAGACATGGAACCTCTT 840
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 QY 841 GAGGAAAGTTCTCAGATGTTCTGCTGGCTCTGAACTTCATGAAGGGGTGTCTGAAG 900
 DB 841 GAGGAAAGTTCTCAGATGTTCTGCTGGCTCTGAACTTCATGAAGGGGTGTCTGAAG 900
 QY 901 ATGAATCCAGATGACAGATTAACCTGTTCCAACTCTGAGAGCTCTTACTTTGATTTCT 960
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 QY 961 TTTCAAGAGGCCCAAAATTAAGAAAGACGCTAATGAAGGAAAGACAGAACGCGCAA 1020
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 DB 1021 CAGGTACTTCCGCTCAAAAGT 1041
 XX AAD03813 standard; cDNA; 1068 BP.
 XX AAD03813;
 XX AC AAD03813;
 XX DT 19-JUN-2001 (first entry)
 XX DE Human kinase cDNA #2.
 XX KW Human; kinase; gene therapy; bioreactor; mental disorder;
 KW biological disorder; ss.
 XX OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..1068
 FT /tag= a
 FT /product= "Human kinase #2"
 FT /note= "The coding region does not include stop codon"
 FT /partial
 XX PN W0200123579-A1.
 XX PD 05-APR-2001.
 XX PF 27-SEP-2000; 2000WO-US026621.
 XX PR 28-SEP-1999; 99US-0156511P.
 XX PA (LEXI-) LEXICON GENETICS INC.
 XX PI Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
 PI Sands AT;
 XX WP1; 2001-266166/27.
 DR P-PSDB; AAB00491.
 XX PT New isolated human kinase polynucleotide useful for generating
 PT antibodies, as reagents in diagnostic assays and for screening for
 PT compounds useful for treating mental, biological or medical diseases.
 XX PS Disclosure; Page 28; 38pp; English.
 XX CC The present sequence is a cDNA encoding novel human protein (NHP) known

as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression

Query Match 98.5%; Score 1025; DB 4; Length 1068;
 Best Local Similarity 100.0%; Pred. No. 1.9e-263;
 Matches 1025; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 841 GAGGAAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTTCATGAAGGGGTGCTGAAG 900
 901 ATGAATCCAGATGACAGATTAACTGTTTCCCAACTCTCGAGAGCTCTACTTTGATTCT 960
 901 ATGAATCCAGATGACAGATTAACTGTTTCCCAACTCTCGAGAGCTCTACTTTGATTCT 960
 961 TTTCAAGAGGCCCAAAATTAAGAAAAAGACGCTAATGAAGGAAAGAAACAGAGACGCCAA 1020
 961 TTTCAAGAGGCCCAAAATTAAGAAAAAGACGCTAATGAAGGAAAGAAACAGAGACGCCAA 1020
 1021 CAGGT 1025
 1021 CAGGT 1025

RESULT 3
 AAD03817
 ID AAD03817 standard; cDNA; 945 BP.
 XX AAD03817;
 XX 19-JUN-2001 (first entry)
 XX Human kinase cDNA #6.
 XX Human; kinase; gene therapy; bioreactor; mental disorder;
 XX biological disorder; BS.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 CDS 1..945
 FT /*tag= a
 FT /product= "Human kinase #6"
 FT /note= "The coding region does not include stop codon"
 FT /partial
 XX MO200123579-Al.
 XX 05-APR-2001.
 XX 27-SEP-2000; 2000MO-US026621.
 XX 28-SEP-1999; 99US-0156511P.
 XX (LEXI-) LEXICON GENETICS INC.
 XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
 PI Sands AT;
 XX WPI; 2001-266166/27.
 DR P-PSDB; AAE00495.
 XX New isolated human kinase polynucleotide useful for generating
 PT antibodies, as reagents in diagnostic assays and for screening for
 PT compounds useful for treating mental, biological or medical diseases.
 XX Claim 3; Page 33; 38pp; English.
 XX The present sequence is a cDNA encoding novel human protein (NHP) known
 CC as human kinase. The human kinases share structural similarity with
 CC animal kinases, more particularly serine or threonine protein kinases.

Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression

Sequence 945 BP; 323 A; 165 C; 202 G; 255 T; 0 U; 0 Other;

Query Match 80.6%; Score 839; DB 4; Length 945;
 Best Local Similarity 90.8%; Pred. No. 9e-214;
 Matches 945; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

QY 1 ATGGAAGATGATAAATTAAGCTAAGCTGAGAGGGCTTATGGGTTGATTCAAA 60
 Db 1 ATGGAAGATGATAAATTAAGCTAAGCTGAGAGGGCTTATGGGTTGATTCAAA 60
 QY 61 TGCAGAACAAACCTCTGGACAGTAGTAGCTGTAAGAAATTTGGGAATCTGAAGAT 120
 Db 61 TGCAGAACAAACCTCTGGACAGTAGTAGCTGTAAGAAATTTGGGAATCTGAAGAT 120
 QY 121 GATCCTGTGTTAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACACAT 180
 Db 121 GATCCTGTGTTAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACACAT 180
 QY 181 CCAATCTTGTGAACCTCATCGAGGTGTCAGGAGAAAAGGAAATGCAATTTAGTTTTT 240
 Db 181 CCAATCTTGTGAACCTCATCGAGGTGTCAGGAGAAAAGGAAATGCAATTTAGTTTTT 240
 QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAACCCCAATGAGTTGCTGAT 300
 Db 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAACCCCAATGAGTTGCTGAT 300
 QY 301 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAATTTCTGTATATACAT 360
 Db 301 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAATTTCTGTATATACAT 360
 QY 361 AACTGTATTACAGAGATATAAACCCTGAAATATTTCTAATACTAAGCAAGGAATAATC 420
 Db 361 AACTGTATTACAGAGATATAAACCCTGAAATATTTCTAATACTAAGCAAGGAATAATC 420
 QY 421 AAGATTGTGACTTCGGGTTTGACAAATTTCTGATTCAGAGATGCTACACCGATTAT 480
 Db 421 AAGATTGTGACTTCGGGTTTGACAAATTTCTGATTCAGAGATGCTACACCGATTAT 480
 QY 481 GTAGCTACAGAGATGATACCGAGTCTCTGAACTTTCTTGGAGATACCTCAGTATGTTCT 540
 Db 481 GTAGCTACAGAGATGATACCGAGTCTCTGAACTTTCTTGGAGATACCTCAGTATGTTCT 540
 QY 541 TCAGTGCATATATGGGCTATTGTTGTTGTTTTCAGAGCTCTCTGACGCCAGCCACTG 600
 Db 541 TCAGTGCATATATGGGCTATTGTTGTTGTTTTCAGAGCTCTCTGACGCCAGCCACTG 600
 QY 601 TGGCCTGGAAATCAGATGTGGACCACTTTATCTGATAATCAGAACACTAGTAGAGACG 660
 Db 601 TGGCCTGGAAATCAGATGTGGACCACTTTATCTGATAATCAGAACACTAGTAGAGACG 660
 QY 661 GGGTTTGGCCATGTTGACCGAGGCTGGTCTCGAACTCTTGACGTCAAGTATCACTGGC 720
 Db 661 GGGTTTGGCCATGTTGACCGAGGCTGGTCTCGAACTCTTGACGTCAAGTATCACTGGC 720
 QY 721 GTAGCCTCTCAAAGTGTGGAATTACAGGAAATTAATCCCAAGACATCAATCAATCTTT 780

Db 651 -----AGGAAATTAATCCAGACATCAATCAATCTTT 684
 QY 781 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAACTCTT 840
 Db 685 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAACTCTT 744
 QY 841 GAGGAAAGTCTCAGATGTTTCATCTGTGGTCTCTGAACTTCAATGAAGGGGTGTCTGAAG 900
 Db 745 GAGGAAAGTCTCAGATGTTTCATCTGTGGTCTCTGAACTTCAATGAAGGGGTGTCTGAAG 804
 QY 901 ATGAATCCAGATCAGATTAACCTGTTCCCACTCTCTGAGAGCTCTCTACTTTGATTCT 960
 Db 805 ATGAATCCAGATCAGATTAACCTGTTCCCACTCTCTGAGAGCTCTCTACTTTGATTCT 864
 QY 961 TTTCAAGAGGCCCAAAATTTAAAGAAAAGCAGTAAATGAAGGAAAGAAACAGAGACGCCAA 1020
 Db 865 TTTCAAGAGGCCCAAAATTTAAAGAAAAGCAGTAAATGAAGGAAAGAAACAGAGACGCCAA 924
 QY 1021 CAGGTACTTCCGCTCAAAAGT 1041
 Db 925 CAGGTACTTCCGCTCAAAAGT 945

RESULT 4
 AAD03814
 ID AAD03814 standard; cDNA; 972 BP.
 XX AAD03814;
 AC AAD03814;
 XX 19-JUN-2001 (first entry)
 DT 19-JUN-2001 (first entry)
 XX Human kinase cDNA #3.
 DE Human; kinase; gene therapy; bioreactor; mental disorder;
 KW biological disorder; ss.
 OS Homo sapiens.
 XX
 FH Location/Qualifiers
 FT 1. 972
 FT /tag= a
 FT /product= "Human kinase #3"
 FT /note= "The coding region does not include stop codon"
 XX
 PN WO200123579-A1.
 XX
 PD 05-APR-2001.
 XX
 PF 27-SEP-2000; 2000WO-US026621.
 XX
 PR 28-SEP-1999; 99US-0156511P.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
 PI Sands AT;
 XX
 DR WPI; 2001-266166/27.
 DR P-PSDB; AAE00492.
 XX
 PT New isolated human kinase polynucleotide useful for generating for
 PT antibodies, as reagents in diagnostic assays and for screening for
 PT compounds useful for treating mental, biological or medical diseases.
 XX
 PS Disclosure; Page 29-30; 38pp; English.
 XX
 CC The present sequence is a cDNA encoding novel human protein (NHP) known
 CC as human kinase. The human kinases share structural similarity with
 CC animal kinases, more particularly serine or threonine protein kinases.
 CC Human kinase cDNA is useful for the detection of mutant human kinase for
 CC the diagnosis of disease, and also as a therapeutic. It is useful for

CC screening drugs effective in the treatment of symptomatic or phenotypic
 CC manifestations perturbing the normal function of NHP in the body. The NHP
 CC nucleotide sequences are useful for generation of antibodies, as reagents
 CC in diagnostic assays, for the identification of other cellular gene
 CC products related to human kinases, and as reagents in assays for
 CC screening compounds that are useful for treating mental, biological or
 CC medical disorders. NHP oligonucleotides are used as probes. The labelled
 CC NHP probes are useful for screening human genomic library for identifying
 CC polymorphisms and as primers in amplification assays to detect mutations
 CC within the exons, introns and splice sites that can be used in
 CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP
 CC products are used to genetically engineer cells in vivo that functions as
 CC bioreactors in the body delivering a continuous supply of NHP to the
 CC body. Nucleotide constructs encoding functional NHPs are used in gene
 CC therapy for the modulation of NHP expression
 XX
 SQ Sequence 972 BP; 323 A; 172 C; 214 G; 263 T; 0 U; 0 Other;

Query Match 79.1%; Score 823; DB 4; Length 972;
 Best Local Similarity 90.6%; Pred. No. 1.7e-209;
 Matches 929; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

Qy 1 ATGCAAAAGTATGAAATTAAGCTAAGACTGAGAGGGTCTTATGGGTTGTATTCAAA 60
 Db |||||||
 Qy 1 ATGCAAAAGTATGAAATTAAGCTAAGACTGAGAGGGTCTTATGGGTTGTATTCAAA 60
 Db |||||||
 Qy 61 TGCAGAAACAAACCTCTGCAACAAGTAGTACTGTGTAAGAAATTTGTGGAATCTGAAGAT 120
 Db |||||||
 Qy 61 TGCAGAAACAAACCTCTGCAACAAGTAGTACTGTGTAAGAAATTTGTGGAATCTGAAGAT 120
 Db |||||||
 Qy 121 GATCCTGTGTTAAGAAATTAAGCTAAGAGAAATACGTATGTTGAAGCAATTAACACAT 180
 Db |||||||
 Qy 121 GATCCTGTGTTAAGAAATTAAGCTAAGAGAAATACGTATGTTGAAGCAATTAACACAT 180
 Db |||||||
 Qy 181 CCAATCTGTGAACCTCATCGAGTGTTCAGGAGAAAGGAAAGCAATTAAGTTT 240
 Db |||||||
 Qy 181 CCAATCTGTGAACCTCATCGAGTGTTCAGGAGAAAGGAAAGCAATTAAGTTT 240
 Db |||||||
 Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAATGCTGAT 300
 Db |||||||
 Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAATGCTGAT 300
 Db |||||||
 Qy 301 GGAGTGATCAAAAGCGTATTAAGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
 Db |||||||
 Qy 301 GGAGTGATCAAAAGCGTATTAAGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
 Db |||||||
 Qy 361 AACTGTATTCACAGATATAAACCTGAAATATTTCTAATACTAGCAAGGAATATC 420
 Db |||||||
 Qy 361 AACTGTATTCACAGATATAAACCTGAAATATTTCTAATACTAGCAAGGAATATC 420
 Db |||||||
 Qy 421 AAGATTTGTGACTTCGGGTTTGCAAAATTTCTGATTCAGGAGATGCTACACCGATTAT 480
 Db |||||||
 Qy 421 AAGATTTGTGACTTCGGGTTTGCAAAATTTCTGATTCAGGAGATGCTACACCGATTAT 480
 Db |||||||
 Qy 481 GTAGCTACGAGATGGTACCGAGCTCCTGAATCTTTGTTGGAGATATCTAGTATGGTTCT 540
 Db |||||||
 Qy 481 GTAGCTACGAGATGGTACCGAGCTCCTGAATCTTTGTTGGAGATATCTAGTATGGTTCT 540
 Db |||||||
 Qy 541 TCAGTCGATATATGGGCTATTTGGTTGTTTTCGAGAGCTCTTCGACGGCCAGCACTG 600
 Db |||||||
 Qy 541 TCAGTCGATATATGGGCTATTTGGTTGTTTTCGAGAGCTCTTCGACGGCCAGCACTG 600
 Db |||||||
 Qy 601 TGGCTCGGAAATCAGATGTGGACCAACTTTATCTGATTAATCAGAACACTAGTAGAGACG 660
 Db |||||||
 Qy 601 TGGCTCGGAAATCAGATGTGGACCAACTTTATCTGATTAATCAGAACACTAGTAGAGACG 660
 Db |||||||
 Qy 661 GGGTTTCGCCCATGTTGACCGAGGCTGTTCTGCAACTTTGAGCTCAAGTGTATCCACCTGCC 720
 Db |||||||
 Qy 651 -----AGGAAATTTAATCCCAAGACATCAATCAATCTTT 684

Qy 781 AAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAACCTTT 840
 Db |||||||
 Qy 685 AAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAACCTTT 744
 Db |||||||
 Qy 841 GAGGAAAGTCTCAGATGTTTCATCCTGTGGCTCTGAACCTTCATGAAGGGGTCTGAAG 900
 Db |||||||
 Qy 745 GAGGAAAGTCTCAGATGTTTCATCCTGTGGCTCTGAACCTTCATGAAGGGGTCTGAAG 804
 Db |||||||
 Qy 901 ATGAATCCAGATGACAGATTAACCTGTTCCCAACTCTCTGGAGAGCTCTTCTGATTTCT 960
 Db |||||||
 Qy 805 ATGAATCCAGATGACAGATTAACCTGTTCCCAACTCTCTGGAGAGCTCTTCTGATTTCT 864
 Db |||||||
 Qy 961 TTTCAAGAGGCCCAAAATTAAGAAAGCAAGCTGTAATGAAGGAAAGAAACAGAACGCCAA 1020
 Db |||||||
 Qy 865 TTTCAAGAGGCCCAAAATTAAGAAAGCAAGCTGTAATGAAGGAAAGAAACAGAACGCCAA 924
 Db |||||||
 Qy 1021 CAGGT 1025
 Db 925 CAGGT 929
 RESULT 5
 RAD30557
 ID AAD30557 standard; cDNA; 1790 BP.
 XX
 AC AAD30557;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Human kinase polypeptide (PKIN-10) cDNA.
 XX
 KW Human; kinase polypeptide; PKIN-10; gene therapy; Addison's disease;
 KW leukaemia; immune disorder; lymphoma; melanoma; developmental disorder;
 KW acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension;
 KW asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis;
 KW cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer;
 KW cholestasis; cardiac; cardiovascular disorder; Niemann-Pick's disease;
 KW lipid disorder; fatty liver; Gaucher's disease; myocardial infarction;
 KW drug screening; transgenic animal; antiinflammatory; hepatotropic;
 KW hypotensive; anti-HIV; enzyme; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CDS 239..1267
 FT /*tag= a
 FT /product= "Human PKIN-10"
 XX
 FN WO200208399-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 20-JUL-2001; 2001WO-US023092.
 XX
 PR 21-JUL-2000; 2000US-0220038P.
 PR 28-JUL-2000; 2000US-022112P.
 PR 04-AUG-2000; 2000US-0222831P.
 PR 11-AUG-2000; 2000US-0224729P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 PA (THOR/) THORNTON M.
 XX
 PI Thornton M, Yue H, Khan FA, Gururajan R, Hafalia AJA, Wallia NK;
 PI Patterson C, Rankumar J, Gandhi AR, Policky JL, Baughn MR;
 PI Tribouley CM, Nguyen DB, Lu Y, Burford N, Lai P, Ding L;
 PI Yao MG, Elliott VS, Recipon SA, Kearney L, Lu DAM, Greenwald SR;
 PI Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL;
 XX
 DR WPI; 2002-206083/26.
 DR P-PSDB; AAE19152.
 XX
 PT New human kinase polypeptide, useful in diagnosis, prevention and

PT treatment of cancer, immune disorder, growth and developmental disorder,
 XX cardiovascular disorder and lipid disorder.
 PS Claim 5; Page 183; 196pp; English.
 XX

CC The present invention relates to an isolated human kinase polypeptide
 CC (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is
 CC useful for diagnosing, treating and preventing cancer (e.g., leukemia,
 CC lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency
 CC syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's
 CC disease, rheumatoid arthritis), a growth and developmental disorder (e.g.
 CC buritis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a
 CC cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial
 CC infarction), and a lipid disorder (e.g., fatty liver, cholestasis,
 CC Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of
 CC drug screening techniques and to analyse the proteome of a tissue or cell
 CC type. PKIN is useful for creating knockin humanised animals or transgenic
 CC animals to model human diseases, in somatic or germline gene therapy, to
 CC generate a transcript image of a tissue or cell type, for detecting
 CC differences in the chromosomal location due to translocation, inversion,
 CC etc., among normal, carrier or affected individuals, and as hybridisation
 CC probes for mapping naturally occurring genomic sequences. PKIN is useful
 CC in southern or northern analysis, dot blot or other membrane-based
 CC technologies, in PCR technologies, in dipstick, pin, multifomat enzyme
 CC linked immunosorbent (ELISA)-like assays and in microarrays utilising
 CC fluids or tissues from patients to detect altered PKIN expression. The
 CC present sequence is human PKIN-10 cDNA

XX Sequence 1790 BP; 581 A; 328 C; 366 G; 515 T; 0 U; 0 Other;

Query Match 78.9%; Score 821; DB 6; Length 1790;
 Best Local Similarity 90.6%; Pred. No. 7.4e-209;
 Matches 927; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

QY 1 ATGGAAGAATGATGAAATAGCTAAGCTGGAGAGGGCTTATGGGTGTTATTTCAA 60
 DB 239 ATGGAAGAATGAAATAGCTAAGCTGGAGAGGGCTTATGGGTGTTATTTCAA 298
 QY 61 TGCAGAACAAACCTCTGGCAAGTAGTAGCTTTAAAAAATTTGGGAATCTGAAGAT 120
 DB 299 TGCAGAACAAACCTCTGGCAAGTAGTAGCTTTAAAAAATTTGGGAATCTGAAGAT 358
 QY 121 GATCCTGTTGTAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACAAT 180
 DB 359 GATCCTGTTGTAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACAAT 418
 QY 181 CCAATCTCTGGAACCTCATCGAGTCTTCAGGAGAAAGAAAGAAATGCAATTTAGTTTT 240
 DB 419 CCAATCTCTGGAACCTCATCGAGTCTTCAGGAGAAAGAAAGAAATGCAATTTAGTTTT 478
 QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATGAGGTTGCTGAT 300
 DB 479 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATGAGGTTGCTGAT 538
 QY 301 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAAATTCCTGATATACAT 360
 DB 539 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAAATTCCTGATATACAT 598
 QY 361 AACTGTATTCCACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGCAATATC 420
 DB 599 AACTGTATTCCACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGCAATATC 658
 QY 421 AGAATTTGCACTTCGGGTTTGGCAAAATCTGATTTCCAGGAGATGCTACACCGATTAT 480
 DB 659 AGAATTTGCACTTCGGGTTTGGCAAAATCTGATTTCCAGGAGATGCTACACCGATTAT 718
 QY 481 GTAGCTACGAGATGGTACCGAGCTCTGAACTTCTTGTGGGATACCTAGTATGTTCT 540
 DB 719 GTAGCTACGAGATGGTACCGAGCTCTGAACTTCTTGTGGGATACCTAGTATGTTCT 778
 QY 541 TCAGTCGATATATGGGCTATTGTTGTTGTTTTTGCAGAGCTCTCTGACAGCCAGCCACTG 600
 DB 779 TCAGTCGATATATGGGCTATTGTTGTTGTTTTTGCAGAGCTCTCTGACAGCCAGCCACTG 838

QY 601 TGGCCTCGAAAATCAGATGTGGACCAACTTTATCTGATATATCAGAAACACTAGTAGAGAGC 660
 DB 839 TGGCCTCGAAAATCAGATGTGGACCAACTTTATCTGATATATCAGAAACACTAGTAGAGAGC 888
 QY 661 GGGTTTCGCCATGTTGACCAAGGCTGGTCTCGAACTCTTTGACGTCAAGTGATCCACCTGCC 720
 DB 889 ----- 888
 QY 721 GTAGCCTCTCAAAAGTGTGGAATTTACAGGAAAATTAATCCCAAGACATCAATCAATCTTT 780
 DB 889 -----AGGAAAATTAATCCCAAGACATCAATCAATCTTT 922
 QY 781 AAAAGTAAACGGGTTTTTCCATGGCAGTCACTATACCTGAGCAGAGACATGGAACCTTT 840
 DB 923 AAAAGTAAACGGGTTTTTCCATGGCAGTCACTATACCTGAGCAGAGACATGGAACCTTT 982
 QY 841 GAGGAAAAGTTCTCAGATGTTTCATCTCTGGCTCTGAACTTTCATGAAGGGGTGTCTGAAG 900
 DB 983 GAGGAAAAGTTCTCAGATGTTTCATCTCTGGCTCTGAACTTTCATGAAGGGGTGTCTGAAG 1042
 QY 901 ATGAATCCAGATGACAGATTAACCTGTTCCAACTCTCTGGAGAGCTCTACTTTGATCT 960
 DB 1043 ATGAATCCAGATGACAGATTAACCTGTTCCAACTCTCTGGAGAGCTCTACTTTGATCT 1102
 QY 961 TTTCAAGAGGCCCAAAATTAAGAGAAAAGCAAGCTTAATGAAGGAAAGAAACAGAGCCCAA 1020
 DB 1103 TTTCAAGAGGCCCAAAATTAAGAGAAAAGCAAGCTTAATGAAGGAAAGAAACAGAGCCCAA 1162
 QY 1021 CAG 1023
 DB 1163 CAG 1165
 RESULT 6
 ABX08936
 ID ABX08936 standard; cDNA; 1678 BP.
 XX AC ABX08936;
 XX DT 21-JAN-2003 (first entry)
 XX DE cDNA encoding human DITHP protein #6.
 KW Human; ss; gene; diagnostic and therapeutic; DITHP; cancer;
 KW arteriosclerosis atherosclerosis; psoriasis; asthma; autoimmune thyroiditis;
 KW autoimmune; inflammatory; anaemia; diabetes mellitus; glomerulonephritis; gout; stroke;
 KW Crohn's disease; rheumatoid arthritis; uveitis; AIDS; allergy;
 KW multiple sclerosis; acquired immunodeficiency disease; neurological disorder; epilepsy;
 KW Alzheimer's disease; dementia; mental retardation; gastrointestinal;
 KW Parkinson's disease; ulcer; cirrhosis; reproductive; infertility;
 KW endometriosis; endocrine disorder; hyperparathyroidism; hyperlipidemia;
 KW hypercholesterolaemia; hypoglycaemia; obesity; Reiter's syndrome;
 KW connective tissue disorder; osteoporosis; infection.
 XX OS Homo sapiens.
 XX WO200279473-A2.
 XX PD 10-OCT-2002.
 XX PF 09-JAN-2002; 2002WO-US001009.
 XX PR 12-JAN-2001; 2001US-0261622P.
 XX PR 16-JAN-2001; 2001US-0261864P.
 XX PR 16-JAN-2001; 2001US-0261865P.
 XX PR 17-JAN-2001; 2001US-0262164P.
 XX PR 17-JAN-2001; 2001US-0262207P.
 XX PR 17-JAN-2001; 2001US-0262208P.
 XX PR 17-JAN-2001; 2001US-0262209P.
 XX PR 17-JAN-2001; 2001US-0262215P.
 XX PR 18-JAN-2001; 2001US-0262102P.

PR 19-JAN-2001; 2001US-0262599P.
 PR 19-JAN-2001; 2001US-0262662P.
 PR 19-JAN-2001; 2001US-0262760P.
 PR 19-JAN-2001; 2001US-0263063P.
 PR 19-JAN-2001; 2001US-0263064P.
 PR 19-JAN-2001; 2001US-0263065P.
 PR 19-JAN-2001; 2001US-0263068P.
 PR 19-JAN-2001; 2001US-0263077P.
 PR 19-JAN-2001; 2001US-0263329P.
 PR 19-JAN-2001; 2001US-0263330P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX Panzer SR, Lincoln SE, Altus CM, Dufour GE, Hillman JL, Jones AL;
 PI Dam TC, Liu TF, Harris B, Flores V, Daffo A, Marwaha R, Chen NJ;
 PI Chang SC, Gerstein EH, Peralta CH, David MH, Lewis SA;
 XX WPI; 2003-040680/03.
 DR P-PSDB; ABU05290.
 XX
 XX New human diagnostic and therapeutic (DTHP) polynucleotides and
 PT polypeptides, useful for diagnosing, preventing or treating diseases,
 PT e.g. cancer, AIDS, Parkinson's disease, or autoimmune/inflammatory
 PT diseases.
 XX
 XX Claim 1; Page 267; 331pp; English.
 PS
 XX This invention relates to the cDNA and protein sequences of fifty six
 CC polynucleotides for diagnostics and therapeutics (DTHP). The human DTHP
 CC polynucleotides and polypeptides are useful for diagnosing, preventing or
 CC treating diseases associated with, as well as effects of exogenous
 CC compounds, on the expression of human molecules, such as cell
 CC proliferative diseases (e.g. cancer, arteriosclerosis, atherosclerosis,
 CC psoriasis, primary thrombocytopenia), autoimmune/inflammatory diseases
 CC (e.g. anaemia, asthma, autoimmune thyroiditis, Crohn's disease, diabetes
 CC mellitus, glomerulonephritis, gout, multiple sclerosis, rheumatoid
 CC arthritis, uveitis, acquired immunodeficiency disease; AIDS; allergies;
 CC neurological disorders (e.g. stroke, Alzheimer's disease, dementia,
 CC mental retardation, Parkinson's disease, epilepsy), gastrointestinal
 CC (e.g. ulcer, cirrhosis), reproductive (e.g. infertility, endometriosis),
 CC endocrine disorders (e.g. hyperparathyroidism, hypercholesterolaemia,
 CC hypoglycaemia, hyperlipidemia, obesity), connective tissue disorders
 CC (e.g. osteoporosis, Reiter's syndrome), or infections (e.g. bacterial,
 CC viral, fungal, parasitic, protozoal). The DTHP sequences may be used to
 CC generate hybridisation probes useful in chromosomal mapping of naturally
 CC occurring genomic sequences. They are also useful in designing probes
 CC useful in diagnostic assays. The polynucleotides are useful as molecular
 CC weight markers, or as antigen to elicit an immune response. The present
 CC sequence represents a human diagnostics and therapeutics (DTHP) cDNA
 CC sequence of the invention
 XX
 SQ Sequence 1678 BP; 541 A; 308 C; 336 G; 493 T; 0 U; 0 Other;
 Query Match 73.3%; Score 762.8; DB 10; Length 1678;
 Best Local Similarity 90.0%; Pred. No. 2.6e-193;
 Matches 925; Conservative 0; Mismatches 2; Indels 101; Gaps 6;
 QY 1 ATGGAAAGTATGAAAAATTAGCTTAAGACTGGAGAGGGCTTATGGGGTTGATTCAA 60
 DB 131 ATGGAGAGTATGAAAAATTAGCTTAAGACTGGAGAGGGCTTATGGGGTTGATTCAA 190
 QY 61 TGCAGA-AACAAAACCTCTGCGAAGTAGTAGCTGTTTAAAAAAATTTCTGGAATCTGAAGA 119
 DB 191 TGCAGATAACAAAACCTCTGCGAAGTAGTAGCTGTTTAAAAAAATTTCTGGAATCTGAAGA 250
 QY 120 TGATCTCTGTTTGAAGAAATAGACACTAAGAGAAATACGTA-TGTTGAACCAATTAAC 178
 DB 251 TGATCTCTGTTTGAAGAAATAGACACTAAGAGAAATACGTA-TGTTGAACCAATTAAC 310
 QY 179 ATCCAAATCTTGAAACCTCATCAGGTGTTTCAGGAGAAAAAGAAATGCAATTTAGTTT 238
 DB 311 ATCCAAATCTTGTAACCTCATCAGGTGTTTCAGGAGAAAAAGAAATGCAATTTAGTTT 370

QY 239 TTGAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTG 298
 DB 371 TTGAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTG 430
 QY 299 ATGGAGTGAATAAAGCGTATTATGCGAACACACTTCAAGCTCTTAAATTTCTGTCTATATAC 358
 DB 431 ATGGAGTGAATAAAGCGTATTATGCGAACACACTTCAAGCTCTTAAATTTCTGTCTATATAC 490
 QY 359 ATAACCTGTATTTCACAGAGATATAAAACCTGAAATATTTCTAAATACTAAACAGGAATAA 418
 DB 491 ATAACCTGTATTTCACAGAGATATAAAACCTGAAATATTTCTAAATACTAAACAGGAATAA 550
 QY 419 TCAAGATTTGTGACTTCGGGTTTGCACAAATTTCTGATTCAGGAGATGCCTACACCGATT 478
 DB 551 TCAAGATTTGTGACTTCGGGTTTGCACAAATTTCTGATTCAGGAGATGCCTACACCGATT 610
 QY 479 ATGTAGCTA-CGAGATGGTACCAGCT-CCTGAACTTCTTGTGGGAGATACT-CAGTATG 535
 DB 611 ATGTAGCTAGGAGATGGTACCAGCTCCTGAACTTCTTGTGGGAGATACTCCAGTATG 670
 QY 536 GTTCTTCAGTCGATATATGGGCTATTGGTGTGTTTTGCGAGAGCTCCTGACAGGCCAGC 595
 DB 671 GTTCTTCAGTCGATATATGGGCTATTGGTGTGTTTTGCGAGAGCTCCTGACAGGCCAGC 730
 QY 596 CACTGTGGCCTGAAATCAGATGTGGACCACTTTATCTGTATTAATCAGAACACTAGTAG 655
 DB 731 CACTGTGGCCTGAAATCAGATGTGGACCACTTTATCTGTATTAATCAGAACACT----- 785
 QY 656 AGACGGGGTTTGGCCATGTTGACAGGCTGGTCTCGAACTCTTGACGCTCAAGTGATCCAC 715
 DB 786 ----- 785
 QY 716 CTGCGCTAGCCTCTCAAAGTGTGGAATTAACAGGAAATTAATCCCAAGACATCAATCAA 775
 DB 786 -----AGGAAATTAATCCCAAGACATCAATCAA 814
 QY 776 TCTTTAAAGTAACGGGTTTTTCATGGGATCAGTATACCTGAGCCAGAGACATGAGAA 835
 DB 815 TCTTTAAAGTAACGGGTTTTTCATGGGATCAGTATACCTGAGCCAGAGACATGAGAA 874
 QY 836 CTCTGAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTCATGAAGGGGTGTC 895
 DB 875 CTCTGAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTCATGAAGGGGTGTC 934
 QY 896 TGAAGATGAATCCAGATGACAGATTAACCTGTTTCCCAACTCCTGGAGAGCTCCTTACTTTG 955
 DB 935 TGAAGATGAATCCAGATGACAGATTAACCTGTTTCCCAACTCCTGGAGAGCTCCTTACTTTG 994
 QY 956 ATTCTTTTCAAGAGGCCCAATTAAGAAAGAAAGACAGTATGAAGGAAAGAAACAGAGAC 1015
 DB 995 ATTCTTTTCAAGAGGCCCAATTAAGAAAGAAAGACAGTATGAAGGAAAGAAACAGAGAC 1054
 QY 1016 GCCAACAG 1023
 DB 1055 GCCAACAG 1062
 RESULT 7
 AAS06725
 ID AAS06725 standard; cDNA; 1083 BP.
 XX
 AC AAS06725;
 XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Polynucleotide sequence encoding human protein kinase #25.
 XX
 KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
 KW metabolic disorder; immune related disease; neurological disorder;
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;
 KW reproductive disorder; gene therapy; sa.
 XX
 OS Homo sapiens.

XX W0200123579-A1.
 XX 05-APR-2001.
 XX 27-SEP-2000; 2000WO-US026621.
 XX 28-SEP-1999; 99US-0156511P.
 XX (LEXI-) LEXICON GENETICS INC.
 XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
 PI Sands AT;
 XX
 DR WPI; 2001-266166/27.
 DR P-PSDB; AAE00490.
 XX
 XX New isolated human kinase polynucleotide useful for generating
 PT antibodies, as reagents in diagnostic assays and for screening for
 PT compounds useful for treating mental, biological or medical diseases.
 XX
 PS Disclosure; Page 34-35; 38pp; English.
 XX
 CC The present sequence encodes a novel human protein (NHP) which is a human
 CC kinase. A polymorphism was identified in the 3' UTR of the present
 CC sequence. The human kinases share structural similarity with animal
 CC kinases, more particularly serine or threonine protein kinases. Human
 CC kinase cDNA is useful for the detection of mutant human kinase for the
 CC diagnosis of disease, and also as a therapeutic. It is useful for
 CC screening drugs effective in the treatment of symptomatic or phenotypic
 CC manifestations perturbing the normal function of NHP in the body. The NHP
 CC nucleotide sequences are useful for generation of antibodies, as reagents
 CC in diagnostic assays, for the identification of other cellular gene
 CC products related to human kinases, and as reagents in assays for
 CC screening compounds that are useful for treating mental, biological or
 CC medical disorders. NHP oligonucleotides are used as probes. The labelled
 CC NHP probes are useful for screening human genomic library for identifying
 CC polymorphisms and as primers in amplification assays to detect mutations
 CC within the exons, introns and splice sites that can be used in
 CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP
 CC products are used to genetically engineer cells in vivo that functions as
 CC bioreactors in the body delivering a continuous supply of NHP to the
 CC body. Nucleotide constructs encoding functional NHPs are used in gene
 CC therapy for the modulation of NHP expression
 XX
 SQ Sequence 1819 BP; 539 A; 368 C; 406 G; 505 T; 0 U; 1 Other;
 Query Match 68.1%; Score 709; DB 4; Length 1819;
 Best Local Similarity 77.0%; Pred. No. 6.2e-179;
 Matches 1025; Conservative 0; Mismatches 0; Indels 306; Gaps 1;
 QY 1 ATGGAAGATGATGAAAAATTAGCTAAGACTGGAGAGGGCTTATGGGGTTGTTATCAAA 60
 DB 138 ATGGAAGATGATGAAAAATTAGCTAAGACTGGAGAGGGCTTATGGGGTTGTTATCAAA 197
 QY 61 TGCAGAAACAAACCTCTGGAACAAGTAGTAGCTGTTAAAAAAATTTGGAAATCTGAAGAT 120
 DB 198 TGCAGAAACAAACCTCTGGAACAAGTAGTAGCTGTTAAAAAAATTTGGAAATCTGAAGAT 257
 QY 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAAGACAT 180
 DB 258 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAAGACAT 317
 QY 181 CCAAACTCTGTGAACCTCATCGAGGTGTTACAGGAGAAAAAGGAAAAATGCAATTTAGTTT 240
 DB 318 CCAAACTCTGTGAACCTCATCGAGGTGTTACAGGAGAAAAAGGAAAAATGCAATTTAGTTT 377
 QY 241 GAATACCTGTGATCATATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300
 DB 378 GAATACCTGTGATCATATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 437
 QY 301 GGAGTGATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAATTTCTGTCTATATACAT 360

DB 438 GGAGTGATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAATTTCTGTCTATATACAT 497
 QY 361 AACTGTATTACAGAGATATAAAACCTGAAATAATTTCTAATACTAAGCAAGGAATATC 420
 DB 498 AACTGTATTACAGAGATATAAAACCTGAAATAATTTCTAATACTAAGCAAGGAATATC 557
 QY 421 AAGATTTGTGACTTCGGGTTTGGACAAATCTG----- 453
 DB 558 AAGATTTGTGACTTCGGGTTTGGACAAATCTGAGTTGGAATTCATCTTTCTCTGGTGCC 617
 QY 454 ----- 453
 DB 618 TCCTTGATTGGCTTAATAGTTGACCTTCTGAAATTTCTTTTCTGCCAATTCAGAGATTTT 677
 QY 454 ----- 453
 DB 678 CTCCTGGCTTGGATCCATTGCTGACACAGATGTTTCCACATGGGGCCAGGCTCATCTCGA 737
 QY 454 ----- 453
 DB 738 ACTTCTGGCCTCAAGTGATCCTTCCACCTCGGCCTCCAAAGTGCTGGATTGCAAGTGTG 797
 QY 454 ----- 453
 DB 798 AGCCACCGTCCCGCAGCCAGATTTTCAAACAAATACTACTGAGAGCTCAACAAGATTGTT 857
 QY 454 -----ATTCCAGGAGATGCTTACAC 474
 DB 858 TTAGTGGGAACACAAATTTTCGAACAAATTTCTTGAGAACGCATTCAGGAGATGCTTACAC 917
 QY 475 GATTATGTAGTACGAGATGGTACCGAGCTCTCGAACTTCTTGTGGGAGATACACTAGTAT 534
 DB 918 GATTATGTAGTACGAGATGGTACCGAGCTCTCGAACTTCTTGTGGGAGATACACTAGTAT 977
 QY 535 GGTTCCTTCAGTCATATATGGGCTATTGGTGTGTTTTTGACAGAGCTCTTGACAGGCGAG 594
 DB 978 GGTTCCTTCAGTCATATATGGGCTATTGGTGTGTTTTTGACAGAGCTCTTGACAGGCGAG 1037
 QY 595 CCACTGTGGCTGGAAATCAGATGTGGACCAACTTTTATCTGATAATCAGAACTAGTA 654
 DB 1038 CCACTGTGGCTGGAAATCAGATGTGGACCAACTTTTATCTGATAATCAGAACTAGTA 1097
 QY 655 GAGACGGGTTTGGCCATGTTGACAGGCTGTTCTGAACTCTTGACGTCAAGTGATCCA 714
 DB 1098 GAGACGGGTTTGGCCATGTTGACAGGCTGTTCTGAACTCTTGACGTCAAGTGATCCA 1157
 QY 715 CCTGCGGTAGCTCTCAAGTGTGGAAATTTACAGGAAAAATTAATCCCAAGACATCAATCA 774
 DB 1158 CCTGCGGTAGCTCTCAAGTGTGGAAATTTACAGGAAAAATTAATCCCAAGACATCAATCA 1217
 QY 775 ATCTTTAAAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGA 834
 DB 1218 ATCTTTAAAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGA 1277
 QY 835 ACTCTTGAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTCTGAAAGGGTGT 894
 DB 1278 ACTCTTGAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTCTGAAAGGGTGT 1337
 QY 895 CTGAAGATGAATCCAGATGACAGATTAACTGTTTCCCACTCTCTGGAGAGCTCTCTACTTT 954
 DB 1338 CTGAAGATGAATCCAGATGACAGATTAACTGTTTCCCACTCTCTGGAGAGCTCTCTACTTT 1397
 QY 955 GATTCTTTTCAAGAGGCCCAAAATTAAGAAAAAGCAGCTAATGAAGGAAAGAAACAGAGA 1014
 DB 1398 GATTCTTTTCAAGAGGCCCAAAATTAAGAAAAAGCAGCTAATGAAGGAAAGAAACAGAGA 1457
 QY 1015 CGCCAAACAGGT 1025
 DB 1458 CGCCAAACAGGT 1468

ADK71927 standard; cDNA; 1266 BP.
ADK71927;
20-MAY-2004 (first entry)
Human kinase and phosphatase KPP-45 cDNA.
human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic;
hypotensive; vasotropic; antiinflammatory; antiangiinal; anti-HIV;
antiallergic; antiasthmatic; immunosuppressive; antichyroid;
dermatologic; antidiabetic; nephrotropic; antitumor; gastrointestinal;
neuroprotective; osteopathic; antirheumatic; antiparkinsonian; anticonvulsant; hepatotropic;
antirheumatic; antiparkinsonian; anticonvulsant; antiparasitic;
antihelminthic; antibacterial; virucide; protozoacide; fungicide;
cardiovascular disease; immune system; neurological; growth; development;
cell proliferation; viral; bacterial; fungal; parasitic; protozoan;
helminthic infection; transgenic; gene therapy; ss; gene.
Homo sapiens.
WO2004018641-A2.
04-MAR-2004.
25-AUG-2003; 2003WO-US026635.
26-AUG-2002; 2002US-0406172P.
25-SEP-2002; 2002US-0413910P.
27-SEP-2002; 2002US-0414296P.
11-OCT-2002; 2002US-0417821P.
(INCY-) INCYTE CORP.
Baughn MR, Richardson TW, Marquis JP, Swarnakar A, Tang YT;
Becha SD, Emerling BM, Jin P, Wilson AD, Yue H, Gietzen KJ;
Chang H, Yang YG, Lee SY, Khare R, Elliott VS, Hafalia AJA;
Chawla NK, Ramkumar J, Gururajan R, Tribouley CM, Chien D, Tran UK;
Murage J;
WPI; 2004-226830/21.
P-PSDB; ADK71968.
New human kinases and phosphatases, useful for diagnosing, treating or
preventing atherosclerosis, hypertension, AIDS, allergy, multiple
sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
or hepatitis.
Claim 5; SEQ ID NO 104; 347pp; English.
The invention relates to a novel isolated polypeptide which is a human
kinase and phosphatase (KPP). The polypeptide of the invention
demonstrates cardiovascular, antiarteriosclerotic, hypotensive,
vasotropic, antiinflammatory, antiangiinal, anti-HIV, antiallergic,
antisthmatic, immunosuppressive, antichyroid, dermatological,
antidiabetic, nephrotropic, antitumor, gastrointestinal, neuroprotective,
osteopathic, antirheumatic, antiparkinsonian, anticonvulsant, antiparasitic,
antihelminthic, antibacterial, virucide, protozoacide and fungicide activities. The
kinase and phosphatase (KPP) polynucleotides, polypeptides, agonists and
antagonists may be useful for diagnosing, treating or preventing
disorders such as cardiovascular diseases, immune system disorders,
neurological disorders, disorders affecting growth and development, cell
proliferative disorders and viral, bacterial, fungal, parasitic, cell
protozoan or helminthic infections. Furthermore, the molecules of the
invention may be useful for creating transgenic animals to model human
disease and during gene therapy. The current sequence is that of a human
KPP cDNA of the invention.
Sequence 1266 BP; 414 A; 234 C; 254 G; 364 T; 0 U; 0 Other;

Query Match 67.4%; Score 702; DB 12; Length 1266;
Best Local Similarity 81.9%; Pred. No. 4e-177;
Matches 927; Conservative 0; Mismatches 0; Indels 205; Gaps 2;
QY 1 ATGAAAAGTATGAAAAATTTAGCTTAAGCTGGAAGAGGGTCTTATGGGGTGTGATTTCAAA 60
DB 54 ATGAAAAGTATGAAAAATTTAGCTTAAGCTGGAAGAGGGTCTTATGGGGTGTGATTTCAAA 113
QY 61 TGCAGAAAACCACTCTGCAAGTAGTAGCTGTTAAAAAATTTGGAATCTGAAGAT 120
DB 114 TGCAGAAAACCACTCTGCAAGTAGTAGCTGTTAAAAAATTTGGAATCTGAAGAT 173
QY 121 GATCCTGTTCTTAAGAAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACAT 180
DB 174 GATCCTGTTCTTAAGAAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACAT 233
QY 181 CCAAAATCTTGTGAACCTCATCGAGGTGTTCCAGGAGAAAAGGAAAATGCAATTTAGTTTTT 240
DB 234 CCAAAATCTTGTGAACCTCATCGAGGTGTTCCAGGAGAAAAGGAAAATGCAATTTAGTTTTT 293
QY 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGGTGCTGAT 300
DB 294 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGGTGCTGAT 353
QY 301 GGAGTGATCAAAAAGCGTATTATGCGCAACACTTTCAAGCTCTTAATTTCTGTCTATATACAT 360
DB 354 GGAGTGATCAAAAAGCGTATTATGCGCAACACTTTCAAGCTCTTAATTTCTGTCTATATACAT 413
QY 361 AACTGTATTACAGAGATATATAAACCCTGAAAATATTCTTAATACTAAGCAAGAAATAATC 420
DB 414 AACTGTATTACAGAGATATATAAACCCTGAAAATATTCTTAATACTAAGCAAGAAATAATC 473
QY 421 AGATTTGTGACTTTCCGGTTCGCAAAATTTCTGA----- 454
DB 474 AGATTTGTGACTTTCCGGTTCGCAAAATTTCTGA----- 533
QY 455 ----- 454
DB 534 TCCTTGATTGGCTTAATAGTTGACCTTCTGAATTTCTTTTCTGCCAATTCAGAGATTTTC 593
QY 455 -----TTCAGAGAGATGCTACCCGATTTATGTAGTACGAG 491
DB 594 TCCTTGCTTGGATCATTTGCTGTTCCAGGAGATGCTACACCGATTATGTAGTACGAG 653
QY 492 ATGTGACCCAGCTCCTGAACTTCTTGTGGGAGATCTCAGTATGTTCTTCAGTCCGATAT 551
DB 654 ATGTGACCCAGCTCCTGAACTTCTTGTGGGAGATCTCAGTATGTTCTTCAGTCCGATAT 713
QY 552 ATGGGCTATTGGTGTGTTTTTTCAGAGCTCTCTGACAGGCCAGCCACTGTGGCTCGAAA 611
DB 714 ATGGGCTATTGGTGTGTTTTTTCAGAGCTCTCTGACAGGCCAGCCACTGTGGCTCGAAA 773
QY 612 ATCAGATGTGGACCAACTTTATCTGATATCAAGACACTAGTAGAGACGGGGTTTCGCCA 671
DB 774 ATCAGATGTGGACCAACTTTATCTGATATCAAGACACT----- 812
QY 672 TGTGTGACCCAGGCTGGTCTCGAACTCTTTCAGCTCAAGTGATCCAGCTGCGTAGCTCTCA 731
DB 813 ----- 812
QY 732 AAGTGTGGAATTAACAGAAAATTAATCCAAAGACATCAATCAATCTTTTAAAGTAACGG 791
DB 813 -----AGGAAAATTAATCCAAAGACATCAATCAATCTTTTAAAGTAACGG 857
QY 792 GTTTTTCATGTCATCAGTATACCTGAGCCAGACATGGAACCTTTGAGAAAAGTT 851
DB 858 GTTTTTCATGTCATCAGTATACCTGAGCCAGACATGGAACCTTTGAGAAAAGTT 917
QY 852 CTCAGATGTTTCATCTCTGCGCTCTCAACTTTCATGAAGGGGTCTCTGAAGATCAATCCAGA 911
DB 918 CTCAGATGTTTCATCTCTGCGCTCTCAACTTTCATGAAGGGGTCTCTGAAGATCAATCCAGA 977
QY 912 TCAGAGATTAACCTGTTCCAACTCTCTGAGAGCTCTCACTTTTGTGATTTCTTTTCAAGAGCG 971

Db 978 TGACAGATTAACTGGTCCCAACTCTCGGAGAGCTCTTACTTTGATTCTTTTCAAGAGGC 1037
 Qy 972 CCAAAATTAAGAAAGACACGCTATGAGGAGAAAGAAACAGAGAGCCCAACAG 1023
 Db 1038 CCAAAATTAAGAAAGACACGCTATGAGGAGAAAGAAACAGAGAGCCCAACAG 1089

RESULT 10
 AAI64248
 ID AAI64248 standard; cDNA; 882 BP.
 XX
 AC AAI64248;
 XX
 DT 08-MAR-2002 (first entry)
 XX
 DE Human kinase 14257 cDNA.
 XX

Protein kinase; enzyme; cytosolic; osteopathic; hepatotropic;
 anti-diabetic; neuroprotective; antiarthritic; dermatological;
 immunosuppressive; anti-inflammatory; antithyroid; antipsoriatic;
 ophthalmological; antiallergic; antiasthmatic; antiatherosclerotic;
 hypotensive; vasotrophic; antiarrhythmic; virucide; anorectic; metabolic;
 immunomodulator; analgesic; cellular proliferative disorder; cancer;
 acute lymphoblastic leukaemia; Hodgkin's disease;
 bone metabolism disorder; osteoporosis; immune system disorder;
 inflammatory; diabetes mellitus; osteoarthritis; asthma;
 cardiovascular disorder; hypertension; coronary artery disease;
 endothelial cell disorder; psoriasis; ss.
 XX
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 FH 5'UTR 1..128
 FT /*tag= a
 FT 129..815
 FT /*tag= b
 FT /*product= "Protein kinase 14275"
 FT 816..882
 FT /*tag= c
 XX
 PN W0200179488-A2.
 XX
 PD 25-OCT-2001.
 XX
 PF 13-APR-2001; 2001WO-US012188.
 XX
 PR 13-APR-2000; 2000US-0196910P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Kapeller-Libermann R;
 XX
 PS WPI; 2002-034355/04.
 DR P-PSDB; AAG78547.
 XX

New 14257 polypeptides (protein kinases), useful as diagnostic targets
 and therapeutic agents for controlling cellular proliferative and/or
 differentiative disorder, bone disorders, immune disorders and
 cardiovascular disorders.
 XX
 PS Claim 2; Fig 1A; 98pp; English.
 XX

The invention relates to an isolated 14257 polypeptide and nucleic acid
 encoding it. The 14257 protein is a protein kinase that acts as a
 modulating agent in regulating a variety of cellular processes, including
 cell proliferation, differentiation, growth and division. The activity of
 the protein of the invention may be described as; cytosolic; osteopathic
 ; hepatotropic; antidiabetic; neuroprotective; antiarthritic;
 dermatological; immunosuppressive; anti-inflammatory; antithyroid;
 antipsoriatic; ophthalmological; antiallergic; antiasthmatic;
 antiatherosclerotic; hypotensive; vasotropic; antiarrhythmic; virucide;
 anorectic; metabolic; immunomodulator and analgesic. The protein of the

CC invention may act as a novel diagnostic target or therapeutic agent
 CC controlling certain disorders, for example kinase-associated or other
 CC 14257-associated disorders. These may include cellular proliferative
 CC disorders such as cancers e.g. acute lymphoblastic leukemia or Hodgkin's
 CC disease. Other disorders include bone metabolism disorders such as
 CC osteoporosis, disorders of the immune system, e.g. inflammatory,
 CC diabetes mellitus, osteoarthritis and asthma. Proteins of the invention
 CC may also be of use as therapeutic agents in cardiovascular disorders such
 CC as hypertension and coronary artery disease, and some endothelial cell
 CC disorders, including psoriasis. The current sequence represents a human
 CC kinase 14257 cDNA
 XX
 SQ Sequence 882 BP; 288 A; 150 C; 198 G; 245 T; 0 U; 1 Other;
 Query Match 61.9%; Score 644; DB 6; Length 882;
 Best Local Similarity 99.2%; Pred. No. 1.le-161;
 Matches 647; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATCGAAAGTATGAAATTTAGCTGAGCTGGAGAGGCTCTTATGGGTTGTATTCAAA 60
 Db 129 ATGGGAAAGTATGAAATTTAGCTGAGCTGGAGAGGCTCTTATGGGTTGTATTCAAA 188
 Qy 61 TGCAGAAACAAACCTCTCGACAAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
 Db 189 TGCAGAAACAAACCTCTCGACABGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 248
 Qy 121 GATCCTGTTTAAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
 Db 249 GATCCTATTGTTAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 308
 Qy 181 CCAATCTTGTGAACCTCATCGAGGTGTTTCAGAGAGAAAGAAATGCAATTTAGTTTTT 240
 Db 309 CCAATCTTGTGAACCTCATCGAGGTGTTTCAGAGAGAAAGAAATGCAATTTAGTTTTT 368
 Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 300
 Db 369 GAATCTGTGATCATGCACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 428
 Qy 301 GGAGTGATCAAAAGCGTATTTATGCGCAAACTTCAAGCTCTTAAATTTCTGTCATATACAT 360
 Db 429 GGAGTGATCAAAAGCGTATTTATGCGCAAACTTCAAGCTCTTAAATTTCTGTCATATACAT 488
 Qy 361 AACTGTATTCACAGAGATATAAAACCTGAAAAATTTCTTAATACTAAGCAAGGATATTC 420
 Db 489 AACTGTATTCACAGAGATATAAAACCTGAAAAATTTCTTAATACTAAGCAAGGATATTC 548
 Qy 421 AAGATTGTGACTTCGGGTTTGACAAATTTCTGATCCAGAGATGCTTACACCGATTAT 480
 Db 549 AAGATTGTGACTTCGGGTTTGACAAATTTCTGATCCAGAGATGCTTACACCGATTAT 608
 Qy 481 GTAGCTACGAGATGGTACCGAGCTCCTGAACTTTTGTGGGAGATACCTCAGTATGTTCT 540
 Db 609 GTAGCTACGAGATGGTACCGAGCTCCTGAACTTTTGTGGGAGATACCTCAGTATGTTCT 668
 Qy 541 TCAGTCGATATATGGGCTATTTGTTGTTTTTTCAGAGCTCCTGACAGGCCAGCCACTG 600
 Db 669 TCAGTCGATATATGGGCTATTTGTTGTTTTTTCAGAGCTCCTGACAGGCCAGCCACTG 728
 Qy 601 TGGCCTGGAAAAATCAGATGAGGACCACTTTTATCTGATAATCAGAACACTAG 652
 Db 729 TGGCCTGGAAAAATCAGATGAGGACCACTTTTATCTGATAATCAGAACACTAG 780

RESULT 11
 ADI40928
 ID ADI40928 standard; cDNA; 1429 BP.
 XX
 AC ADI40928;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Human kinase and phosphatase KPP-41 encoding cDNA SEQ ID NO:94.
 XX

human; kinase and phosphatase, KPP; enzyme; cardiovascular; antiarteriosclerotic; hypotensive; vasotropic; antiinflammatory; antiangiogenic; anti-allergic; antiasthmatic; immunosuppressive; anti-HIV; antitubercular; antidiabetic; nephrotropic; antitumor; dermatologic; antidiabetic; osteopathic; antitumor; gastrointestinal; neuroprotective; osteopathic; antiarthritic; uropathic; ophthalmological; antirheumatic; antiparkinsonian; nootropic; anticonvulsant; hepatotropic; CNS; antiparasitic; haemostatic; cytostatic; antilipaeamic; antiparasitic; antihelminthic; antibacterial; vitidic; prozoacide; fungicide; gene therapy; kinase modulator; phosphatase modulator; cardiovascular disease; immune system disorder; neurological disorder; growth and development disorder; cell proliferative disorder; infection; gene; ss.

Homo sapiens.

Key	Location/Qualifiers
CDS	70. .621
	/*tag= a
	/product= "kinase and phosphatase KPP-41"

WO2004009778-A2.

29-JAN-2004.

18-JUL-2003: 2003WO-US022650.

19-JUL-2002: 2002US-0397354P

02-AUG-2002; 2002US-0400509P.
02-AUG-2002; 2002US-0400783P

15-AUG-2002; 2002US-0404027P.

(INCY-) INCYTE CORP.

Hafalia AJA, Emerli

Elliott VS, Jin P, Hawkins PR, Swarnakar A, Chawla NK, Tran UK;
 Gururajan R, Ding L, Marquis JP, Thornton MB, Forsythe IJ, Lee EA;
 Gietzen KJ, Ramkumar J;

WPI; 2004-132950/13.

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new human kinases and phosphatases, useful for diagnosing, treating or preventing atherosclerosis, hypertension, AIDS, allergy, multiple sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer or hepatitis.

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The present sequence encodes a human kinase and phosphatase (KPP) protein. KPP sequences have cardiovascular, antiarteriosclerotic, hypotensive, vasotropic, antiinflammatory, antiangiinal, anti-HIV, anti-allergic, antiasthmatic, immunosuppressive, antithyroid, dermatological, antidiabetic, antineoplastic, antigout, gastrointestinal, neuroprotective, osteopathic, antiarthritic, uterotropic, ophthalmological, antirheumatic, antiparkinsonian, noctropic, anticonvulsant, hepatotropic, CNS, antipsoriasis, haemostatic, cytostatic, antilipaeimic, antiparasitic, antimelanitic, antibacterial, virucide, protozoacide and fungicide activities, and can be used in gene therapy, and as kinase modulators and phosphatase modulators. KPP proteins, polynucleotides, agonists and antagonists can be used for diagnosing, treating or preventing disorders associated with aberrant expression of KPP, such as cardiovascular diseases (e.g. atherosclerosis, hypertension, vasculitis, angina pectoris or congestive heart failure), immune system disorders (e.g. AIDS, allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout, irritable bowel syndrome, multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid arthritis, Sjögren's syndrome or uveitis), neurological disorders (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, dementia or epilepsy), disorders affecting growth and development (e.g. cirrhosis, hepatitis, mixed connective tissue disease, psoriasis or primary thrombocytopenia), cell proliferative disorders (e.g.

Db 910 ACACAGGAAATTAATCCCAAGACATCAATCTTTAAAGTAACGGGTTTTTCCAT 969
 Qy 802 GGCATAGTATACCTGAGCCAGAGACATGGAATCTCTGAGGAAAGTTCTCAGATGTT 861
 Db 970 GGCATAGTATACCTGAGCCAGAGACATGGAATCTCTGAGGAAAGTTCTCAGATGTT 1029
 Qy 862 CATCTGTGGCTCTGAATCTCATGAAGGGGTCTCTGAAGATGATCCAGATGACAGATTA 921
 Db 1030 CATCTGTGGCTCTGAATCTCATGAAGGGGTCTCTGAAGATGATCCAGATGACAGATTA 1089
 Qy 922 ACCTGTTCCCAACTCCTGGAGAGCTCTTACTTTCATTTCTTTCAAGAGGCCCAATTTAAA 981
 Db 1090 ACCTGTTCCCAACTCCTGGAGAGCTCTTACTTTCATTTCTTTCAAGAGGCCCAATTTAAA 1149
 Qy 982 AGAAAGCAGCTAATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1023
 Db 1150 AGAAAGCAGCTAATGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1191

RESULT 12
 ABX34679
 ID ABX34679 standard; cDNA; 1281 BP.
 AC ABX34679;
 XX

DT 13-FEB-2003 (first entry)
 XX
 DE Human mddt cDNA SEQ ID 240.
 XX

KW MDDT; human; disease detection and treatment molecule polypeptide;
 KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
 KW haemostatic; nephrotropic; antianemic; antiproliferative; hepatotropic;
 KW gene therapy; protein replacement therapy; cell proliferative disorder;
 KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
 KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
 KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
 KW psoriasis; hepatitis; gene; ss.
 XX

OS Homo sapiens.
 XX
 PN WO200279449-A2.
 XX
 PD 10-OCT-2002.
 XX

PF 27-MAR-2002; 2002WO-US009944.
 XX
 PR 28-MAR-2001; 2001US-0279619P.
 PR 29-MAR-2001; 2001US-0280067P.
 PR 29-MAR-2001; 2001US-0280068P.
 PR 16-MAY-2001; 2001US-0291280P.
 PR 17-MAY-2001; 2001US-0291829P.
 PR 17-JUN-2001; 2001US-0291849P.
 PR 19-JUN-2001; 2001US-0299428P.
 PR 20-JUN-2001; 2001US-0299776P.
 PR 20-JUN-2001; 2001US-0300001P.
 XX

(INCY-) INCYTE GENOMICS INC.

PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tudson O, Yap PE, Amshay SR;
 PI Dufour GE, Hillman JL, Yu JY, Tudson O, Yap PE, Amshay SR;
 PI Paralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RV, Urashka ME;
 XX

DR WPI; 2003-058431/05.
 DR P-PSDB; ABU11689.
 XX

XX New purified disease detection and treatment molecule proteins and
 PT polynucleotides, useful for diagnosing, treating or preventing cancers
 PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
 PT or hepatitis.
 XX

PS Claim 1; SEQ ID NO 240; 339pp + Sequence Listing; English.

XX This invention describes a novel disease detection and treatment molecule
 CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
 CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
 CC antianemic, antiproliferative and hepatotropic activity. The polynucleotides
 CC and the polypeptides of the invention can be used for gene therapy,
 CC protein replacement therapy and are useful for treating a variety of
 CC diseases or conditions. These polypeptides or polynucleotides are
 CC particularly useful for diagnosing, treating or preventing cell
 CC proliferative disorders (e.g. cancers including adenocarcinoma,
 CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
 CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
 CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
 CC hepatitis. ABX3440-ABX34835 encode the MDDT polypeptides represented in
 CC ABU11450-ABU11845, described in the disclosure of the invention. NOTE:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SQ Sequence 1281 BP; 428 A; 191 C; 317 G; 345 T; 0 U; 0 Other;
 Query Match 52.2%; Score 543.2; DB 8; Length 1281;
 Best Local Similarity 99.5%; Pred. No. 1.1e-134;
 Matches 545; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGGAAAGTATGAAAAAATTAGCTAAGCTGGAGAGGGTCTTATGGGGTTGTATTTCAA 60
 Db 704 ATGGAAAGTATGAAAAAATTAGCTAAGCTGGAGAGGGTCTTATGGGGTTGTATTTCAA 763
 Qy 61 TGCAGAACAAACCTCTGCACAGTAGTAGCTTTAAAAAATTTGGGAATCTGAAGAT 120
 Db 764 TGCAGAACAAACCTCTGCACAGTAGTAGCTTTAAAAAATTTGGGAATCTGAAGAT 823
 Qy 121 GATCCTCTTCTTAAGAAAAATAGCACTAAGAGAAATAGCTATGTTGAAAGCAATTTAAACAT 180
 Db 824 GATCCTCTTCTTAAGAAAAATAGCACTAAGAGAAATAGCTATGTTGAAAGCAATTTAAACAT 883
 Qy 181 CCAAACTCTGTGAACCTCATCGAGGTCTTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
 Db 884 CCAAACTCTGTGAACCTCATCGAGGTCTTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 943
 Qy 241 GAATACCTGTGATCATACACCTTTTAAATGAGCTGGAAGAGAACCCCAATGGAATGCTGAT 300
 Db 944 GAATACCTGTGATCATACACCTTTTAAATGAGCTGGAAGAGAACCCCAATGGAATGCTGAT 1003
 Qy 301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTGATATACAT 360
 Db 1004 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTGATATACAT 1063
 Qy 361 AACTGTATTACAGAGATATAAAACCTGAAAAATTTCTAATACTAAGCAAGGAATAATC 420
 Db 1064 AACTGTATTACAGAGATATAAAACCTGAAAAATTTCTAATACTAAGCAAGGAATAATC 1123
 Qy 421 AAGATTTGTGACTTCGGGTTTGCACAAATTTGATTTCCAGGAGATGCTACACCGATTTAT 480
 Db 1124 AAGATTTGTGACTTCGGGTTTGCACAAATTTGATTTCCAGGAGATGCTACACCGATTTAT 1183
 Qy 481 GTAGCTACGAGATGGTACCGAGCTCTCGAACTCTTCTGTGGAGATACCTCAGTATGGTTCT 540
 Db 1184 GCAGCTACGAGATGGTACCGAGCTCTCGAACTCTTCTGTGGAGATACCTCAGTATGGTTCT 1243
 Qy 541 TCAGTCCA 548
 Db 1244 TCAGTCCA 1251

RESULT 13
 AAF44669
 ID AAF44669 standard; cDNA; 911 BP.
 XX
 AC AAF44669;
 XX
 DT 27-MAR-2001 (first entry)

XX DE Novel protein kinase cDNA, SEQ ID NO: 49.
 XX KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; cardiac; renal; antiinflammatory; antiaesthetic;
 KW dermatological; antidiabetic; antifertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
 XX OS Homo sapiens.
 XX WO2000073469-A2.
 XX PD 07-DEC-2000.
 XX PF 26-MAY-2000; 2000WO-US014842.
 XX FR 28-MAY-1999; 99US-0136503P.
 XX FA (SUGEN-) SUGEN INC.
 XX PI Plowman GD, Martinez R, Whyte D, Sudersanam S;
 XX WPI; 2001-032161/04.
 XX DR P-PSDB; AAB65642.
 XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 PT neurodegenerative diseases and/or cancers.
 XX Example 4; Fig 2; 310pp; English.
 XX The present sequence encodes a novel protein kinase. The nucleic acids
 CC and the protein kinases they encode may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays. The kinase polypeptides may be used as antigens in the production
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies
 CC and kinase antagonists may also be used to down regulate kinase
 CC expression and activity. Diseases related to kinase expression and
 CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
 CC disorders, complications of organ transplantation, myocardial infarction,
 CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
 CC stress related disorders, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
 CC disorders
 XX Sequence 911 BP; 293 A; 182 C; 178 G; 258 T; 0 U; 0 Other;
 Query Match 51.6%; Score 537; DB 4; Length 911;
 Best Local Similarity 87.0%; Pred.No. 4.4e-133;
 Matches 643; Conservative 0; Mismatches 0; Indels 96; Gaps 1;
 QY 285 AATGGAGTGTGGTGGAGTGTGATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAA 344
 DB 1. AATGGAGTGTGTGGTGGAGTGTGATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAA 60
 QY 345 TTCTCTGTATATACATCAATCAATGTTTACAGAGATATAAACCCTGAAATATTCTAATAAC 404
 DB 61 TTCTCTGTATATACATCAATCAATGTTTACAGAGATATAAACCCTGAAATATTCTAATAAC 120
 QY 405 TAAGCAAGGAATTAATCAAGATTTGTGACTTCGGGTTTGCAAAATTCGATTCGAGGAGA 464
 DB 121 TAAGCAAGGAATTAATCAAGATTTGTGACTTCGGGTTTGCAAAATTCGATTCGAGGAGA 180
 QY 465 TGCCTACCGGATTTATGTAGTACGAGATGGTACCGAGTCTCTGAATCTTTGTGGAGA 524
 DB 181 TGCCTACCGGATTTATGTAGTACGAGATGGTACCGAGTCTCTGAATCTTTGTGGAGA 240

QY 525 TACTCAGTATGGTCTTCTCAGTCGATATATGGGCTATTGGTTGTTGTTTTCGAGAGCTCCT 584
 DB 241 TACTCAGTATGGTCTTCTCAGTCGATATATGGGCTATTGGTTGTTGTTTTCGAGAGCTCCT 300
 QY 585 GACAGGCCAGCCACTGTGGCTCGGAAATCAGATGTGACCAACTTTTATCTGATAATCAG 644
 DB 301 GACAGGCCAGCCACTGTGGCTCGGAAATCAGATGTGACCAACTTTTATCTGATAATCAG 360
 QY 645 AAGACTAGTAGAGACGGGGTTTCGCCATGTTGACAGGCTGGTCTCGAACTCTTGAGTC 704
 DB 361 AACTT
 QY 705 AAGTGATCCACCTGCCGTAGCCTCTCAAAGTCTGGAATTTACAGAAATTAATCCCAAG 764
 DB 367 -AGGAAATTAATCCCAAG 384
 QY 765 ACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTCAGGCCAGA 824
 DB 385 ACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATACCTCAGGCCAGA 444
 QY 825 AGACATGGAACCTTTGAGGAAAGTTCTCAGATGTTTCATCTCTGCTGCTGAATTCAT 884
 DB 445 AGACATGGAACCTTTGAGGAAAGTTCTCAGATGTTTCATCTCTGCTGCTGAATTCAT 504
 QY 885 GAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTAACTGTTCCCACTCTCGGAGAG 944
 DB 505 GAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTAACTGTTCCCACTCTCGGAGAG 564
 QY 945 CTCTACTTTGATTTCTTTTCAAGAGGCCCAAAATTAAGAAAGAACGTAATGAAGGAAG 1004
 DB 565 CTCTACTTTGATTTCTTTTCAAGAGGCCCAAAATTAAGAAAGAACGTAATGAAGGAAG 624
 QY 1005 AAACAGAACGCCCAACAG 1023
 DB 625 AAACAGAACGCCCAACAG 643
 RESULT 14
 ADI29367
 ID ADI29367 standard; cDNA; 911 BP.
 AC ADI29367;
 XX 22-APR-2004 (first entry)
 DE Human MARK3-associated cDNA #37.
 XX Human; ss; antisense gene therapy; MARK3;
 KW MAP/microtubule affinity-regulating kinase 3; cancer;
 KW Alzheimer's disease; neurodegenerative disorder;
 KW hyperproliferative disorder; cytostatic.
 XX Homo sapiens.
 XX US2003232771-A1.
 PD 18-DEC-2003.
 PF 17-JUN-2002; 2002US-00174319.
 XX 17-JUN-2002; 2002US-00174319.
 PR (ISIS-) ISIS PHARM INC.
 PA Ward DT, Freier SM, Dobie KW;
 PI WPI; 2004-052188/05.
 DR P-PSDB; ADI29249.
 XX New antisense compound targeted to a nucleic acid molecule encoding
 PT microtubule-affinity-regulating kinases (MARK3), useful for modulating
 PT expression of MARK3 or for treating cancer or Alzheimer's disease.

PS Disclosure; Fig 2; 233pp; English.

XX The invention relates to a compound comprising a sequence comprising 8-80
 CC base pairs (bp) targeted to a nucleic acid encoding MARK3
 CC (MAP/microtubule affinity-regulating kinase 3), that specifically
 CC hybridizes with the nucleic acid encoding MARK3 and inhibits expression
 CC of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a
 CC composition comprising the compound and a carrier or diluent, inhibiting
 CC the expression of MARK3 in cells or tissues, treating an animal having or
 CC suspected of having a disease or condition associated with MARK3 and
 CC screening for an antisense compound. The antisense oligonucleotide is
 CC useful for preparing a composition for treating hyperproliferative
 CC disorder, particularly cancer and neurodegenerative diseases e.g.
 CC Alzheimer's disease. The present sequence is a MARK3 associated cDNA
 CC included in the figures but not mentioned anywhere else in the
 CC specification.

XX Sequence 911 BP; 293 A; 182 C; 178 G; 258 T; 0 U; 0 Other;

SQ

Query Match 51.6%; Score 537; DB 12; Length 911;
 Best Local Similarity 87.0%; Pred. No. 4.4e-133;
 Matches 643; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

QY 285 AAATGGAGTTGCTGATGGAGTCAAAAGCGTATTATATGCGCAACACTTCAAGCTCTTAA 344
 DB 1 AAATGGAGTTGCTGATGGAGTCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAA 60

QY 345 TTCTCTGTCATATACATAACTGTATTACAGAGATATAAAACCTGAAATATTCTTAATAAC 404
 DB 61 TTCTCTGTCATATACATAACTGTATTACAGAGATATAAAACCTGAAATATTCTTAATAAC 120

QY 405 TAAGCAAGGAATATCAAGATTTGTGACTTCGGTGTTCGCAAAATCTGATTCAGGAGA 464
 DB 121 TAAGCAAGGAATATCAAGATTTGTGACTTCGGTGTTCGCAAAATCTGATTCAGGAGA 180

QY 465 TGCTACACCGATATATAGTACGATGGTACCGAGCTCCTGAACCTTTGTGGGAGA 524
 DB 181 TGCTACACCGATATATAGTACGATGGTACCGAGCTCCTGAACCTTTGTGGGAGA 240

QY 525 TACTCAGTATGTTCTTCAGTCGATATATGGCTTATGTTGTGTTTTCGACAGCTCCT 584
 DB 241 TACTCAGTATGTTCTTCAGTCGATATATGGCTTATGTTGTGTTTTCGACAGCTCCT 300

QY 585 GACAGGCCAGCACTGTGGCTGGAAATCAGATGTGGACCAACTTTATCTGATAATCAG 644
 DB 301 GACAGGCCAGCACTGTGGCTGGAAATCAGATGTGGACCAACTTTATCTGATAATCAG 360

QY 645 AACCTAGTAGAGAGCGGGTTTCCCAATGTTGACAGGCTGCTCGAACTCTTGACGTC 704
 DB 361 AACACT-----

QY 705 AAGTGATCCACCTGCGCTAGCTCTCAAGTGTGGAATTACAGGAAATTAATCCCAAG 764
 DB 367 -----AGGAAATTAATCCCAAG 384

QY 765 ACATCAATCAATCTTTAAAGTAACGGGTTTTTCATGGCATCAGTATACCTGAGCCAGA 824
 DB 385 ACATCAATCAATCTTTAAAGTAACGGGTTTTTCATGGCATCAGTATACCTGAGCCAGA 444

QY 825 AGACATGGAACCTTTCAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACCTCAT 884
 DB 445 AGACATGGAACCTTTCAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACCTCAT 504

QY 885 GAAGGGGTGTCGAAGATGAATCAGATGACAGATTAACCTGTTCCCACTCTCTGGAGAG 944
 DB 505 GAAGGGGTGTCGAAGATGAATCAGATGACAGATTAACCTGTTCCCACTCTCTGGAGAG 564

QY 945 CTCCTACTTTGATTTCTTTTCAAGAGGGCCCAATTAAGAAAGAAACGATTAATGAAGGAG 1004
 DB 565 CTCCTACTTTGATTTCTTTTCAAGAGGGCCCAATTAAGAAAGAAACGATTAATGAAGGAG 624

QY 1005 AACACAGAGAGCCCAACAG 1023.

|||||

DB 625 AACAGAGAGGCGCAACAG 643

RESULT 15

AAAD03812

ID AAD03812 standard; cDNA; 561 BP.

XX AAD03812;

DT 19-JUN-2001 (first entry)

XX Human kinase cDNA #1.

DE Human; kinase; gene therapy; bioreactor; mental disorder;

XX biological disorder; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..561

FT /tag= a

FT /product= "Human kinase #1"

FT /note= "The coding region does not include stop codon"

FT /partial

XX W0200123579-A1.

XX 05-APR-2001.

XX 27-SEP-2000; 2000WO-US026621.

XX 28-SEP-1999; 99US-0156511P.

XX (LEXI-) LEXICON GENETICS INC.

XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;

XX Sands AT;

XX WPI; 2001-266166/27.

XX P-PSDB; AAE00490.

XX New isolated human kinase polynucleotide useful for generating for

PT antibodies, as reagents in diagnostic assays and for screening for

PT compounds useful for treating mental, biological or medical diseases.

XX Disclosure; Page 27; 38pp; English.

XX The present sequence is a cDNA encoding novel human protein (NHP) known

CC as human kinase. The human kinases share structural similarity with

CC animal kinases, more particularly serine or threonine protein kinases.

CC Human kinase cDNA is useful for the detection of mutant human kinase for

CC the diagnosis of disease, and also as a therapeutic. It is useful for

CC screening drugs effective in the treatment of symptomatic or phenotypic

CC manifestations perturbing the normal function of NHP in the body. The NHP

CC nucleotide sequences are useful for generation of antibodies, as reagents

CC in diagnostic assays, for the identification of other cellular gene

CC products related to human kinases, and as reagents in assays for

CC screening compounds that are useful for treating mental, biological or

CC medical disorders. NHP oligonucleotides are used as probes. The labelled

CC NHP probes are useful for screening human genomic library for identifying

CC polymorphisms and as primers in amplification assays to detect mutations

CC within the exons, introns and splice sites that can be used in

CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP

CC products are used to genetically engineer cells in vivo that functions as

CC bioreactors in the body delivering a continuous supply of NHP to the

CC body. Nucleotide constructs encoding functional NHPs are used in gene

CC therapy for the modulation of NHP expression

XX

SQ Sequence 561 BP; 189 A; 87 C; 112 G; 173 T; 0 U; 0 Other;

Query Match 43.7%; Score 454.4; DB 4; Length 561;
 Best Local Similarity 99.8%; Pred. No. 4.3e-111;
 Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGAAGAGTATGAAAAATTAGCTAAGACTGGAGAAGGGTCTTATGGGGTTGTATTCAAA	60
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Db			
Qy	61	TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTAAAAAATTTGTGGAATCTGAAGAT	120
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Qy	121	GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTTAAACAT	180
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Qy	121	GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTTAAACAT	180
Db			
Qy	181	CCAAATCTTGTGAACCTCATCGAGGTGTTCAAGAGAAAAAGAAAAATGCATTTAGTTTTT	240
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Qy	181	CCAAATCTTGTGAACCTCATCGAGGTGTTCAAGAGAAAAAGAAAAATGCATTTAGTTTTT	240
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Qy	241	GAATCTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT	300
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Qy	241	GAATCTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT	300
Db			
Qy	301	GGAGTGATCAAAAGCGTATTATGSCAACACTTCAAGCTCTTAATTTCTGTCATATACAT	360
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Qy	301	GGAGTGATCAAAAGCGTATTATGSCAACACTTCAAGCTCTTAATTTCTGTCATATACAT	360
Db			
Qy	361	AACTGTATTTCACAGAGATATAAAACCTGAAATATTCTAATACTAAAGCAAGGAATAATC	420
Db			
Qy	361	AACTGTATTTCACAGAGATATAAAACCTGAAATATTCTAATACTAAAGCAAGGAATAATC	420
Db			
Qy	421	AAGATTTGTGACTTCGGGTTTGCACAAATTCGTATT	456
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Search completed: April 21, 2005, 21:13:01
 Job time : 582.772 secs

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4	1025	98.5	1068	6	AX107714	Sequence
5	839	80.6	945	6	AR492170	Sequence
6	839	80.6	945	6	AX107722	Sequence
7	823	79.1	972	6	AR492167	Sequence
8	823	79.1	972	6	AX107716	Sequence
9	821	78.9	1790	6	AX746179	Sequence
10	762.8	73.3	1678	6	AX698820	Sequence
11	757	72.7	1083	6	AX166534	Sequence
12	709	68.1	1819	6	AR492171	Sequence
13	709	68.1	1819	6	AX107724	Sequence
14	645.6	62.0	687	6	AX286069	Sequence
15	645.6	62.0	882	6	AX286067	Sequence
16	537	51.6	911	6	AX056404	Sequence
17	454.4	43.7	561	6	AR492165	Sequence
18	454.4	43.7	561	6	AX107712	Sequence
19	454.4	43.7	594	6	AR492168	Sequence

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				Gaps	0;
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Db	1	ATGGAARAAGTATGAAAANAATTAGCTTAAGACTGGAGAAAGGGTCTTATGGGGTGTGATTCAAAA	60		
Qy	61	TGCAGAAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAAATCTGAAGAT	120		
Db	61	TGCAGAAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGTGGAAATCTGAAGAT	120		
Qy	121	GATCCTGTGTTTAAAGAAAATAGCACTAAAGAGAAATACGTATGTTGAAGCAAAATTA AAAACAT	180		
Db	121	GATCCTGTGTTTAAAGAAAATAGCACTAAAGAGAAATACGTATGTTGAAGCAAAATTA AAAACAT	180		
Qy	181	CCAAATCTTGTAACCTCATCGAGGTGTTTCAGAGAAAAGGAAAATGCATTTTAGTTTTT	240		
Db	181	CCAAATCTTGTAACCTCATCGAGGTGTTTCAGAGAAAAGGAAAATGCATTTTAGTTTTT	240		
Qy	241	GAATATCTGTGATCATACACTTTTTTAAATGAGCTGGAAAGAAACCCCAATGAGGTGCTGAT	300		

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Db 241 GAATAGTGTATCATACACTTTTAAATGAGCTGGAAAGAACCCAAATGGAGTTGCTGAT 300
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Qy 361 AACTGTATTTCAGAGATATATAAAGCTGAAATATTTCTAAATACCTAGCAGGGAATATC 420
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ACCESSION AX107720
VERSION AX107720.1 GI:13923201
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and
Sands, A.T.
JOURNAL Human kinase proteins and polynucleotides encoding the same
Patent: WO 0123579-A 9 05-APR-2001;
Lexicon Genetics Incorporated (US)

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FEATURES             source
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ORIGIN

Query Match      100.0%; Score 1041; DB 6; Length 1041;
Best Local Similarity 100.0%; Pred. No. 2.7e-243;
Matches 1041; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAAAGATGATGAAATTTAGCTAGCACTGGAGAGGGTCTTATGGGTGTTGTTTCAAA 60
Db 1 ATGAAAGATGATGAAATTTAGCTAGCACTGGAGAGGGTCTTATGGGTGTTGTTTCAAA 60
Qy 61 TGCAGAAACAAAACCTCTGGCAAGTAGTAGCTGTTTAAAAAATTTTGTGGAATCTGAAGAT 120
Db 61 TGCAGAAACAAAACCTCTGGCAAGTAGTAGCTGTTTAAAAAATTTTGTGGAATCTGAAGAT 120
Qy 121 GATCCTGTTTAAAGAAATAGCACTTAAGAGAAATAGCTATGTTGAAGCAATTAAGACAT 180
Db 121 GATCCTGTTTAAAGAAATAGCACTTAAGAGAAATAGCTATGTTGAAGCAATTAAGACAT 180
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Db 181 CCAAACTCTGTGAACCTCATCGAGGTGTTTTCAGGAGAAAGGAAATGCAATTTAGTTTT 240
Qy 241 GAATATCTGTGATCATACCTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300
Db 241 GAATATCTGTGATCATACCTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300
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Db 301 GGAGTCAATCAAAAGCGTATATGGCAAAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
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DEFINITION Sequence 3 from patent US 6716616.
ACCESSION AR492166
VERSION AR492166.1 GI:47260676
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1068)
AUTHORS Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B.
and Sands,A.T.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: US 6716616-A 3 06-APR-2004;
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Best Local Similarity 100.0%; Pred. No. 2.2e-239;
Matches 1025; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Sequence 3 from Patent WO0123579.
ACCESSION AX107714
VERSION AX107714.1 GI:13923198
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Donoho,G., Turner,C.A., Nehls,M., Friedrich,G., Zambrowicz,B. and Sands,A.T.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0123579-A 3 05-APR-2001;
Lexicon Genetics Incorporated (US)
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Query Match 98.5%; Score 1025; DB 6; Length 1068;
Best Local Similarity 100.0%; Pred. No. 2.2e-239;
Matches 1025; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
LOCUS AR492170
DEFINITION Sequence 11 from patent US 6716616.
ACCESSION AR492170
VERSION AR492170.1 GI:47260680
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

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Unclassified.
1 (bases 1 to 945)
Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B.
and Sands,A.T.
Human kinase proteins and polynucleotides encoding the same
Patent: US 6716616-A 11 06-APR-2004;
FEATURES
source location/Qualifiers
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Best Local Similarity 90.8%; Pred. No. 5.1e-194;
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DEFINITION Sequence 11 from Patent W00123579.
ACCESSION  AX107722
VERSION     AX107722.1 GI:13923202
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and
JOURNAL     Sands, A.T.
            Human kinase proteins and polynucleotides encoding the same
            Patent: WO 0123579-A 11 05-APR-2001;
            Lexicon Genetics Incorporated (US)
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Best Local Similarity 90.6%; Pred. No. 5.1e-194;
Matches 945; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

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DEFINITION Sequence 5 from patent US 6716616.
ACCESSION  AR492167
VERSION     AR492167.1 GI:47260677
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 972)
AUTHORS     Donoho, G., Turner, C.A. Jr., Nehls, M.C., Friedrich, G., Zambrowicz, B.
            and Sands, A.T.
TITLE       Human kinase proteins and polynucleotides encoding the same
JOURNAL     Patent: US 6716616-A 5 06-APR-2004;
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 Db |||||
 QY 481 GTAGCTACGAGATGTAACGAGCTCTGAACTTTCTGATTCGAGAGATGCTACACCGATTAT 540
 Db |||||
 QY 481 GTAGCTACGAGATGTAACGAGCTCTGAACTTTCTGATTCGAGAGATGCTACACCGATTAT 540
 Db |||||
 QY 541 TCAGTCGATATATGGCTTATTTGTTGTTTTCAGAGCTCTTGAAGCCAGCCACTG 600
 Db |||||
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 Db |||||
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 QY 601 TGGCTCGAAATCAGATGTCGACCACTTTATCTGATATCAGAACTAGTAGAGAGC 660
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 QY 661 GGGTTTCGCCATGTTGACAGGCTGGTCTCGAACTCTTGACGTCAAGTGATCCACCTGCC 720
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 Db |||||
 QY 721 GTAGCCTCTCAAGCTGCTGGAATTAAGGAAATTAATCCAGACATCAATCAATCTTT 780
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 Db |||||
 QY 781 AAAAGTAAACGGGTTTCCATGTCATCAGTATACCTGAGCCAGACATGGAACCTCTT 840
 Db |||||
 QY 841 GAGGAAAGTCTCAGATGTTCACTGCTGGCTCTGAACCTTCAATGAAGGGTGTCTGAAG 900
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 Db |||||
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 QY 961 TTTCAAGAGCCCAATTTAAAGAAAGCAAGCACTGTAATGAAGGAGAAACAGAGAGCCCAA 1020
 Db |||||
 QY 961 TTTCAAGAGCCCAATTTAAAGAAAGCAAGCACTGTAATGAAGGAGAAACAGAGAGCCCAA 1020
 Db |||||
 QY 1021 CAGGT 1025
 Db |||||
 QY 925 CAGGT 929

RESULT 8
 AX107716
 LOCUS
 DEFINITION
 Sequence 5 from Patent WO0123579.
 AX107716 972 bp DNA linear PAT 30-APR-2001

AX107716
 AX107716.1 GI:13923199
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 Doncho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and
 Sands, A.T.
 Human kinase proteins and polynucleotides encoding the same
 Patent: WO 012579-A 5 05-APR-2001;
 Lexicon Genetics Incorporated (US)
 Location/Qualifiers
 1.972
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Query Match 79.1%; Score 823; DB 6; Length 972;
 Best Local Similarity 90.6%; Pred.No. 4.1e-190;
 Matches 929; Conservative 0; Mismatches 0; Indels 96; Gaps 1;
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 QY 1 ATGGAAGCTATGAAATTTAGCTAAGACTGGAGAGGGTCTTATGGGGTTGTTTCAAA 60
 Db |||||
 QY 61 TGCAGAAACAAACCTCTGCAACAGTAGTAGCTGTTTAAAAATTTGTGGAATCTGAAGT 120
 Db |||||
 QY 61 TGCAGAAACAAACCTCTGCAACAGTAGTAGCTGTTTAAAAATTTGTGGAATCTGAAGT 120
 Db |||||
 QY 121 GATCTCTGTTTAAAGAAATAGCACTAAGAGAAATACGTAATGTTGAAGCAATTTAAAAACAT 180
 Db |||||
 QY 121 GATCTCTGTTTAAAGAAATAGCACTAAGAGAAATACGTAATGTTGAAGCAATTTAAAAACAT 180
 Db |||||
 QY 181 CCAAAATCTTGTGAACCTCTCATCGAGGTGTTTCAGGAGAAAGAAAGAAATGCAATTTAGTTT 240
 Db |||||
 QY 181 CCAAAATCTTGTGAACCTCTCATCGAGGTGTTTCAGGAGAAAGAAAGAAATGCAATTTAGTTT 240
 Db |||||
 QY 241 GAATCTGTGATCATACATTTTAAATGAGCTGGAAGAAACCCAAATGGAATGCTCAT 300
 Db |||||
 QY 241 GAATCTGTGATCATACATTTTAAATGAGCTGGAAGAAACCCAAATGGAATGCTCAT 300
 Db |||||
 QY 301 GGAGTGATCAAAAGCGTATTATGGAACACATTTCAAGCTCTTAATTTCTGTCATATACAT 360
 Db |||||
 QY 301 GGAGTGATCAAAAGCGTATTATGGAACACATTTCAAGCTCTTAATTTCTGTCATATACAT 360
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 QY 361 AACTGTATTTCAGAGATATAAACTCTGAAATATTTCTAATACTTAAGCAAGGAATATC 420
 Db |||||
 QY 421 AAGATTTGTGACTTCGGGTTTGCACAAATTTCTGATTCAGGAGATGCTACACCGATTAT 480
 Db |||||
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 Db |||||
 QY 481 GTAGCTACGAGATGTAACGAGCTCTGAACTTTCTGATTCGAGAGATGCTACACCGATTAT 540
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 Db |||||
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 Db |||||
 QY 601 TGGCTCGAAATCAGATGTCGACCACTTTATCTGATATCAGAACTAGTAGAGAGC 660
 Db |||||
 QY 661 GGGTTTCGCCATGTTGACAGGCTGGTCTCGAACTCTTGACGTCAAGTGATCCACCTGCC 720
 Db |||||
 QY 661 GGGTTTCGCCATGTTGACAGGCTGGTCTCGAACTCTTGACGTCAAGTGATCCACCTGCC 720
 Db |||||
 QY 721 GTAGCCTCTCAAGCTGCTGGAATTAAGGAAATTAATCCAGACATCAATCAATCTTT 780

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Qy      781  AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAACCTCTT 840
Db      685  AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAACCTCTT 744
Qy      841  GAGGAAAGTTCTCAGATGTTTCATCTGTGCTCTGAACTTCATGAGGGGTGTCGAAG 900
Db      745  GAGGAAAGTTCTCAGATGTTTCATCTGTGCTCTGAACTTCATGAGGGGTGTCGAAG 804
Qy      901  ATGAATCCAGATGACAGATTAACCTGTTCCCACTCTCTGGAGAGCTCTCTACTTTGATTCT 960
Db      805  ATGAATCCAGATGACAGATTAACCTGTTCCCACTCTCTGGAGAGCTCTCTACTTTGATTCT 864
Qy      961  TTTCAAGAGGCCAAATTAAGAAAAAGCACGTAATGAAGGAAGAAAAAGAGAGCGCAA 1020
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Qy      1021  CAGGT 1025
Db      925  CAGGT 929

RESULT 9
AX746179 LOCUS 1790 bp DNA linear PAT 13-JUN-2003
DEFINITION Sequence 30 from Patent WO0208399.
ACCESSION AX746179
VERSION AX746179.1 GI:31746165
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Yue, H., Khan, F.A., Gururajan, R., Hafalia, A.J., Chawla, N.K., Arivu, C.S., Ramesh, J., Gandhi, A.R., Policky, J.L., Baughn, M.R., Tribouley, C.M., Bandman, O., Nguyen, D.B., Lu, Y., Burford, N., Lal, P., Ding, L., Yao, M.G., Elliott, V.S., Recipon, S.A., Kearney, L., Lu, D.A., Greenwald, S.R., Tang, Y.T., Xu, Y., Walsh, R.T., Gietzen, K.J., Yang, J., Jackson, J.L. and Thornton, M.
TITLE Human kinases
JOURNAL Patent: WO 0208399-A 30 31-JAN-2002;
INCYTE INCYTE Genomics, Inc. (US); Thornton, Michael (US)
FEATURES
source /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 1698381CB1"

ORIGIN
Query Match 78.9%; Score 821; DB 6; Length 1790;
Best Local Similarity 90.6%; Pred. No. 1.3e-189;
Matches 927; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

Qy      1 ATGGAAGATGAAAAATAGCTAAGACTGAGAGGGTCTTATGGGTTGTATTCAAA 60
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Qy      61 TGCAGAAACAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGGAACTCTGAAGAT 120
Db      299 TGCAGAAACAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGGAACTCTGAAGAT 358
Qy      121 GATCCTGTTGTAGAAAAATAGCACTAAGAAATAGTATGTTGAAGCAATTAACAT 180
Db      359 GATCCTGTTGTAGAAAAATAGCACTAAGAAATAGTATGTTGAAGCAATTAACAT 418
Qy      181 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAAAGAAAAATGCATTTAGTTT 240
Db      419 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAAAGAAAAATGCATTTAGTTT 478

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Qy      241 GAATACCTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
Db      479 GAATACCTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 538
Qy      301 GGAGTGAATCAAAAGCGTATTATGGCAAAACACTTCAAGCTCTTAAATTTCTGTCAATACAT 360
Db      539 GGAGTGAATCAAAAGCGTATTATGGCAAAACACTTCAAGCTCTTAAATTTCTGTCAATACAT 598
Qy      361 AACTGTATTCAAGAGATATAAAACCTGAAATATTCTAATACTAAGCAAGGAATAATC 420
Db      599 AACTGTATTCAAGAGATATAAAACCTGAAATATTCTAATACTAAGCAAGGAATAATC 658
Qy      421 AAGATTGTGACTTTCGGGTTTGGCAAAATCTCTGATCCAGGAGATGCTTACACCGATTAT 480
Db      659 AAGATTGTGACTTTCGGGTTTGGCAAAATCTCTGATCCAGGAGATGCTTACACCGATTAT 718
Qy      481 GTACTACGAGATGGTACCGAGCTCTCGAACTTCTGTGGGAGATACCTCAGTATGGTTCT 540
Db      719 GTACTACGAGATGGTACCGAGCTCTCGAACTTCTGTGGGAGATACCTCAGTATGGTTCT 778
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Db      779 TCAGTCGATATATGGGCTATTGGTTGTTGTTTTCGAGAGCTCTCTGACAGGCGACCCACTG 838
Qy      601 TGGCTGGAAAAATCAGATGTGGACCAACTTTATCTGATATATCAGAACACTAGTAGAGACG 660
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Qy      661 GGGTTTCGCCATGTTGACACGAGCTGGTCTCGAACTCTTGAGCTCAAGTGATCCACCTGCC 720
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Qy      721 GTAGCCTCTCAAAAGTGTGGAATTTACAGGAAAAATTAATCCCAAGACATCAATCAATCTTT 780
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Qy      781 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGCAAGACATGGAACCTCTT 840
Db      923 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGCAAGACATGGAACCTCTT 982
Qy      841 GAGGAAAGTTCTCAGATGTTTCATCTGTGCTCTGAACTTCATGAAGGGGTGTCGAAG 900
Db      983 GAGGAAAGTTCTCAGATGTTTCATCTGTGCTCTGAACTTCATGAAGGGGTGTCGAAG 1042
Qy      901 ATGAATCCAGATGACAGATTAACCTGTTCCCACTCTCTGGAGAGCTCTCTACTTTGATTCT 960
Db      1043 ATGAATCCAGATGACAGATTAACCTGTTCCCACTCTCTGGAGAGCTCTCTACTTTGATTCT 1102
Qy      961 TTTCAAGAGGCCCAATTAAGAAAAAGCAAGCTAATGAAGGAAGAAAAAGAGAGAGCGCAA 1020
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Qy      1021 CAG 1023
Db      1163 CAG 1165

RESULT 10
AX698820 LOCUS 1678 bp DNA linear PAT 02-APR-2003
DEFINITION Sequence 6 from Patent WO02079473.
ACCESSION AX698820
VERSION AX698820.1 GI:29499608
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Panzer, S.R., Lincoln, S.E., Altus, C.M., Dufour, G.E., Hillman, J.L., Jones, A.L., Dam, T.C., Liu, T.F., Harris, B., Flores, V., Daffo, A., Marwaha, R., Chen, A.J., Chang, S.C., Gerstin, J.E., Peralta, C.H., David, M.H. and Lewis, S.A.

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TITLE Molecules for diagnostics and therapeutics
JOURNAL Patent: WO 02079473-A 6 10-OCT-2002;
Incyte Genomics, Inc. (US)

FEATURES

source
Location/Qualifiers
1..1678
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: LI:058298.1:2001JAN12"

ORIGIN

Query Match 73.3%; Score 762.8; DB 6; Length 1678;
Best Local Similarity 90.0%; Pred. No. 2e-175;
Matches 925; Conservative 0; Mismatches 2; Indels 101; Gaps 6;

QY 1 ATGGAAGATGATCAAAATATAGCTAGAGCTGAGAGGGTCTTATGGGGTTGTATTTCAA 60
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QY 131 ATGGAGAGATGAAATATAGCTAGAGCTGAGAGGGTCTTATGGGGTTGTATTTCAA 190
DB |||||
QY 61 TCAGA-AACAAACCTCTGGCAAGTAGTAGCTGTAAATAATTTGTGGAATCTGAAGA 119
DB |||||
QY 191 TCAGATACAAACCTCTGGCAAGTAGTAGCTGTAAATAATTTGTGGAATCTGAAGA 250
DB |||||
QY 120 TCATCTCTGTGTAGAAATAGCACTAGAGAAATACGTA-TGTTGAAGCAATTTAAAC 178
DB |||||
QY 251 TGATCTCTGTGTAGAAATAGCACTAGAGAAATACGTA-TGTTGAAGCAATTTAAAC 310
DB |||||
QY 179 ATCCAAATCTTGTGAACCTCATCGAGGTGTTTCAGAGAGAAAGGAAATGCAATTTAGTTT 238
DB |||||
QY 311 ATCCAAATCTTGTGAACCTCATCGAGGTGTTTCAGAGAGAAAGGAAATGCAATTTAGTTT 370
DB |||||
QY 239 TTGAATCTCTGATCATACACTTTTAATAGCTGGAAAGAAACCCAAATGAGTTGCTG 298
DB |||||
QY 371 TTGAATCTCTGATCATACACTTTTAATAGCTGGAAAGAAACCCAAATGAGTTGCTG 430
DB |||||
QY 299 ATGGAGTGAATCAAAAGCTTATTTAGGCAACACTTCAGCTCTTAATTTCTGTCATATAC 358
DB |||||
QY 431 ATGGAGTGAATCAAAAGCTTATTTAGGCAACACTTCAGCTCTTAATTTCTGTCATATAC 490
DB |||||
QY 359 ATACTGTATTCAGAGATATAAACTGAAATATTTCTAATACTAAGCAAGGAATAA 418
DB |||||
QY 491 ATACTGTATTCAGAGATATAAACTGAAATATTTCTAATACTAAGCAAGGAATAA 550
DB |||||
QY 419 TCAAGATTTGATCTCGGGTTTGCACAAATCTGATTCAGAGATGCTTACCGGAT 478
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QY 551 TCAAGATTTGATCTCGGGTTTGCACAAATCTGATTCAGAGATGCTTACCGGAT 610
DB |||||
QY 479 ATGTAGCTA-CGAGATGGTACCGAGCT-CCTGAACTTCTTTGTGGAGATACT-CAGTATG 535
DB |||||
QY 611 ATGTAGCTAGCGAGATGGTACCGAGCTCCCTGAACTTCTTTGTGGAGATACTCCAGTATG 670
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QY 536 GTTCTTCAGTCGATATAGGCTATTTGGTGTGTTTTCAGAGCTCCTGACAGGCCAGC 595
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QY 671 GTTCTTCAGTCGATATAGGCTATTTGGTGTGTTTTCAGAGCTCCTGACAGGCCAGC 730
DB |||||
QY 596 CACTGTGGCTTGGAAATCAGATGTGCAACCTTTATCTGATTAATCAGAACACTAGTAG 655
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QY 731 CACTGTGGCTTGGAAATCAGATGTGCAACCTTTATCTGATTAATCAGAACACT 785
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QY 656 AGACGGGGTTTCGCCATTTGACCGAGCTGGTCTCGAACTCTTGACGTCAAATGATCCAC 715
DB |||||
QY 786 ----- 785
DB |||||
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DB |||||
QY 786 -----AGGAAATTAATCCCAAGCATCAATCAA 814
DB |||||
QY 776 TCTTTAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAAA 835
DB |||||
QY 815 TCTTTAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAAA 874
DB |||||
QY 836 CTCTTGAGGAAAGTTCTCAGATGTTTCATCTCTGGCTCTGAATTTCAATGAGGGGTGTC 895
DB |||||

Db 875 CTCCTGAGGAAAGTTCTCAGATGTTTCATCTCTGTGGCTCTGAACCTTCATGAAGGGTGTCT 934
QY 896 TGAAGATGAATCCAGATGACAGATTAACCTCTTCCCAACTCTCTGAGAGCTCCTTACTTTG 955
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QY 935 TGAAGATGAATCCAGATGACAGATTAACCTCTTCCCAACTCTCTGAGAGCTCCTTACTTTG 994
Db |||||
QY 956 ATTCTTTTCAAGAGCCCAATTAATAAGAAAGCACGTAATGAAGGAGAGAAACAGAGAC 1015
Db |||||
QY 995 ATTCTTTTCAAGAGCCCAATTAATAAGAAAGCACGTAATGAAGGAGAGAAACAGAGAC 1054
Db |||||
QY 1016 GCCAACAG 1023
Db |||||
QY 1055 GCCAACAG 1062
Db |||||

RESULT 11
AX166534
LOCUS AX166534 1083 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 25 from Patent WO0138503.
ACCESSION AX166534
VERSION AX166534.1 GI:14546879
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Plowman, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R.,
Planagan, P. and Clary, D.S.
TITLE Novel human protein kinases and protein kinase-like enzymes
JOURNAL Patent: WO 0138503-A 25 31-MAY-2001;
Sugen, Inc. (US)
FEATURES
Location/Qualifiers
1..1083
/organism="Homo sapiens"
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ORIGIN

Query Match 72.7%; Score 757; DB 6; Length 1083;
Best Local Similarity 86.1%; Pred. No. 5.1e-174;
Matches 927; Conservative 0; Mismatches 0; Indels 150; Gaps 2;

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QY 61 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTGTAAATAATTTGTGGAATCTGAAGAT 120
DB |||||
QY 121 GATCCTGTGTAGAAATAGCACTAGAGAAATACGTAATGTTGAGCAATTTAAACAT 180
DB |||||
QY 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAGAAAGGAAATGCAATTTAGTTT 240
DB |||||
QY 241 GAAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 300
DB |||||
QY 301 GGAGTATCAAAAGCTTATGCAACACTTCAGCTCTTAATTTCTGTCATATACAT 360
DB |||||
QY 361 AACTGTATTCACAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATAATC 420
DB |||||
QY 421 AAGATTTGCTACTTCGGGTTTGCAAAATTTCTGA ----- 454
DB |||||

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Db 421 AAGATTGTGACTTCGGGTTGCACAAATTCAGTAATTCACATGTTGGAGAAATTGAC 480
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Db 481 TTACTCGATCTGATTGATGCAATTTGCCAGTTCCAGAGATGCTTACACCGATTATGTAGCT 540
Qy 487 ACAGATGTTACCGAGCTCTCGAACTTCTGTGGAGATACCTAGTATGTTCTTCAGTC 546
Db 541 ACAGATGGTACCAGCTCTCGAACTTCTGTGGAGATACCTAGTATGTTCTTCAGTC 600
Qy 547 GATATATGGGCTATTTGGTTGTTTTCAGAGCTCTCGAGAGCCAGCCACTGTGGCCT 606
Db 601 GATATATGGGCTATTTGGTTGTTTTCAGAGCTCTCGAGAGCCAGCCACTGTGGCCT 660
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Db 661 GGAATATCAGATGTGGACCAACTTTATCTGATAATCAGAACACT- 704
Qy 667 CGCATGTTGACAGGCTGGTCTCGAACTCTTGACGTCAGTATCCACCTGCCGTAGCC 726
Db 705 ----- 704
Qy 727 TCTCAAAGTCTGGAATTTACAGGAAATTTAATCCAAAGACATCAATCAATCTTTAAAAGT 786
Db 705 -----AGGAAATTTAATCCAAAGACATCAATCAATCTTTAAAAGT 744
Qy 787 AACGGGTTTTTCCATGGCATCAGTATACCTGAGCGAGAGACATGGAACCTTTGAGGAA 846
Db 745 AACGGGTTTTTCCATGGCATCAGTATACCTGAGCGAGAGACATGGAACCTTTGAGGAA 804
Qy 847 AAGTTCAGATGTTTATCTGTGGCTCTGAACTTTCATGAAGGGGTCTCGAAGATGAAT 906
Db 805 AAGTTCAGATGTTTATCTGTGGCTCTGAACTTTCATGAAGGGGTCTCGAAGATGAAT 864
Qy 907 CCAGATCAGAGATTAACTGTTCCAACTCTCTGAGAGCTCTTACTTTGATTTTCAA 966
Db 865 CCAGATCAGAGATTAACTGTTCCAACTCTCTGAGAGCTCTTACTTTGATTTTCAA 924
Qy 967 GAGGCCCAATTTAAAGAAAGCAGCTAATGAAGGAAAGAAACAGAGCCCAACAG 1023
Db 925 GAGGCCCAATTTAAAGAAAGCAGCTAATGAAGGAAAGAAACAGAGCCCAACAG 981

RESULT 12
AR492171
LOCUS AR492171 1819 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 13 from patent US 6716616.
ACCESSION AR492171
VERSION AR492171.1 GI:47260681
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1819)
AUTHORS Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B.
and Sands,A.T.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: US 6716616-A 13 06-APR-2004;
FEATURES
source Location/Qualifiers
1..1819
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 68.1%; Score 709; DB 6; Length 1819;
Best Local Similarity 77.0%; Pred. No. 2.6e-162;
Matches 1025; Conservative 0; Mismatches 0; Indels 306; Gaps 1;

Qy 1 ATGGAAGATGATAAATAGCTTAAGACTGAGAGGGCTTATGGGTTGTAATCAAA 60
Db 138 ATGGAAGATGATAAATAGCTTAAGACTGAGAGGGCTTATGGGTTGTAATCAAA 197
Qy 61 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
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Db 198 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 257
Qy 121 GATCCTGTTTGAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTTAAACAT 180
Db 258 GATCCTGTTTGAAGAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTTAAACAT 317
Qy 181 CCAATCTTGTGAACCTCATCGAGGTGTTTCAGGAGAAAGAAAGAAATGCAATTTAGTTTT 240
Db 318 CCAATCTTGTGAACCTCATCGAGGTGTTTCAGGAGAAAGAAAGAAATGCAATTTAGTTTT 377
Qy 241 GAATACGTGATCATACACCTTTTAAATGAGCTGGAAGAAACCCAAATGAGGTGCTGAT 300
Db 378 GAATACGTGATCATACACCTTTTAAATGAGCTGGAAGAAACCCAAATGAGGTGCTGAT 437
Qy 301 GGAGTGATCAAAAGCGTATTTATGCGAAACACTTCAAGCTCTTAAATTTCTGTCAATACAT 360
Db 438 GGAGTGATCAAAAGCGTATTTATGCGAAACACTTCAAGCTCTTAAATTTCTGTCAATACAT 497
Qy 361 AACTGTATTCAAGAGATATAAAACCTGAAATAATTTCTAATACTAAGCAAGGAATATC 420
Db 498 AACTGTATTCAAGAGATATAAAACCTGAAATAATTTCTAATACTAAGCAAGGAATATC 557
Qy 421 AAGATTGTGACCTTCGGGTTTGCACAAATTTCTG- 453
Db 558 AAGATTGTGACCTTCGGGTTTGCACAAATTTCTGAGTTGGAATCTTCTCTGTTGCTGCC 617
Qy 454 ----- 453
Db 618 TCCTTGATTGGCTTAATAGTTGACCTTCTGAATTTCTTTTCTGCCAATTCAGAGATTTT 677
Qy 454 ----- 453
Db 678 CTCCTGGCTTGGATCCATTGCTGACACAGTGTGTTTACCATGGGGCCAGGCTCATCTCGA 737
Qy 454 ----- 453
Db 738 ACTTCTGGCTCAAGTGATCCTTCCACTCGGCTCCCAAAGTCTCGATTTGCAAGTTGTG 797
Qy 454 ----- 453
Db 798 AGCCACGTCGCCAGCCAGATTTTCAACAATACTACTGAGAGCTCACAGAGATTGTT 857
Qy 454 -----ATTCCAGAGATGCTTACACC 474
Db 858 TTAGTGGGAACAACAATTTGCAACAATTTCTTGAGAACGCATTCAGGAGATGCCACACC 917
Qy 475 GATTATGATAGTAGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACCTAGTAT 534
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Qy 655 GAGACGGGGTTTCGCATGTTGACAGGCTGGTCTCGAACTCTTGAAGTCAAGTATCCA 714
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Qy 835 ACTCTTGAGAAAGTTCTCAGATGTTCTGCTGCTGCTGAACTTCTGAAGGCTGT 894
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QY 895 CTGAAGATCAATCCAGATGACAGATTAACCTGTTCCCACTCTCTGAGAGCTCTCTACTTTT 954

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Db 1398 GATTCCTTTTCAAGAGGCCCAATTAAGAGAAAGCACGTAATGAAGGAAAGAAACAGAAGA 1457

QY 1015 CGCCACACAGGT 1025

Db 1458 CGCCACACAGGT 1468

RESULT 13

AX107724 1819 bp DNA linear PAT 30-APR-2001

LOCUS Sequence 13 from Patent WO0123579.

DEFINITION AX107724

ACCESSION AX107724.1 GI:13923203

VERSION

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and Sands, A.T.

TITLE Human kinase proteins and polynucleotides encoding the same

JOURNAL Patent: WO 0123579-A 13 05-APR-2001;

LEXICON Genetex Incorporated (US)

FEATURES Location/Qualifiers

1..1819

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 68.1%; Score 709; DB 6; Length 1819;

Best Local Similarity 77.0%; Pred. No. 2.6e-162;

Matches 1025; Conservative 0; Mismatches 0; Indels 306; Gaps 1;

QY 1 ATGGAAGAAGTATGAAAATTAAGTAAAGCTGAGAGAGGGCTTATGGGTTGATTCAAA 60

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QY 61 TGCAGAAACAAACCTCTGACAAAGTAGTAGCTGTTAAAGAAATTTGTTGGAATCTGAGAT 120

Db 198 TGCAGAAACAAACCTCTGACAAAGTAGTAGCTGTTAAAGAAATTTGTTGGAATCTGAGAT 257

QY 121 GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAGACAT 180

Db 258 GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAGACAT 317

QY 181 CCAAACTCTGTAACCTCATCGAGTCTTACGAGAAAGAAAGAAATGCAATTTAGTTTTT 240

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QY 241 GAATACCTGTCATACACTTTTAAATGAGCTGGAAGAAACCCCAATGAGTTGCTGAT 300

Db 378 GAATACCTGTCATACACTTTTAAATGAGCTGGAAGAAACCCCAATGAGTTGCTGAT 437

QY 301 GGAGTGNATCAAGAGCGTATTAATGGCAACCTTCAAGCTCTTAATTTCTGTCAATACAT 360

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QY 361 AACTGTATTCACAGAGATATAAAGCTGAAATATTTCTAATTAAGCAAGCAAGTAATC 420

Db 498 AACTGTATTCACAGAGATATAAAGCTGAAATATTTCTAATTAAGCAAGCAAGTAATC 557

QY 421 AAGATTGTGACTTCGGGTTTGCACAAATTCG----- 453

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Db 978 GGTTCCTTCAGTCATATATGGGCTATTTGGTTGTTGTTTTCGAGAGCTCTCTGACAGGCCAG 1037

QY 595 CCACTGTGGCTCGAAAATCAGATGTGGACCAACTTTATCTGATATATCAGAACACTAGTA 654

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Db 1098 GAGACGGGGTTTCGCCATGTTGACAGGCTGGTCTCGAACTCTTTCAGCTCAAGTGATCCA 1157

QY 715 CCTGCGTAGCCTCTCAAAAGTCTGGAATTCAGGAGAAATTAATCCCAAGACATCAATCA 774

Db 1158 CCTGCGTAGCCTCTCAAAAGTCTGGAATTCAGGAGAAATTAATCCCAAGACATCAATCA 1217

QY 775 ATCTTTAAAGTAACGGGTTTTCATATGTCATCAGTATACCTGAGCCAGACATGGAA 834

Db 1218 ATCTTTAAAGTAACGGGTTTTCATATGTCATCAGTATACCTGAGCCAGACATGGAA 1277

QY 835 ACTCTTGAGAAAAGTTCTCAGATGTTTATCTCTGTGGCTCTGAACTTTCATGAAGGGTGT 894

Db 1278 ACTCTTGAGAAAAGTTCTCAGATGTTTATCTCTGTGGCTCTGAACTTTCATGAAGGGTGT 1337

QY 895 CTGAAGATGAATCCAGATGACAGATTTAACCTGTTCCCACTCTCGAGAGCTCTCTACTTTT 954

Db 1338 CTGAAGATGAATCCAGATGACAGATTTAACCTGTTCCCACTCTCGAGAGCTCTCTACTTTT 1397

QY 955 GATTCCTTTTCAAGAGGCCCAATTAAGAGAAAGCAACGTAATGAAGGAAAGAAACAGAAGA 1014

Db 1398 GATTCCTTTTCAAGAGGCCCAATTAAGAGAAAGCAACGTAATGAAGGAAAGAAACAGAAGA 1457

QY 1015 CGCCACACAGGT 1025

Db 1458 CGCCACACAGGT 1468

RESULT 14

AX286069 687 bp DNA linear PAT 20-NOV-2001

LOCUS Sequence 3 from Patent WO0179488.

DEFINITION AX286069

ACCESSION AX286069

VERSION AX286069.1 GI:17045995

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	1	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS	Kapeller-Libermann, R.	
TITLE	14257, protein kinase molecules and uses therefor	
JOURNAL	Patent: WO 0179488-A 1 25-OCT-2001;	
FEATURES	Millennium Pharmaceuticals, Inc. (US)	
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Best Local Similarity	99.4%;	Pred. No. 7.7e-147;
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Qy	61	TGCAGAAACAAACCTCTGGAACAGTAGTCTGTTAAAAAATTTGGAAATCTGAAGAT 120
Db	61	TGCAGAAACAAACCTCTGGAACAGTAGTCTGTTAAAAAATTTGGAAATCTGAAGAT 120
Qy	121	GATCCTGTTTAAAGAAATAGCACTAAGAGAAATACATATGTTGAAGCAATTAACACAT 180
Db	121	GATCCTATTTTAAAGAAATAGCACTAAGAGAAATACATATGTTGAAGCAATTAACACAT 180
Qy	181	CCAATCTTGTGAACCTCATCGAGGTGTTCAAGAGAAAGAAAGAAATGCAATTTAGTTTTT 240
Db	181	CCAATCTTGTGAACCTCATCGAGGTGTTCAAGAGAAAGAAAGAAATGCAATTTAGTTTTT 240
Qy	241	GAATACCTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGGTTGCTGAT 300
Db	241	GAATACCTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGGTTGCTGAT 300
Qy	301	GGAGTGATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTCTATATACAT 360
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Qy	361	AACGTATTACAGAGATATAAAACCTGAAATATTTCTTAATCTAAGCAAGGAATATC 420
Db	361	AACGTATTACAGAGATATAAAACCTGAAATATTTCTTAATCTAAGCAAGGAATATC 420
Qy	421	AAGATTGTTGACTTCGGGTTTGCAAAATCTGATTCCAGAGATGCTTACACCGATTAT 480
Db	421	AAGATTGTTGACTTCGGGTTTGCAAAATCTGATTCCAGAGATGCTTACACCGATTAT 480
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Qy	541	TCAGTCGATATATGGGCTATTGGTTGTTTTCAGAGCTCCTGACAGCCGACCTG 600
Db	541	TCAGTCGATATATGGGCTATTGGTTGTTTTCAGAGCTCCTGACAGCCGACCTG 600
Qy	601	TGGCCTCGAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACACTAG 652
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LOCUS	AX286067	882 bp DNA linear PAT 20-NOV-2001
DEFINITION	Sequence 1 from Patent WO0179488.	
ACCESSION	AX286067	
VERSION	AX286067.1	G1:17045993
KEYWORDS		
SOURCE		
ORGANISM		
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	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	

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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_est2.*
3: gb_hc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	405	42.9	670	6	BY733578 BY733578
3	401.8	42.5	1691	3	AK016781 Mus muscu
4	390.6	41.3	825	6	CB315094 AGENCOURT
5	361	38.2	536	5	BU686325 UI-CF-DU1
c 6	360.2	38.1	689	6	BY752739 BY752739
7	333.6	35.3	500	1	AI385966 ml34h09.y
8	319.4	33.8	824	3	BU221831 603750354
9	316.8	33.5	757	7	CK482747 AGENCOURT
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11	306.8	32.5	598	2	AV986182 AV986182
12	296.2	31.3	806	7	CK472415 AGENCOURT
13	289.2	30.6	597	5	BP016186 BP016186
14	275.8	29.2	1956	3	AY383681 Rattus no
15	269.8	28.6	565	6	CB400506 OSTF177F1
16	261.2	27.6	1462	9	AY412140 Homo sapi
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19	255	27.0	718	1	AA286088 vc33b05.r
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23	247.8	26.2	504	5	BK304025 BX304025
24	242	25.6	1462	9	AY412141 Pan trogl

25	239	25.3	485	2	AV960213	AV960213
26	238.2	25.2	722	7	CK237628	CK237628 AGENCOURT
27	232.6	24.6	790	7	CK597959	CK597959 AGENCOURT
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29	227.2	24.0	1064	5	BU120363	BU120363 603142234
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c 31	226	23.9	774	5	BM110560	BM110560 BM110560
32	224.2	23.7	2005	3	AK090045	AK090045 Mus muscu
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35	222.6	23.6	1893	3	AK050990	AK050990 Mus muscu
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39	216.2	22.9	432	6	CB757579	CB757579 AMGNNUC:N
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ALIGNMENTS

RESULT 1
LOCUS CB169554 695 bp mRNA linear EST 30-JAN-2003
DEFINITION RUC603000752.R1 CSEQFXN20 testes Bos taurus cdna, mRNA sequence.
ACCESSION CB169554
VERSION CB169554.1 GI:28155681
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE 1 (bases 1 to 695)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Adelson, D.L. and Gill, C.A. Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
TITLE Bovine ESTs (Adelson and Gill) Bovinae; Bos.
JOURNAL Unpublished (2003)
COMMENT Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
USA
Tel: 9798452616
Fax: 9798456970
Email: david.adelson@tamu.edu.

FEATURES
source Location/Qualifiers
1..695
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="testes"
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normalized Rd 1 library, sequenced 3' with M13R primer."

ORIGIN
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Best Local Similarity 92.8%; Pred. No. 1.8e-111;
Matches 504; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

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QY 301 GGAGTGATCAAAAGCGTATTATGCGAAACACTTCAAGCTCTTAATTTCTGTCTATATACAT 360
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QY 421 AAGATTGTGATCTCGGTTTGGCAAAATTTCTGATCCAGAGATGCTACACCGATTAT 480
Db 123 AAGATCTGTGACTTTGGGTTTGCACGAATTTCTGATTCAGGAGATGCTACACTGACTAC 64
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Db 3 TCA 1

RESULT 2
BY733578
LOCUS BY733578
DEFINITION BY733578.1 GI:27146705
ACCESSION BY733578
VERSION BY733578.1
KEYWORDS 670 bp mRNA linear EST 17-DEC-2002
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 670)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamana,K., I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Buit,C.,
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusica,V.,
Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,
Santelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K.,
Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M.,
Verardo,R., Wagner,L.G., Wainwright,C., Wang,Y., Watanabe,Y.,
Wells,C., Wilming,L.G., Wyshaw-Boris,A., Yanagisawa,M., Yang,I.,
Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P.,
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M.,
Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K.,

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Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K.,
Shingawa,A., Tasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
JOURNAL PUBMED
MEDLINE
COMMENT
Contact: Yoshihide Hayashizaki
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Fax: 81-45-503-9216
Email: genome-resescg.riken.jp, URL: http://genome.gsc.riken.jp/
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
FEATURES
Location/Qualifiers
source 1..670
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ORIGIN
Query Match 42.9%; Score 405; DB 6; Length 670;
Best Local Similarity 85.6%; Pred. No. 3.5e-92;
Matches 450; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
QY 1 ATGGAAAAGTATGAAAATTTAGCTAGACTGGAGAGGGTCTTATGGGGTTGTATTCAAA 60
Db 145 ATGGAAAAGTATGAAAAGCTAGCTAGATCGGAGAGGGTCTTATGGCGTGTGTATTCAG 204
QY 61 TCGAGAAACAAACCTCTGACCAAGTAGTAGCTGTGTAAAAAATTTGTGAATCTGAAGAT 120
Db 205 TCGAGAAACAAATCTTCTGCAACAGTAGTAGCGATCAAAAAATTCGTGGAATCTGAAGAT 264
QY 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACACAT 180
Db 265 GATCCTGTTGTTAAGAAAAATAGCACTTGGCGGAATCCCTGCTGCTGAGCAGCTTGAACAC 324

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Qy	181	CCAAATCTGTGAACCTCATCGAGTGTTCAGAGAAAGAAATGCAATTTAGTTT	240
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Qy	241	GAATACTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT	300
Db	385	GAGTACTGTGATCATACACTTTTAAACGAGCTGGAGAGAAACCCAAACGAGTTTCTGAT	444
Qy	301	GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT	360
Db	445	GGAGTGATTAAGAGTGTCTATGTCGCAACCTTCAAGCCCTTAATTTCTGTCACAAAGCAC	504
Qy	361	AACGTATTTCACAGAGATATAAACCTGAAATTTCTTAATACTACGAGGAATATC	420
Db	505	AATGTATTTCATCGGATGTAAACCTGAAACATCTCTAAACCAAGCAAGGATGATA	564
Qy	421	AAGATTTTGTGACTTCGGGTTTGCACAAATTTCTGATTCAGAGAGATCCCTACACCGATTAT	480
Db	565	AAGATTTTGTGACTTTGATTTGCAGGATTTCTAATTCAGAGAGCGCTACACAGACTAT	624
Qy	481	GTAGCTACGAGATGGTACCGAGCTCTGAATCTTCTTGTGGAGATA	526
Db	625	GTTGCCACAGGTGTGACCGAGCCGCAACTTCTCGTGGGAGACA	670
RESULT 3			
AK016781			
LOCUS			
DEFINITION			
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177 ATGGAATAATGAAAAATGGAAGATTGGAAGGCTCTATGGGTAGTGTCAAG 236
61 TGCAGAAACAAACCTCTGGACAGTAGTACTGTTAAAAATTTGGATCTGAAGAT 120
237 TGCAGAAACAGGACACGGGTGAGATGCTGGCCATCAAGAGGTTCTTGGAAACGAGAT 296
121 GATCCTGTGTTAAAGAAATAGCACTAAGAGAAATACGTATGTTGAAAGCAATTAACAT 180
297 GACCTGTGTCATAAGAAATACGCTTCGAGAAATCGCATGCTCAAGCACTCAGCAC 356
181 CCAATCTGTGAACCTCATCGAGGTGTTTACGAGAAAGAAATGCAATTTAGTTT 240
357 CCCAACCTGTGCTCAACCTCTGGAAGTCTTCCGAGGAAAGCGAGGCTTCACTGCTGTC 416
241 GAATCTGTGATCATATACATTTTAAATGAGCTGGAAGAAACCAATGAGTTGCTGAT 300
417 GAGTACTGCGACCAACAGCGTCTTCAAGCTGATCGGATCGGATCAGAGGGGGGTACACGAG 476
301 GGAGTGATCAAAAGCGTATTATGCAACACATTCAGCTCTTAATTTCTGTCTATATACAT 360
477 CCTCTGTGAAGAACATAAATTCGACACACTGACGCTGTAAATTTCTGCCATAACAT 536
361 AACTGTATTACAGAGATATAAAACCTGAAATATTCTTAATACTAAGCAAGGAATATC 420
537 AACTGTCATACAGAGACGTGAAGCCGGAATATTTCTCATCAACAAACAGTCAGCCATT 596
421 AAGATTGTCATCTCGGTTTGCACAAATCTGATT---CCAGAGATGCTCACACCGAT 477
597 AAGCTCTGTGACTTTGGGTTGCGACGGCTTCTACTGGACAGGTGACTACTACACGGAC 656
478 TAGTAGTACGAGATGATGACGAGCTCTGAACTTCTTGTGGAGATATCTCAGTATGTT 537
657 TACGTGCCACCGGTGTACCGCTCACCGAGCTGTAGTGGGAGACACGCGATGTT 716
538 TCCTCAGTCGATATATGGCTATTTGTTGTTTTCGACAGCTCTCGACAGCCAGCCA 597
717 CCCCCTGTAGATGTCGGCAATTTGGCTGTGTGTTGCTGAGTTACTGTCCGGAGTGCCT 776
598 CTGTGGCTCGAAATCAGATGTGACCAACTTTTCTGTGATATCAACAACTAGGAATA 657
777 CTATGGCCAGGAATACTGACGTGGATCAGCTTACTGTGATAGGAATAACCTTGGGGGAC 836
658 TTAATCCAGACATCAATCAATCTTTAAAGTAAACGGGTTTTTCCATGGCATCAGTATA 717
837 CTCAATCCAGGACACGAGCAAGTATTAGCATGAATCAATCTTCACTGAGGTGAAAT 896
718 CTTGAGCCAGACATGGAACCTCTTGAAGAAAGTTCTCAGATGTTATCTCTGCTGCT 777
897 CCAGACCTGAAGACATGGAACAATTGAGTTGAAATTTCCAAACATCTCTACTCTGCA 956
778 CTGAACCTTCATGAAGGGGTGCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCTCA 837
957 CTGGCTCTTAAAGGCTGCTCCATGATGATCTGCTGAGAGGCTGATCGGAACAG 1016
838 CTCCTGGAGAGCTCTTACTTTGATTTCTTTTCAAGAGG 874
1017 CTGTTGAGCATCCATATTTTGACAGCATTCGAGAAG 1053

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RESULT 4
CB315094
LOCUS
DEFINITION
  CB315094 825 bp mRNA linear EST 04-MAR-2003
  IMAGE:6888377 5', mRNA sequence.
VERSION
  CB315094
KEYWORDS
  EST.
  Rattus norvegicus (Norway rat)
  Rattus norvegicus
  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
  Rattus.

```

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 825)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-i@mail.nih.gov
Tissue Procurement: John C. Marshall, M.D., Ph.D.
CDNA Library Preparation: CLONTECH
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: L10M3144 row: i column: 16
High quality sequence stop: 468.

FEATURES
source

Location/Qualifiers
1..825
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/mol_type="mRNA"
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/clone="IMAGE:6888377"
/tissue_type="Pituitary"
/lab_host="DH10B"
/clone_lib="NICHDRr Pit1"
/notes="Vector: pDNR-LIB; Site 1: SfiI; Site 2: SfiI; 5'
and 3' adaptors were used in Cloning as follows: 5'
adaptor sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-dr(30)BN-3'
(where B = A, C, G, or T). Average
insert size 1.23 kb (range 0.5-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 41.3%; Score 390.6; DB 6; Length 825;
Best Local Similarity 83.3%; Pred. No. 1.7e-88;
Matches 455; Conservative 0; Mismatches 90; Indels 1; Gaps 1;
QY 361 AACTGTATTCACAGATATATAACCTGAAATATTCTAATACTAAGCAAGAAATATC 420
DB 96 AGCTGTATCCATCGGACGCTAAACCCGAAACATCTTAATAGCCAAGAGGTGATA 155
QY 421 AAGATTGTGACTTCGGGTTTGACAAATTTCTGATTCAGAGATGCTTACACCGATTAT 480
DB 156 AAGATTGTGACTTCGGATTTCGACGATTTCTAATTCAGAGATGCTTACAGACTAT 215
QY 481 GTAGCTACGAGATGGTACCGAGCTCTCGAACTTTCTGTGGAGATATCTCAGTATGTTCT 540
DB 216 GTTGCCACCAAGGTGTACCGAGCCCTGAACTTTCTGTGGAGACACGAAGTACGGCTCC 275
QY 541 TCGTGTATATATGGCTATTGTTGTTGTTTTCAGAGCTCTTTCAGAGCCAGCCACTG 600
DB 276 TCTGTGACATATGCGCTGTGCGCTGTGTTTTCAGAGCTCTTTCAGCGCTCAGCCACTC 335
QY 601 TGGCTGGAATAATCAGATGTGACCAACTTTATCTGATATCAGAACACTTAGGAAATTA 660
DB 336 TGCCAGGAAATCAGATGTGACCACTTTATCTGATCATCAGGACATTTGGAAAGCTG 335
QY 661 ATCCCAAGACATCAATCAATCTTTAAAGTAAAGGGTTTTTCCATGGCATCAGTATACCT 720
DB 396 ATCCCAAGGATCAGTCTATCTTTAAAGTAAACAGTTTTCGTTGGCATCAGCATACCC 455
QY 721 GAGCCAGAGACATGGAACCTCTTGAGGAAAGTTCTCAGATGTTTCTCTGTGGCTCTG 780
DB 456 GAACCTGAGGACATGAGACTCTTGAAGAAATAATCTCAAAATGTTTCAGGCTATGGCTTTA 515
QY 781 AACTTTCATG-AAAGGGGTGTCTGAAGATGAATCAGATGACAGATTAACCTGTTTCCCAACT 839
DB 516 AGTTTTCATGAAGGGGTGTCTGAAGATGATCTCTGATGAGAGGCTGACCTGTGCCAGCT 575
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ORIGIN

Query Match 35.3%; Score 333.6; DB 1; Length 500;
 Best Local Similarity 82.3%; Pred. No. 5.3e-74;
 Matches 408; Conservative 0; Mismatches 84; Indels 4; Gaps 2;

QY 135 GAAATAGCACTAAGAGAAATACGTATGCTTCAAGCAATTAACCAATCAAACTCTGTGAA 194
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 Db 2 GAAATAGCCCTGCGGAAATCCGTATGCTGAAG---TTGAACACCAACCAACCTCGTGA 58
 |||||
 QY 195 CCTCATCGAGTGTTCAGAGAAAAAGAAATGCATTAGTTTGAATACTGTGATCA 254
 |||||
 Db 59 CCTCATCGAGTGTTCAGAGAAAGAGAAAGATGCACTAGTTTGTAGTACTGTATCA 118
 |||||
 QY 255 TACACTTTTAAATGAGCTGGAAGAAAGAAACCCAAATGGAGTGTCTGATGAGATGATCAAAAG 314
 |||||
 Db 119 CACACTGTAAACGAGCTGGAGAGAAACCCAAACGGAGTTTCTGATGAGTGATTAAGA 178
 |||||
 QY 315 CGTATTATGCAACACTTCAAGCTCTTAATTTCTGTCAATATACATCACTATTCACAG 374
 |||||
 Db 179 TGTGCTATGGCAACCCCTTCAAGCCCTTAACCTTCTGTCAAGCACCAATTTATTCATCG 238
 |||||
 QY 375 AGATATAAAGCTGAAATATTTCTAATAAATAAGCAAGGAATAATCAAGATTTCGTGACTT 434
 |||||
 Db 239 GGATGTAAACCTGAAACATCTTAATAACCAAGCAAGGATGATAAGATTTCGTGACTT 298
 |||||
 QY 435 CGGTTTGCACAAATTCGATTCAGGAGATGCTTACACCGATATATGTAGCTACGAGATG 494
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 Db 299 TGGATTTCACCAATTCCTAATTCAGGAGACGCTTACACACTATGTTGACCAAGTG 358
 |||||
 QY 495 GTACCGAGCTCTGAACCTTCTTGGGAGATACCTCAGTATGTTCTTCAGTGCATATATG 554
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 Db 359 GTACCGAGCCCTCGAATCTTCGTGGGAGACCAAGTACGGTTCCTCTGTAGACGTGTG 418
 |||||
 QY 555 GGCTATTGTTGTTGTTTTCAGAGCTCTCTGACAGGCGAGCCACTGTGGCCCTGGAATATC 614
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 Db 419 GGCCGTGCGTGTGTTTATGACAGAGCTTCTGACGTGTGACCACTCTGGCCCGG-AAATA 477
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 QY 615 AGATGTGGACCACTT 630
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 Db 478 CGAGCTGGACCACTT 493
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RESULT 8
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 LOCUS 603750354F1 CSEQH04 Gallus gallus linear EST 25-NOV-2002
 DEFINITION 824 bp mRNA clone CHEST661113 5', mRNA
 sequence.

ACCESSION BU221831.1 GI:25410266

VERSION EST.

KEYWORDS Gallus gallus (chicken)

SOURCE Gallus gallus

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 824)

AUTHORS Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,

Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.

TITLE A Comprehensive Collection of Chicken cDNAs

JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)

MEDLINE 22335534

PUBMED 12445392

COMMENT Contact: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

1. .824

FEATURES

source

/organism="Gallus gallus"
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 /strain="White Leghorn, Hisex"
 /db_xref="taxon:9031"
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 /lab_host="DH10B"
 /clone_lib="CSEQH04"
 /note="Organ: whole embryo; Vector: pBluescript II KS(+);
 Site 1: EcoRI; Site 2: NotI; This normalized library was
 constructed from 1 million independent clones. cDNA
 synthesis was initiated using an oligo(dT) primer, using
 methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was bluntended, ligated to NotI adapters, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

ORIGIN

Query Match 33.8%; Score 319.4; DB 5; Length 824;
 Best Local Similarity 67.2%; Pred. No. 2.4e-70;
 Matches 483; Conservative 0; Mismatches 231; Indels 5; Gaps 2;

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 Db 2 TCCTACGGCGTGTCTTCAAGTCCGCAACAGGGAGACGGGGCAGATCGTGGCCATCAAG 61
 |||||
 QY 100 AAATTTGTGGAATCTGAAGATGATCCTGTGTTTAAAGAAATAGCACATAAGAGAAATACGT 159
 |||||
 Db 62 AAGTTCCTCGAGTCCGAGAGAGCCCGGTGATCCGGAAGATCGCGCTCGGGAGTCCGC 121
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 QY 160 ATGTTGAAGCAATTAACATCCAAATCTTGTGTAACCTCATCGAGGTGTTTCAGAGAAAA 219
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 Db 122 ATGCTGAAGCAACTGAAACACCCCAACCTGTGTAACCTGTGGAGGTGTTTCAGAGAAAG 181
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 QY 220 AGGAAATGCAATTTAGTTTGTGTAATCTGTGATCATACACTTTTAAATAGCTGGAAGA 279
 |||||
 Db 182 AGGAAGCTGCACCTGGTCTTTGAGTACTGTGACACACACCGTCTCCACGAGCTGGAAG 241
 |||||
 QY 280 AACCAATAGAGTGTGCTGATGGAGTATCAAAAGCGTATTATGGCAAAACACTTCAAGCT 339
 |||||
 Db 242 CACCCCGGGGGTCCGGAGAGCTGTCAGNGCATTACCTGGCAGACCCCTCCAACT 301
 |||||
 QY 340 CTTAATTTCTCATATACATACTGTAATTCACAGAGATATAAAACCTGAAAAATATTCTA 399
 |||||
 Db 302 GTGAACCTTTGTCAAAACACAACTGCATCCATCGAGATGTAAAGCCAGAAACATCCTG 361
 |||||
 QY 400 ATAATTAAGCAAGAAATATCAAGATTGTGACTTCGGGTTTGCACAAATTCGATT--- 456
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 Db 362 ATAACGAAGCACTCCATCATCAAACTCTGTGACTTCGGATTGCTGCATGCTGACTGGC 421
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 QY 457 CCAGGAGATGCCCTACACCGCATTTAGTACTACAGATGTTGACCGAGCTCCTGAACTTCTT 516
 |||||
 Db 422 CCAGGTGATTACTACACAGACTACGTGGCAACCGAGGTGTACCGCTCCACAGAGCTGTG 481
 |||||
 QY 517 GTGGAGATACTCAGTATGTTTCTTCAATCGATATATGGGCTATTTGGTGTGTTTTCGA 576
 |||||
 Db 482 GTGGGGACACGAGTATGGCCCTCTCTGTGACGCTGTGGGCAATAGGCTGTGTCTTTGG 541
 |||||
 QY 577 GAGCTCTGACAGCCAGCCACTGTGGCCCTGGAAAAATCAGATGTGGACCACTTTATCTG 636
 |||||
 Db 542 GAGCTGCTCTCCGGGTGGCCACTGTGGCCCGGCAAGTCAGACGTGGACCACTGTACCTC 601
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 QY 637 ATAATCAGAACACTTAGGAAATTAATCCCAAGACATCAATCAATCTTTAA--AAGTAAAG 694
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 /lab_host="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene mouse testis (#937308)"
 /note="Organ: testis; Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"

ORIGIN

Query Match 33.5%; Score 316.8; DB 1; Length 938;
 Best Local Similarity 82.9%; Pred. No. 1.1e-69;
 Matches 398; Conservative 0; Mismatches 77; Indels 5; Gaps 3;

Qy 135 GAAATAGCCTAAGAGAAATACGTATGTTGAAGCAATTAACATCCAAATCTGTGAA 194
 Db 1 GAAATAGCCTGCGGGAATCCGTGTCTGAAG---TTGAACACACCAACCTCGTGA 57

Qy 195 CCTCATCGAGTGTTCAGAGAAAGAAAGAAATGCATTAGTTTGAATCTGTGATCA 254
 Db 58 CCTCATCGAGTGTTCAGAGAAAGAAAGATGCACTAGTTTGAATCTGTGATCA 117

Qy 255 TACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGATGGAGTGATCAAAAG 314
 Db 118 CACACTGTAAACGAGCTGGAGAGAAACCCAAACGGAGTTCTGATGGAGTGATTAAG 177

Qy 315 CGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCATATACATCTGATTTACAG 374
 Db 178 TGTGCTATGGCAACCTTCAAGCCCTTAACCTTCTGTCAAGCACAAATTTGATTCATCG 237

Qy 375 AGATATAAACCTGAAATATTTCTAATACTAAGCAAGGAATATCAAGATTTGGAATT 434
 Db 238 GGATGTAAACCTGAAACATCTTAATAACCAAGCAAGGAGTGAATAAGATTTGGAATT 297

Qy 435 CGGTTTGGCAAAATTTCTGATTCAGGAGATGCCCTACACCGCATTTATGTAGCTACGAGATG 494
 Db 298 TGGATTTGCAGCAATTTCTAATTCAGGAGAGCGCTACACAGCTATGTTGCCACCGTG 357

Qy 495 GTACCGAGCTCTGAATCTTGTGGGAGATCACTCAGTATGGTTCTTCAGTCGATATATG 554
 Db 358 GTACCGAGCCCCGAACTTCTCGTGGGAGACACGAAGTACGGTTCCTCTGTAGACGTGTG 417

Qy 555 GGCTATTGTTGTGTTTTCAGAGCTCTTCAGAGCCGACGACCTGTGGCTGGAAATC 614
 Db 418 GGCCGTGGCTGTGTTTTCAGAG-CTCCTGACGGGTGAG-CACTCTGGCCGGGAAAC 475

RESULT 11
 AV986182 598 bp mRNA linear EST 14-MAR-2002
 LOCUS
 DEFINITION AV986182 Nori Satoh unpublished cDNA library, larva Ciona
 intestinalis cDNA clone cilv41b18 5', mRNA sequence.

AV986182
 AV986182.1 GI:19475050
 EST.
 Clona intestinalis
 Clona intestinalis
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
 Phlebobranchia; Cionidae; Ciona.

1 (bases 1 to 598)
 Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
 Expressed genes in Ciona intestinalis
 Unpublished (2000)
 Contact: Nori Satoh
 Department of Zoology
 Kyoto University
 Sakyo-ku, Kyoto 606-8502, Japan

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 Tel: 81-75-753-4081
 Fax: 81-75-705-1113

Email: satoheascidian.zool.kyoto-u.ac.jp.

FEATURES

source
 1. 598
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 /clone="cilv41b18"
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ORIGIN

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 Best Local Similarity 70.7%; Pred. No. 3.7e-67;
 Matches 423; Conservative 0; Mismatches 172; Indels 3; Gaps 1;

Qy 11 ATGAAAAATAGCTTAAGACTGGAGAGGGTCTTATGGGTTGTATTCAAATGCGAAACA 70
 Db 1 ATGGAAGATAGGTAAAGTAGGGGAAGGATCTATGGCATTTGTTTAAATGTGGAACC 60

Qy 71 AAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTTGGAAATCTGAAGATGATCCTGTTG 130
 Db 61 GTGACTCGGACAAATTTGTGCCCATCAAAAAATTTGTGAGTCAAGAGATGACCCGTGA 120

Qy 131 TTAAGAAAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACATCCAATCTTG 190
 Db 121 TCAGAAAAATCGCGCTGAGGGAATCAGAATGTTTAAAGCAATTTGAACACACAATAACTTGG 180

Qy 191 TGAACCTCATCGAGTGTTCAGGAGAAAAAGAAAAATGCATTTAGTTTTCGAATCTGTG 250
 Db 181 TGAACCTGATTGAAGTTTTCGTCGAAAAACGCAATTTACATCTTGTGTTTGAAGTATGTTG 240

Qy 251 ATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGATGAGAGTGATCA 310
 Db 241 ATCATACAGTTTAAATGAATTTGCAACACACATGAGAGGAGTACCAGAACATCATGTGA 300

Qy 311 AAACGCTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCATATACATAACTGTATTTC 370
 Db 301 AACGTATTGTTGGCAAGTTCTTCAAGCTGTCTCACTTTTGGCATCAGCATAAATTTGATAC 360

Qy 371 ACAGAGATATAAACCTTGAAATATTCTAATACTTAAGCAAGGAATTAATCAAGATTTGTG 430
 Db 361 ATCGTGAITGAACACGAGAAACATATTAATCATTAAGCAAGGTGTTATCAAGTTGTG 420

Qy 431 ACTTCGGGTTTGCAAAATTTCTGA---TTCCAGAGATGCCCTACACCGATTTATGTAGCTA 487
 Db 421 ACTTTGGATTGCAAGAATTTTAACTGCTCTGCGACGATTACACCGACTATGTGGCCA 480

Qy 488 CGAGATGTTACCGAGCTCCTGAACTTCTTGTGGAGATACATCAGTATGTTTCTTCAGTCG 547
 Db 481 CTAGTGTGTACAGACACCTGAGCTCCTCGTGGGGACACTCAGTATGGCCCTCCAGTGG 540

Qy 548 ATATATCGGCTATTGTTGTTTTCAGAGCTCCTGACAGCGCCAGCCACTGTGGCC 605
 Db 541 ATGTGTGGCAATAGTTGCGTATTGCCGAGTTGTTGTGCGGACAGGCATATATGGCC 598

RESULT 12

CK472415

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 806)

NIH-MGC

http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

**JOURNAL
COMMENT**

Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs@mail.nih.gov
Tissue Procurement: Howard Jacobs
cDNA Library Preparation: Express Genomics
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAMI5022 row: e column: 17
High quality sequence stop: 657.
Location/Qualifiers
1. .806
/organism="Rattus norvegicus"
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/clone="IMAGE:7127611"
/tissue_type="kidney, pooled"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 236"
/note="Organ: kidney; Vector: pExpress-1; Site: 1: EcorV;
Site: 2: NotI; RNA obtained from pooled kidney tissue from
a mix of male and female animals at 8 wk old. Tissues were
snap-frozen and kept at -80C for two days before RNA
extraction and purification (Tri-reagent method). cDNA was
primed using oligo-dT primer:
5'-pGACTAGTCTTCGAGCGGCCCGCC(T)25-3' and cloned into
the EcorV/NotI sites of pExpress-1. Size-selection >1.4Kb
resulted in an average insert size of 2.2 Kb. This primary
library is normalized (non-normalized primary library is
NIH MGC 235) and was constructed by Express Genomics
(Frederick, MD). Note: this is a NIH MGC library."

ORIGIN

Query Match	31.3%	Score 296.2	DB 7	Length 806
Best Local Similarity	67.3%	Pred. No. 2e-64		
Matches 434	Conservative 0	Mismatches 208	Indels 3	Gaps 1
152	AAATAGCTATGTTGAAGCAATTAATAACATCCAAATCTTTGTGAACCTCATCGAGGTGTCA	211		
1	AAATCCGATGCTCAAGCAACTACGCATCCCAACTCGTCAGCCTCTCGAAGTCTTCC	60		
212	GGAGAAAAAGGAAATGCAATTTAGTTTGTGAATACTGTGATCATACACTTTTAAATGAGC	271		
61	GCAGGAAGCGGGCGCTTCACCTGGTGTGAGTACTGCCACCACACGGGTGCTTTCAGGAGC	120		
272	TGGAAGAAACCCAAATGAGTTGCTGTGAGGTGATCAAAAGCGTATTATGCGCAACAC	331		
121	TGGAAGATATCAGAGGGGGTACAGAGCGCTCTCGTGAACAATAACTTGGCAGACAC	180		
332	TTCAAGCTCTTAATTTCTGTCATPATACATAACTGTATTACAGAGATATAAAACCTGAAA	391		
181	TGCAGGCTGTGAATTTCTGCATAAACAACAACCTGTCATACAGAGATGTGAAGCCGGAA	240		
392	ATATTCTAATAACTAGCAAGGAATAATCAAGATTGTCAGCTTCGGGTTTGCACAATTC	451		
241	ACATCTCATCAACCAACACTCAGTCATTAAGCTCTGTGACTTTGGGTTTGCACGGCTTC	300		
452	TGATTT---CCAGAGATGCTTACACCGATATGTAGTACTACGAGATGGTACCGAGCTCTCG	508		
301	TCACGTGACCTGGTGACTACTACACTGACTACGTGGCCACCGAGTGGTACCGCTCACCTG	360		
509	AACTTCTCTGTGGAGATACCTCAGTATGGTTCTTTCAGTCGATATATCGGCTATTGGTTG	568		
361	AGCTGCTAGTGGAGACACACAGTATGGCCCCCAGTAGTGTCTGGCANAATTTGGGTGTG	420		
569	TTTTTTCAGAGCTCTCTGA CAGGCCAGCCACTGTGGCTGGAAAAATCAGATGTGGACCAAC	628		
421	TGTTTGTCTGAGTTGCTGTC CGAGGTGCTCTGTGGCCAGAAAAATCCGATGTGGACGAGC	480		

Qy	629	TTTATCTGATATTCAGAACACTAGGAAATTAATCCCAAGACATCAATCAATCTTTTAAA	688
Db	481	TCTATCTGATAAGGAAACCCCTGGGGGACCTCATTTCCAGGCAACCAAGTATTTAGCA	540
Qy	689	GTAACGGGTTTTTCATGGCATCAGTATACTCTGACCCAGAAGACATGGAACTCTTTGAGG	748
Db	541	TGATCAGTACTTCAGTGGGGTGAAATTCAGACCCCTGAAGACATGGAAACACTTGAGT	600
Qy	749	AAAAGTTCTCAGATGTTTCATCCTGTGGCTCTGAACTTCATGAAGG	793
Db	601	TGAAGTTTCCAAACATCTCCTTACTCTGCTCTGGGCTTCTTAAGGG	645
RESULT 13			
BP016186			
LOCUS			
DEFINITION			
BP016186 Nori Satoh unpublished cDNA library, young adult Ciona			
intestinalis cDNA clone ciad64e08 5', mRNA sequence.			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
Ciona intestinalis			
Ciona intestinalis			
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;			
Phlebobranchia; Cionidae; Ciona.			
1 (bases 1 to 597)			
Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.			
Expressed genes in Ciona intestinalis			
Unpublished (2000)			
Contact: Nori Satoh			
Department of Zoology			
Kyoto University			
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan			
Tel: 81-75-753-4081			
Fax: 81-75-705-1113			
Email: satoh@ascidian.zool.kyoto-u.ac.jp.			
Location/Qualifiers			
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adult"			
FEATURES			
source			

[illegible]

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 Db 338 ATCATGTTAAAGCTATTGTTGGCAAGTCTTCAAGCTGTTCACTTTTGCCATCAGCAT 397
 Qy 362 ACTGTATTACAGAGATATAAAACCTGAAATATTCTAATAAATAAGCAAGCAATAATCA 421
 Db 398 ATTGTATACATCGTGATGTAAACAGAGACATATTATCACTAAGCAAGGTGTATCA 457
 Qy 422 AGATTGTGACTTCGGGTTTGACAAATTTCTGA---TTCCAGGAGATCCCTACACCGATT 478
 Db 458 AGTTGTGTGACTTTGGATTGCAAGAAATTTAACTGGTCTCTGGCGCAGCATTACACCGACT 517
 Qy 479 ATGTAGCTACAGATGGTACCGAGCTCTGCACTTCTTGTGGGAGATCACTCAGTATGTT 538
 Db 518 ATGTGGCCACTAGTGGTACAGAGCACCTGAGCTCTCTCGTGGGACACTCAGTATGGCC 577
 Qy 539 CTTCAGTCGATATATGGGC 557
 Db 578 CTNCAGTGGATGTGGGC 596

RESULT 14
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 ACCESSION AY383681
 VERSION AY383681.1 GI:37654267
 KEYWORDS
 SOURCE
 ORGANISM
 Rattus norvegicus (Norway rat)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 1956)
 Xu, C.S., Chang, C.F., Han, H.P., Wang, G.P., Chai, L.Q., Yuan, J.Y.,
 Yang, K.J., Zhao, L.F., Ma, H.H., Wang, L., Wang, S.F., Xing, X.K.,
 Shen, G.M., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.
 Liver regeneration after PH
 Unpublished
 2 (bases 1 to 1956)
 Xu, C.S., Chang, C.F., Han, H.P., Wang, G.P., Chai, L.Q., Yuan, J.Y.,
 Yang, K.J., Zhao, L.F., Ma, H.H., Wang, L., Wang, S.F., Xing, X.K.,
 Shen, G.M., Shi, J.B., Rahman, S., Wang, Q.N. and Zhang, J.B.
 Direct Submission
 Submitted (09-SEP-2003) Henan Bioengineering Key Lab, Henan Normal
 University, No. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R.
 China

FEATURES

source
 1..1956
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 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
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ORIGIN

Query Match 29.2%; Score 275.8; DB 3; Length 1956;
 Best Local Similarity 61.6%; Pred. No. 3.7e-59;
 Matches 458; Conservative 0; Mismatches 282; Indels 3; Gaps 1;
 Qy 1 ATGGAAGAAGTATGAAAAATAGCTAAAGACTGAGAGGGCTTATGGGGTGTATTCAA 60
 Db 1 ATGGAAGAAGTATGAAACCTTAGGATTGGTTGGAAGGGGAGTTACGGAATGGTGAAG 60
 Qy 61 TGCAGAAACAAAACCTCTGGACAAAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
 Db 61 TGTAGGAACAAAGACAGCTGGGAAGAAATTTGTGCCATTAAAGAGTTCTTTAGAGAGCGATGAC 120
 Qy 121 GATCCTGTTGTAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
 Db 121 GATAAAAATGGTTAAAGAAAGATCGCTATCGAGAAATCAAGTTTACTAAAGCAACTCGCGGAT 180
 Qy 181 CCAAAATCTTGTGAACCTCATCGAGGTGTTCAAGAGAAAAAGAAAAATCATTTAGTTT 240
 Db 181 GAAAAATTTGTGAACCTGTTTGGAAAGTGTGAAGAAAAAGAACGCTTGGTACTTGTACTT 240
 Qy 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT 300
 Db 241 GAATTTGTTGACCACACAGATTCTTGTAGACTTGAACCTCTTCCCAAATGGAGTAGACTAT 300
 Qy 301 GGAGTGATCAAAAGCGTATTATGCAACACACTTCAAGCTCTTAATTTCTGTCTATATACAT 360
 Db 301 CAAGTAGTTCAAAGTAGTATTTGTTTTCAGATCATTAATGGAATTTGGAATTTGCCATAGT 360
 Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTCTTAATAACTAAGCAAGGAATAATC 420
 Db 361 AATATCATACAGAGATATAAAACCCGAGNATATATTAGTCTCACAGTCTGGCGTTGTA 420
 Qy 421 AAGATTGTGACTTCGGGTTTGGCAAAATTTCTGAT---TCCAGAGATGCTCTACACCGAT 477
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 Db 481 TATGTGGCCACCCGGTGGTACAGAGCTCCAGAACTGCTGGTGGTATGTCAAGTACGCGC 540
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 Qy 658 TTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATA 717
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 Qy 718 CCTGAGCCAGAGACATGGAAC 740
 Db 721 CCTGAGATCAAGACATAGAAGC 743
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 ACCESSION CB400506
 VERSION CB400506.1 GI:30742233
 KEYWORDS
 SOURCE
 ORGANISM
 Caenorhabditis elegans
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
 1 (bases 1 to 565)
 Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M.,
 Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T.,
 Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
 Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V.,

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 21, 2005, 23:37:20 ; Search time 3580.63 Seconds
(without alignments)
1602.273 Million cell updates/sec

Title: US-10-766-691-11

Perfect score: 945

Sequence: 1 atggaagatgataaaatt.....aggtaattccgctcaaaagt 945

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5633728 seqs, 3035525691 residues

Total number of hits satisfying chosen parameters: 11267456

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	945	100.0	945	19	US-10-766-691-11
2	929	98.3	972	19	US-10-766-691-5
3	927	98.1	1790	17	US-10-333-314-30
4	868.8	91.9	1678	18	US-10-250-889-6
5	839	88.8	1041	19	US-10-766-691-9
6	823	87.1	1068	19	US-10-766-691-3
7	647	68.5	887	9	US-09-834-496A-3
8	647	68.5	882	9	US-09-834-496A-1
9	507	53.7	1819	19	US-10-766-691-13
10	454.4	48.1	561	19	US-10-766-691-1
11	454.4	48.1	594	19	US-10-766-691-7
12					Sequence 11, Appl
13					Sequence 5, Appli
14					Sequence 30, Appl
15					Sequence 6, Appli
16					Sequence 9, Appli
17					Sequence 3, Appli
18					Sequence 1, Appli
19					Sequence 13, Appl
20					Sequence 1, Appli
21					Sequence 7, Appli

12 415.4 44.0 1612 17 US-10-363-616-146 Sequence 146, App
13 413.8 43.8 1363 10 US-09-960-706-1079 Sequence 1079, Ap
14 413.8 43.8 2944 18 US-10-357-930-24573 Sequence 24573, A
15 287 30.4 1701 16 US-10-174-794-5 Sequence 5, Appli
16 287 30.4 3080 16 US-10-174-794-3 Sequence 3, Appli
17 283.8 30.0 2095 17 US-10-369-022-21 Sequence 21, Appl
18 283.8 30.0 2095 18 US-10-757-262-107 Sequence 107, Appl
19 227.4 24.1 1513 18 US-10-620-052A-33 Sequence 33, Appl
20 163.4 17.3 1635 14 US-10-072-036-112 Sequence 112, App
21 163.4 17.3 1635 14 US-10-072-036-114 Sequence 114, App
22 163 17.2 1297 11 US-09-969-034-4494 Sequence 4494, Ap
23 163 17.2 1297 16 US-10-295-681-28 Sequence 28, Appl
24 161.8 17.1 2213 17 US-10-440-464-137 Sequence 137, App
25 161.8 17.1 2213 17 US-10-641-643-1037 Sequence 1037, Ap
26 161.8 17.1 2734 18 US-10-723-860-7854 Sequence 7854, Ap
27 161.4 17.1 1322 9 US-09-925-300-324 Sequence 324, App
28 159.8 16.9 1297 16 US-10-295-681-30 Sequence 30, Appl
29 157 16.6 2213 16 US-10-295-681-40 Sequence 40, Appl
30 155.6 16.5 1050 9 US-09-954-456-84 Sequence 84, Appl
31 155.6 16.5 1050 9 US-09-954-456-718 Sequence 718, App
32 155.6 16.5 1050 9 US-09-954-456-1165 Sequence 1165, Ap
33 155.6 16.5 1050 11 US-09-968-007A-985 Sequence 985, App
34 155.6 16.5 1050 15 US-10-177-293-40 Sequence 40, Appl
35 155.6 16.5 1050 16 US-10-204-041-7 Sequence 7, Appli
36 155.6 16.5 1050 17 US-10-172-118-668 Sequence 668, App
37 155.6 16.5 1050 17 US-10-189-266-4 Sequence 4, Appli
38 155.6 16.5 1050 17 US-10-342-887-668 Sequence 668, App
39 155.6 16.5 1050 18 US-10-723-860-2447 Sequence 2447, Ap
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41 155.6 16.5 1050 19 US-10-843-641A-3745 Sequence 3745, Ap
42 155.6 16.5 1050 19 US-10-843-641A-4192 Sequence 4192, Ap
43 155.6 16.5 1050 19 US-10-843-641A-4192 Sequence 4192, Ap
44 155.6 16.5 1235 18 US-10-733-878-420 Sequence 7455, Ap
45 155.6 16.5 1235 18 US-10-751-736-4 Sequence 420, App
Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-10-766-691-11
; Sequence 11, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10766,691
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 945
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-11

Query Match 100.0%; Score 945; DB 19; Length 945;
Best Local Similarity 100.0%; Pred. No. 2.8e-238;
Matches 945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAAGATGAAAATTAGCTAGACGGAGCGCTTATGGGTGTTATTCAAA 60
|||||

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Db 1 ATGGAAGATGATGAAAAATAGCTAAGACTGCGAAGGGCTTATGGGTTGTATTCAA 60
Qy 61 TGCAGAAACAAACCTCTGCGAAGTACTAGCTGTTAAAAATTTGGGATCTGAGAT 120
Db 61 TGCAGAAACAAACCTCTGCGAAGTACTAGCTGTTAAAAATTTGGGATCTGAGAT 120
Qy 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATAGCTGTTGGAAGCAATTAACACAT 180
Db 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATAGCTGTTGGAAGCAATTAACACAT 180
Qy 181 CCAATCTTTGGAACCTCATCGAGTGTTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
Db 181 CCAATCTTTGGAACCTCATCGAGTGTTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGATGGCTGAT 300
Db 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGATGGCTGAT 300
Qy 301 GGAGTGATCAAAAGCGTATTATGCAACACCTTCAAGCTCTTAAATTTCTGTCTATATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGCAACACCTTCAAGCTCTTAAATTTCTGTCTATATACAT 360
Qy 361 AACTGTATTCCAGAGATATAAAACCTGAAATAATTTCTAAATCAAGCAAGGAATAATC 420
Db 361 AACTGTATTCCAGAGATATAAAACCTGAAATAATTTCTAAATCAAGCAAGGAATAATC 420
Qy 421 AAGATTTGTGACTTCGGGTTTGCACAAATTTCTGATCCAGGAGATGCTACACCGATTAT 480
Db 421 AAGATTTGTGACTTCGGGTTTGCACAAATTTCTGATCCAGGAGATGCTACACCGATTAT 480
Qy 481 GTAGCTACGAGATGCTACCGAGCTCTTGAACCTTCTGTTGGGAGATCTCAGTATGGTTCT 540
Db 481 GTAGCTACGAGATGCTACCGAGCTCTTGAACCTTCTGTTGGGAGATCTCAGTATGGTTCT 540
Qy 541 TCAGTCGATATATGGGCTATTGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 600
Db 541 TCAGTCGATATATGGGCTATTGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 600
Qy 601 TGGCCTGGAAAAATCAGATGTTGGGCTTAAATGAGTAAACCGGTTTTTCCATGGCATCAGTATACCT 660
Db 601 TGGCCTGGAAAAATCAGATGTTGGGCTTAAATGAGTAAACCGGTTTTTCCATGGCATCAGTATACCT 660
Qy 661 ATCCCAAGACATCAATCAATCTTTTAAAGTAACCGGTTTTTCCATGGCATCAGTATACCT 720
Db 661 ATCCCAAGACATCAATCAATCTTTTAAAGTAACCGGTTTTTCCATGGCATCAGTATACCT 720
Qy 721 GAGCCAGAGACATGGAACCTCTTGAGGAAAAAGTTCTCAGATGTTCACTCTGGGCTCTG 780
Db 721 GAGCCAGAGACATGGAACCTCTTGAGGAAAAAGTTCTCAGATGTTCACTCTGGGCTCTG 780
Qy 781 AACTTCATGAAGGGTCTGTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCACTC 840
Db 781 AACTTCATGAAGGGTCTGTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCACTC 840
Qy 841 CTGAGAGCTCTCTACTTTGATCTTTTCAAGAGGCCCAATTAAGAAAAAGCACGTAAT 900
Db 841 CTGAGAGCTCTCTACTTTGATCTTTTCAAGAGGCCCAATTAAGAAAAAGCACGTAAT 900
Qy 901 GAAGGAAGAAACAGAACGCCAACAGGTACTTCCGCTCAAAAAGT 945
Db 901 GAAGGAAGAAACAGAACGCCAACAGGTACTTCCGCTCAAAAAGT 945
```

RESULT 2

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US-10-766-691-5
; Sequence 5, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
```

```
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: Lex-0046-USA
; CURRENT APPLICATION NUMBER: US/10/766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 972
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-766-691-5

Query Match 98.3%; Score 929; DB 19; Length 972;
Best Local Similarity 100.0%; Pred. No. 4,7e-234;
Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAAGATGATGAAAAATAGCTAAGACTGCGAAGGGCTTATGGGTTGTATTCAA 60
Db 1 ATGGAAGATGATGAAAAATAGCTAAGACTGCGAAGGGCTTATGGGTTGTATTCAA 60
Qy 61 TGCAGAAACAAACCTCTGCGAAGTACTAGCTGTTAAAAATTTGGGATCTGAGAT 120
Db 61 TGCAGAAACAAACCTCTGCGAAGTACTAGCTGTTAAAAATTTGGGATCTGAGAT 120
Qy 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATAGCTGTTGGAAGCAATTAACACAT 180
Db 121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATAGCTGTTGGAAGCAATTAACACAT 180
Qy 181 CCAATCTTTGGAACCTCATCGAGTGTTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
Db 181 CCAATCTTTGGAACCTCATCGAGTGTTCAGGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGATGGCTGAT 300
Db 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGATGGCTGAT 300
Qy 301 GGAGTGATCAAAAGCGTATTATGCAACACCTTCAAGCTCTTAAATTTCTGTCTATATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGCAACACCTTCAAGCTCTTAAATTTCTGTCTATATACAT 360
Qy 361 AACTGTATTCCAGAGATATAAAACCTGAAATAATTTCTAAATCAAGCAAGGAATAATC 420
Db 361 AACTGTATTCCAGAGATATAAAACCTGAAATAATTTCTAAATCAAGCAAGGAATAATC 420
Qy 421 AAGATTTGTGACTTCGGGTTTGCACAAATTTCTGATCCAGGAGATGCTACACCGATTAT 480
Db 421 AAGATTTGTGACTTCGGGTTTGCACAAATTTCTGATCCAGGAGATGCTACACCGATTAT 480
Qy 481 GTAGCTACGAGATGCTACCGAGCTCTTGAACCTTCTGTTGGGAGATCTCAGTATGGTTCT 540
Db 481 GTAGCTACGAGATGCTACCGAGCTCTTGAACCTTCTGTTGGGAGATCTCAGTATGGTTCT 540
Qy 541 TCAGTCGATATATGGGCTATTGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 600
Db 541 TCAGTCGATATATGGGCTATTGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 600
Qy 601 TGGCCTGGAAAAATCAGATGTTGGGCTTAAATGAGTAAACCGGTTTTTCCATGGCATCAGTATACCT 660
Db 601 TGGCCTGGAAAAATCAGATGTTGGGCTTAAATGAGTAAACCGGTTTTTCCATGGCATCAGTATACCT 660
Qy 661 ATCCCAAGACATCAATCAATCTTTTAAAGTAACCGGTTTTTCCATGGCATCAGTATACCT 720
Db 661 ATCCCAAGACATCAATCAATCTTTTAAAGTAACCGGTTTTTCCATGGCATCAGTATACCT 720
Qy 721 GAGCCAGAGACATGGAACCTCTTGAGGAAAAAGTTCTCAGATGTTCACTCTGGGCTCTG 780
Db 721 GAGCCAGAGACATGGAACCTCTTGAGGAAAAAGTTCTCAGATGTTCACTCTGGGCTCTG 780
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QY 781 AACTTCATGAGGGGTCTGAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTC 840
Db 781 AACTTCATGAGGGGTCTGAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTC 840
QY 841 CTGAGAGCTCTACTCTTTGATTCTTTTCAAGAGGGCCCAAAATTAAGAGAAAAGCAGTAAT 900
Db 841 CTGAGAGCTCTACTCTTTGATTCTTTTCAAGAGGGCCCAAAATTAAGAGAAAAGCAGTAAT 900
QY 901 GAAGGAAGAAACAGAGAGCGCAACAGGT 929
Db 901 GAAGGAAGAAACAGAGAGCGCAACAGGT 929

RESULT 3

US-10-333-314-30

; Sequence 30, Application US/10333314

; Publication No. US20030211093A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry
; APPLICANT: KHAN, Farrah A.; GURURAJAN, Rajagopal
; APPLICANT: HAFALIA, April J.A.; CHAWLA, Narinder K.
; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Javalaxmi
; APPLICANT: GANDHI, Ameena R.; POLICKY, Jennifer L.
; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.
; APPLICANT: THORNTON, Michael B.; BANDMAN, Olga
; APPLICANT: NGUYEN, Danielle B.; LU, Yan
; APPLICANT: BURFORD, Neil; LAL, Preeti G.
; APPLICANT: DING, Li; YAO, Monique G.
; APPLICANT: ELLIOTT, Vicki S.; RECIPON, Shirley A.
; APPLICANT: KEARNEY, Liam; LU, Dyung Aina M.
; APPLICANT: GREENWALD, Sara R.; TANG, Y. Tom
; APPLICANT: XU, Yuming; WALSH, Roderick T.
; APPLICANT: GIZTEN, Kimberly J.; YANG, Junming
; APPLICANT: JACKSON, Jennifer L.

; TITLE OF INVENTION: HUMAN KINASES

; FILE REFERENCE: PI-0162 USN

; CURRENT APPLICATION NUMBER: US/10/333,314

; CURRENT FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: PCT/US01/23092

; PRIOR FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 60/220,038

; PRIOR FILING DATE: 2000-07-21

; PRIOR APPLICATION NUMBER: US 60/222,112

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: US 60/222,831

; PRIOR FILING DATE: 2000-08-04

; PRIOR APPLICATION NUMBER: US 60/224,729

; PRIOR FILING DATE: 2000-08-11

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: PERL Program

; SEQ ID NO 30

; LENGTH: 1790

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No: 1698381CB1

US-10-333-314-30

Query Match 98.1%; Score 927; DB 17; Length 1790;
Best Local Similarity 100.0%; Pred. No. 2.2e-233;
Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAAAGATGAAATTAAGCTAAGCTGAGAGGGTCTATGGGGTTGTTTCAAA 60
Db 239 ATGAAAGATGAAATTAAGCTAAGCTGAGAGGGTCTATGGGGTTGTTTCAAA 298
QY 61 TGCAGAAACAAACCTCTGGCAAGTAGTACTGTAAAAAATTTGTGGAATCTGAAGAT 120
Db 299 TGCAGAAACAAACCTCTGGCAAGTAGTACTGTAAAAAATTTGTGGAATCTGAAGAT 358
QY 121 GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180

Db 359 GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 418
QY 181 CCAAAATCTTGTGAACCTCATCGAGGTGTTTCAGAGGAAAAAGGAAATCATTTAGTTTTT 240
Db 419 CCAAAATCTTGTGAACCTCATCGAGGTGTTTCAGAGGAAAAAGGAAATCATTTAGTTTTT 478
QY 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTGTCTGAT 300
Db 479 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTGTCTGAT 538
QY 301 GGAGTGAATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAAATTTCTGTGCATATACAT 360
Db 539 GGAGTGAATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAAATTTCTGTGCATATACAT 598
QY 361 AACTGTATTTCACAGAGATATAAAACCTGAAATATTTCTAAATACTAAGCAAGGAATAATC 420
Db 599 AACTGTATTTCACAGAGATATAAAACCTGAAATATTTCTAAATACTAAGCAAGGAATAATC 658
QY 421 AAGATTTGTGACTTCGGGTTTGCACAAATTCGTATTCAGAGATGCTCTACACCGATTAT 480
Db 659 AAGATTTGTGACTTCGGGTTTGCACAAATTCGTATTCAGAGATGCTCTACACCGATTAT 718
QY 481 GTACCTACGAGATGTCACCGAGCTCCTGAACTCTTGTGGGAGATACCTCAGTATGTTCT 540
Db 719 GTACCTACGAGATGTCACCGAGCTCCTGAACTCTTGTGGGAGATACCTCAGTATGTTCT 778
QY 541 TCAGTTCGATATATGGGCTATTGGTTGTGTTTTTTCAGAGCTCCTGACAGGCGCAGCACTG 600
Db 779 TCAGTTCGATATATGGGCTATTGGTTGTGTTTTTTCAGAGCTCCTGACAGGCGCAGCACTG 838
QY 601 TGGCTCGAAAAATCAGATGTCGACCAAACTTTATCTGATAATCAGAAACACTAGGAAAAATTA 660
Db 839 TGGCTCGAAAAATCAGATGTCGACCAAACTTTATCTGATAATCAGAAACACTAGGAAAAATTA 898
QY 661 ATCCCAAGACATCAATCAATCTTTAAAGTAACGGTTTTTCCATGGCATCATGATACCT 720
Db 899 ATCCCAAGACATCAATCAATCTTTAAAGTAACGGTTTTTCCATGGCATCATGATACCT 958
QY 721 GAGCCAGAAGACATGGAACCTCTTTGAGGAAAAAGTTCTCAGATGTTCACTCTGTGGCTCTG 780
Db 959 GAGCCAGAAGACATGGAACCTCTTTGAGGAAAAAGTTCTCAGATGTTCACTCTGTGGCTCTG 1018
QY 781 AACTTCATGAAGGGGTGTCGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTC 840
Db 1019 AACTTCATGAAGGGGTGTCGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTC 1078
QY 841 CTGAGAGCTCTACTTTTGTGATTTCTTTTCAAGAGGCCCAAAATTAAGAGAAAAGCAGTAAT 900
Db 1079 CTGAGAGCTCTACTTTTGTGATTTCTTTTCAAGAGGCCCAAAATTAAGAGAAAAGCAGTAAT 1138
QY 901 GAAGGAAGAAACAGAGAGCGCAACAG 927
Db 1139 GAAGGAAGAAACAGAGAGCGCAACAG 1165

RESULT 4

US-10-250-889-6

; Sequence 6, Application US/10250889

; Publication No. US20040115629A1

; GENERAL INFORMATION:

; APPLICANT: PANZER, Scott R.; LINCOLN, Stephen E.;
; APPLICANT: ALTUS, Christina M.; DUFOUR, Gerard E.;
; APPLICANT: JACKSON, Jennifer L.; JONES, Anissa L.;
; APPLICANT: DAM, Tam C.; LIU, Tommy F.;
; APPLICANT: HARRIS, Bernard; FLORES, Vincent Z.;
; APPLICANT: DAFPO, Abel; MARWAHA, Rakesh;
; APPLICANT: CHEN, Alice J.; CHANG, Simon C.;
; APPLICANT: GERSTIN, Jr., Edward H.; PERALTA, Careyna H.;
; APPLICANT: DAVID, Marie H.; LEWIS, Samantha A.
; TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PT-1195 USN
; CURRENT APPLICATION NUMBER: US/10/250,889

```

; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: PCT/US02/01009
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/261,622
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/261,864
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/261,865
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/262,207
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,208
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,209
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,164
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,215
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/263,102
; PRIOR FILING DATE: 2001-01-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 1678
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: LI:058298.1:2001JAN12
US-10-250-889-6

Query Match      91.9%; Score 868.8; DB 18; Length 1678;
Best Local Similarity 99.2%; Pred. No. 4.5e-218;
Matches 925; Conservative 0; Mismatches 2; Indels 5; Gaps 5;

QY 1 ATGGAAGAGTATGAAAATTAGCTTAAGCTGAGAGAGGCTTATGGGTTGTATTCAAA 60
DB 131 ATGGAAGAGTATGAAAATTAGCTTAAGCTGAGAGAGGCTTATGGGTTGTATTCAAA 190
QY 61 TGCAGA-AACAAAACCTCTGACAAAGTAGTAGCTGTTAAAAAATTTCTGGAATCTGAAGA 119
DB 191 TGCAGATAACAAAACCTCTGACAAAGTAGTAGCTGTTAAAAAATTTCTGGAATCTGAAGA 250
QY 120 TGATCCTGTTGTTAAGAAAATAGCACTAAGAAAATACGTA-TGTTGAAGCAATTAAGAAC 178
DB 251 TGATCCTGTTGTTAAGAAAATAGCACTAAGAAAATACGTA-TGTTGAAGCAATTAAGAAC 310
QY 179 ATCCAAATCTTGTGAACCTCATCGAGGTGTTTCAGGAGAAAAGCAAAATGCAATTTAGTTT 238
DB 311 ATCCAAATCTTGTGAACCTCATCGAGGTGTTTCAGGAGAAAAGCAAAATGCAATTTAGTTT 370
QY 239 TTGAATCTGTGATCATACATTTTAAATGAGCTGGAAGAAAACCCAAATGGAAGTTGCTG 298
DB 371 TTGAATCTGTGATCATACATTTTAAATGAGCTGGAAGAAAACCCAAATGGAAGTTGCTG 430
QY 299 ATGGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTATTTCTGTCATATAC 358
DB 431 ATGGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTATTTCTGTCATATAC 490
QY 359 ATAACTGTATTCAAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAA 418
DB 491 ATAACTGTATTCAAGAGATATAAAACCTGAAAATATTCTAATAACTAAGCAAGGAATAA 550
QY 419 TCAAGATTTGTGACTTCGGGTTTGCAACAATTTCTGATTCAGAGAGTGCCTACCGGATT 478
DB 551 TCAAGATTTGTGACTTCGGGTTTGCAACAATTTCTGATTCAGAGAGTGCCTACCGGATT 610
QY 479 ATGTAGCTA-CGAGATGGTACCAGGCT-CCTGAACCTTCTTGTGGGAGATAC-CAGTATG 535
DB 611 ATGTAGCTAGCGAGATGGTACCAGGCTCCCTGNACTTCTTGTGGGAGATACCTCCAGTATG 670

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QY 536 GTTCTTCAGTCGATATATGGGCTATTGTTGTGTTTTTGACAGAGCTCTGACAGCCAGC 595
DB 671 GTTCTTCAGTCGATATATGGGCTATTGTTGTGTTTTTGACAGAGCTCTGACAGCCAGC 730
QY 596 CACTGTGGCCCTGGAAAATCAGATGTGACCAACTTTATCTGATTAATCAGAACTAGGAA 655
DB 731 CACTGTGGCCCTGGAAAATCAGATGTGACCAACTTTATCTGATTAATCAGAACTAGGAA 790
QY 656 AATTAATCCCAAGACATCAATCTTTAAAGTAAACGGGTTTTTCCATGGCATGAGTA 715
DB 791 AATTAATCCCAAGACATCAATCTTTAAAGTAAACGGGTTTTTCCATGGCATGAGTA 850
QY 716 TACCTGAGCCAGAAAGACATGGAACCTCTTGAGGAAAAGTTCTCAGATGTTTCATCTGTGG 775
DB 851 TACCTGAGCCAGAAAGACATGGAACCTCTTGAGGAAAAGTTCTCAGATGTTTCATCTGTGG 910
QY 776 CTCTGAACCTTCATGAAGGGGTGCTGAAGATGAATCCAGATGACAGATTAACCTGTCCC 835
DB 911 CTCTGAACCTTCATGAAGGGGTGCTGAAGATGAATCCAGATGACAGATTAACCTGTCCC 970
QY 836 AACTCTCGAGAGCTCTCTACTTTGATTTCTTTCAAGAGGCCCAAAATTAAGAAAAGCAC 895
DB 971 AACTCTCGAGAGCTCTCTACTTTGATTTCTTTCAAGAGGCCCAAAATTAAGAAAAGCAC 1030
QY 896 GTAATGAAGGAAGAAAACAGAGAGCGCAACAG 927
DB 1031 GTAATGAAGGAAGAAAACAGAGAGCGCAACAG 1062

RESULT 5
US-10-766-691-9
; Sequence 9, Application US/10766691
; Publication No: US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10/766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-9

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Query Match      88.8%; Score 839; DB 19; Length 1041;
Best Local Similarity 90.8%; Pred. No. 2.5e-210;
Matches 945; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

QY 1 ATGGAAGATGAAAATTAAGCTTAAGCTGGAAGAGGTTCTTATGGGTTGTATTCAAA 60
DB 1 ATGGAAGATGAAAATTAAGCTTAAGCTGGAAGAGGTTCTTATGGGTTGTATTCAAA 60
QY 61 TGCAGAAAACAAACCTCTGGACAAAGTAGTAGCTCTTAAAAAATTTGTGGATCTGAAGAT 120
DB 61 TGCAGAAAACAAACCTCTGGACAAAGTAGTAGCTCTTAAAAAATTTGTGGATCTGAAGAT 120
QY 121 GATCCTGTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
DB 121 GATCCTGTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180

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Qy 181 CCAATCTTGTGAACCTCATCGAGGTGTCAGGAGAAAGGAAATGCATTAGTTT 240
Db 181 CCAATCTTGTGAACCTCATCGAGGTGTCAGGAGAAAGGAAATGCATTAGTTT 240
Qy 241 GAATACCTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATGAGTTGCTGAT 300
Db 241 GAATACCTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATGAGTTGCTGAT 300
Qy 301 GGAGTGATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGCGCAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAGCAAGGAAATATC 420
Db 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAGCAAGGAAATATC 420
Qy 421 AAGATTGTGACTTCGGGTGTCACAAATCTGATTCAGGAGATGCTACACCGATTAT 480
Db 421 AAGATTGTGACTTCGGGTGTCACAAATCTGATTCAGGAGATGCTACACCGATTAT 480
Qy 481 GTAGTACGAGATGGTACCGAGTCTCTGAACTTCTTGTGGAGATACCTCAGTATGTTCT 540
Db 481 GTAGTACGAGATGGTACCGAGTCTCTGAACTTCTTGTGGAGATACCTCAGTATGTTCT 540
Qy 541 TCAGTCGATATATGGGCTATTGTTGTGTTTTCAGAGCTCTTCAGAGCCAGCCACTG 600
Db 541 TCAGTCGATATATGGGCTATTGTTGTGTTTTCAGAGCTCTTCAGAGCCAGCCACTG 600
Qy 601 TGGCTCGAAATACAGATGTGGACCAACTTTATCTGATATATCAACACT- 650
Db 601 TGGCTCGAAATACAGATGTGGACCAACTTTATCTGATATATCAACACTAGTAGAGAG 660
Qy 651 ----- 650
Db 661 GGGTTTCGCCATGTTGACCGGTGCTCGAACTCTTGAGCTCAAGTGATCCACCTGCC 720
Qy 651 -----AGGAAATTAATCCAGACATCAATCAATCTTT 684
Db 721 GTAGCTCTCAAAAGTGTGGAAATTAACAGGAAATTAATCCAGACATCAATCAATCTTT 780
Qy 685 AAAAGTAAACGGGTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAACCTTT 744
Db 781 AAAAGTAAACGGGTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAACCTTT 840
Qy 745 GAGGAAAGTTCTCAGATGTTTCATCTCTGCTGCTGAACTTCAATGAAGGGGTGCTGAAG 804
Db 841 GAGGAAAGTTCTCAGATGTTTCATCTCTGCTGCTGAACTTCAATGAAGGGGTGCTGAAG 900
Qy 805 ATGAATCCAGATGACAGATTAACCTGTTCCCACTCTCTGAGAGCTCTCTATTGATTTCT 864
Db 901 ATGAATCCAGATGACAGATTAACCTGTTCCCACTCTCTGAGAGCTCTCTATTGATTTCT 960
Qy 865 TTTCAAGAGCCCAAAATTAAGGAAAGCAGTAAATGAAGGAAAGAAACAGAGAGCCAA 924
Db 961 TTTCAAGAGCCCAAAATTAAGGAAAGCAGTAAATGAAGGAAAGAAACAGAGAGCCAA 1020
Qy 925 CAGGTACTTCCGCTCAAAAGT 945
Db 1021 CAGGTACTTCCGCTCAAAAGT 1041

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RESULT 6

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US-10-766-691-3
; Sequence 3, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and

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; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10/766,691
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: homo sapiens
; US-10-766-691-3

```

Query Match 87.1%; Score 823; DB 19; Length 1068;

Best Local Similarity 90.6%; Pred. No. 4.2e-206;

Matches 929; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

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Qy 1 ATGGAAGATGATGAAAAATTTAGCTAAGACTGGAGAGGGTCTTATGGGGTTGTATTCAAA 60
Db 1 ATGGAAGATGATGAAAAATTTAGCTAAGACTGGAGAGGGTCTTATGGGGTTGTATTCAAA 60
Qy 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTTTAAAAAATTTTGGAAATCTGAAGAT 120
Db 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTTTAAAAAATTTTGGAAATCTGAAGAT 120
Qy 121 GATCCTGTTCTTAAGAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAAGACAT 180
Db 121 GATCCTGTTCTTAAGAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAAGACAT 180
Qy 181 CCAATCTTGTGAACCTCATCGAGGTGTTCCAGGAGAAAGGAAATTCATTTAGTTTTT 240
Db 181 CCAATCTTGTGAACCTCATCGAGGTGTTCCAGGAGAAAGGAAATTCATTTAGTTTTT 240
Qy 241 GAATACCTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATGAGTTGCTGAT 300
Db 241 GAATACCTGATCATACACTTTTAAATGAGCTGGAAGAAACCAATGAGTTGCTGAT 300
Qy 301 GGAGTGATCAAAAGCGTATTATGSCAAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGSCAAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAGCAAGGAAATATC 420
Db 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAGCAAGGAAATATC 420
Qy 421 AAGATTGTGACTTCGGGTTTGCACAAATTTCTGATTCAGAGATGCTCTACACCGATTAT 480
Db 421 AAGATTGTGACTTCGGGTTTGCACAAATTTCTGATTCAGAGATGCTCTACACCGATTAT 480
Qy 481 GTAGTACGAGATGGTACCGAGCTCTCGAACTTCTTGTGGAGATACCTCAGTATGTTCT 540
Db 481 GTAGTACGAGATGGTACCGAGCTCTCGAACTTCTTGTGGAGATACCTCAGTATGTTCT 540
Qy 541 TCAGTCGATATATGGGCTATTGTTGTGTTTTCAGAGCTCTTCAGAGCCAGCCACTG 600
Db 541 TCAGTCGATATATGGGCTATTGTTGTGTTTTCAGAGCTCTTCAGAGCCAGCCACTG 600
Qy 601 TGGCTCGAAATACAGATGTGGACCAACTTTATCTGATATATCAACACTAGTAGAGAG 660
Db 601 TGGCTCGAAATACAGATGTGGACCAACTTTATCTGATATATCAACACTAGTAGAGAG 660
Qy 651 ----- 650
Db 661 GGGTTTCGCCATGTTGACCGGTGCTCGAACTCTTGAGCTCAAGTGATCCACCTGCC 720
Qy 651 -----AGGAAATTAATCCAGACATCAATCAATCTTT 684
Db 721 GTAGCTCTCAAAAGTGTGGAAATTAACAGGAAATTAATCCAGACATCAATCAATCTTT 780
Qy 685 AAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAACCTTT 744

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Db 781 AAAAGTAAAGGGTTTTCATGCAATCAGTATACCTGAGCCAGAAACATGGAACCTCTT 840
QY 745 GAGGAAAAGTTTCTCAGATGTTTCTGCTGCTCTGAATCTCATGAGGGGTCTCTGAAG 804
Db 841 GAGGAAAAGTTTCTCAGATGTTTCTGCTGCTCTGAATCTCATGAGGGGTCTCTGAAG 900
QY 805 ATGAATCCAGATGACAGATTAACTCTGCTCCCACTCTGAGAGCTCTCTACTTTGATTTCT 864
Db 901 ATGAATCCAGATGACAGATTAACTCTGCTCCCACTCTGAGAGCTCTCTACTTTGATTTCT 960
QY 865 TTTCAAGAGGCCCAATTAAGAAAAGCAGCGTAATGAAGGAAGAAAACAGAGAGCCCAA 924
Db 961 TTTCAAGAGGCCCAATTAAGAAAAGCAGCGTAATGAAGGAAGAAAACAGAGAGCCCAA 1020
QY 925 CAGGT 929
Db 1021 CAGGT 1025

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RESULT 7
US-09-834-496A-3
; Sequence 3, Application US/09834496A
; Patent No. US20020090701A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann
; TITLE OF INVENTION: 14257 NOVEL PROTEIN KINASE MOLECULES AND
; FILE REFERENCE: 381552000900
; CURRENT APPLICATION NUMBER: US/09/834,496A
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/196,910
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-834-496A-3

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Query Match 68.5%; Score 647; DB 9; Length 687;
Best Local Similarity 99.2%; Pred. No. 7.8e-160;
Matches 650; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGAAAAGTATGAAAATTAAGCTAAGCTGAGAGGGGTCTTATGGGGTTGTTATTCAAA 60
Db 1 ATGGAAAAGTATGAAAATTAAGCTAAGCTGAGAGGGGTCTTATGGGGTTGTTATTCAAA 60
QY 61 TGCAGAAACAAACCTCTGGACAGTAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 120
Db 61 TGCAGAAACAAACCTCTGGACAGTAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 120
QY 121 GATCCTGTTGTTAAGAAAATAGCAATAGCAATAGCTATGTTGAAGCAATTAAGCAAT 180
Db 121 GATCCTATGTTAAGAAAATAGCAATAGCAATAGCTATGTTGAAGCAATTAAGCAAT 180
QY 181 CCAATCTCTGACCTCATCGAGGTCTTCCAGAGAAAAGAAAATGCAATTTAGTTTTT 240
Db 181 CCAATCTCTGACCTCATCGAGGTCTTCCAGAGAAAAGAAAATGCAATTTAGTTTTT 240
QY 241 GAATCTGTGATCATACACTTTTAAATAGCTGGAAGAAACCAATGAGTTGCTGAT 300
Db 241 GAATCTGTGATCATGCACTTTTAAATAGCTGGAAGAAACCAATGAGTTGCTGAT 300
QY 301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTATATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTATATACAT 360
QY 361 AACTGTATTACAGAGATATAAACCCTGAAATATTCTTAATTAACTAAGCAAGGAATATC 420
Db 361 AACTGTATTACAGAGATATAAACCCTGAAATATTCTTAATTAACTAAGCAAGGAATATC 420

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QY 421 AAGATTGTGACTTCGGGTTTGCAAAATTCGATTCAGGAGATGCCTACACGATTAT 480
Db 421 AAGATTGTGACTTCGGGTTTGCAAAATTCGATTCAGGAGATGCCTACACGATTAT 480
QY 481 GTAGCTACGAGATGGTACCGAGCTCCTGAACCTTCTTGTGGGAGATATCTCAGTATGGTTCT 540
Db 481 GTAGCTACGAGATGGTACCGAGCTCCTGAACCTTCTTGTGGGAGATATCTCAGTATGGTTCT 540
QY 541 TCAGTCCGATATATGGGCTATTGGTTGTTTTCAGAGCTCCTGACAGGCCAGCCACTG 600
Db 541 TCAGTCCGATATATGGGCTATTGGTTGTTTTCAGAGCTCCTGACAGGCCAGCCACTG 600
QY 601 TGGCCTGGAATAATCAGATGTGGACCAACTTTATCTGATAATCAGAAACACTAGGAA 655
Db 601 TGGCCTGGAATAATCAGATGTGGACCAACTTTATCTGATAATCAGAAACACTAGGTA 655

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RESULT 8
US-09-834-496A-1
; Sequence 1, Application US/09834496A
; Patent No. US20020090701A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann
; TITLE OF INVENTION: 14257 NOVEL PROTEIN KINASE MOLECULES AND
; FILE REFERENCE: 381552000900
; CURRENT APPLICATION NUMBER: US/09/834,496A
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/196,910
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 882
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (129)...(815)
US-09-834-496A-1

```

```

Query Match 68.5%; Score 647; DB 9; Length 882;
Best Local Similarity 99.2%; Pred. No. 8.8e-160;
Matches 650; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ATGGAAAAGTATGAAAATTAAGCTAAGCTGAGAGGGGTCTTATGGGGTTGTTATTCAAA 60
Db 129 ATGGGAAAAGTATGAAAATTAAGCTAAGCTGAGAGGGGTCTTATGGGGTTGTTATTCAAA 188
QY 61 TGCAGAAACAAACCTCTGGACAGTAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 120
Db 189 TGCAGAAACAAACCTCTGGACAGTAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT 248
QY 121 GATCCTGTTGTTAAGAAAATAGCAATAGCAATAGCTATGTTGAAGCAATTAAGCAAT 180
Db 249 GATCCTATGTTAAGAAAATAGCAATAGCAATAGCTATGTTGAAGCAATTAAGCAAT 308
QY 181 CCAATCTCTGACCTCATCGAGGTCTTCCAGAGAAAAGAAAATGCAATTTAGTTTTT 240
Db 309 CCAATCTCTGACCTCATCGAGGTCTTCCAGAGAAAAGAAAATGCAATTTAGTTTTT 368
QY 241 GAATCTGTGATCATACACTTTTAAATAGCTGGAAGAAACCAATGAGTTGCTGAT 300
Db 369 GAATCTGTGATCATGCACTTTTAAATAGCTGGAAGAAACCAATGAGTTGCTGAT 428
QY 301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTATATACAT 360
Db 429 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTATATACAT 488
QY 361 AACTGTATTACAGAGATATAAACCCTGAAATATTCTTAATTAACTAAGCAAGGAATATC 420
Db 489 AACTGTATTACAGAGATATAAACCCTGAAATATTCTTAATTAACTAAGCAAGGAATATC 548

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Qy 421 AAGATTGTGACTTCGGGTTGGCAAAATTCGATTCAGAGAGATGCTACACCGATTAT 480
Db 549 AAGATTGTGACTTCGGGTTGGCAAAATTCGATTCAGAGAGATGCTACACCGATTAT 608
Qy 481 GTAGCTACGAGATGCTACCGAGCTCCTGAACCTCTGTGGGAGATACCTCAGTATGGTTCT 540
Db 609 GTAGCTACGAGATGCTACCGAGCTCCTGAACCTCTGTGGGAGATACCTCAGTATGGTTCT 668
Qy 541 TCAGTCGATATATGGGCTATTTGGTTGTGTTTTTCAGAGCTCCTGACAGGCCAGCCACTG 600
Db 669 TCAGTCGATATATGGGCTATTTGGTTGTGTTTTTCAGAGCTCCTGACAGGCCAGCCACTG 728
Qy 601 TGGCCTGGAAAATCAGATGTGGCAACCTTTATCTGATATCAGAACACTAGGAA 655
Db 729 TGGCCTGGAAAATCAGATGTGGCAACCTTTATCTGATATCAGAACACTAGGTA 783

RESULT 9

US-10-766-691-13
; Sequence 13, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 1819
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-13

Query Match 53.7%; Score 507; DB 19; Length 1819;
Best Local Similarity 69.8%; Pred. No. 9,8e-123;
Matches 929; Conservative 0; Mismatches 0; Indels 402; Gaps 2;

Qy 1 ATGGAAGAAGTATGAAAAATTAGCTAAGACTGGAGAAGGGCTTATGGGGTTGTATCAAA 60
Db 138 ATGGAAGAAGTATGAAAAATTAGCTAAGACTGGAGAAGGGCTTATGGGGTTGTATCAAA 197
Qy 61 TGCAGAACAAACCTCTGGCAAGTAGTAGCTGTAAAAAATTTGGGAATCTGAAGAT 120
Db 198 TGCAGAACAAACCTCTGGCAAGTAGTAGCTGTAAAAAATTTGGGAATCTGAAGAT 257
Qy 121 GATCCTGTGTTAAGAAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAAGACAT 180
Db 258 GATCCTGTGTTAAGAAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAAGACAT 317
Qy 181 CCAAACTCTGTGAACCTCATCGAGGTGTTACAGAGAAAAAGAAAAATGCAATTTAGTTTTT 240
Db 318 CCAAACTCTGTGAACCTCATCGAGGTGTTACAGAGAAAAAGAAAAATGCAATTTAGTTTTT 377
Qy 241 GAATATCTGTGATCATACATTTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
Db 378 GAATATCTGTGATCATACATTTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 437
Qy 301 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAATTTCTGTGCATATACAT 360
Db 438 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAATTTCTGTGCATATACAT 497

RESULT 10

US-10-766-691-1
; Sequence 1, Application US/10766691
; Publication No. US20050042626A1

Qy 361 AACTGTATTACAGAGATATAAAACCTGAAAAATATTTCTAATAACTAAGCAAGGAATATC 420
Db 498 AACTGTATTACAGAGATATAAAACCTGAAAAATATTTCTAATAACTAAGCAAGGAATATC 557
Qy 421 AAGATTTTGCACTTCGGGTTTGCACAAATTCCTG----- 453
Db 558 AAGATTTTGCACTTCGGGTTTGCACAAATTCCTGAGTTGGACTTCATCTTTCTCTGGTGCC 617
Qy 454 ----- 453
Db 618 TCCTTGATTGGCTTAATAGTTGACCTTCTGAAATCTTTTTCTGCCAAATTCAGAGATTTTT 677
Qy 454 ----- 453
Db 678 CTCCTGGCTTTGGATCCATTGCTGACACAGTGTTCACCAATGGGGCCCGAGGCTCATCTCGA 737
Qy 454 ----- 453
Db 738 ACTTCTGGCCTCAAGTGATCCTTCCACCTCGGCCCTCCAAAGTGCTGGATTGCAAGTGTC 797
Qy 454 ----- 453
Db 798 AGCCACGCTGCCCGCCAGATTTTTCACAAATAACTACTGAGAGCTCACAAGATTGTTT 857
Qy 454 -----ATTCCAGAGATGCCCTACACC 474
Db 858 TTAGTGGGAACACAAATTTTCGAACAAATTCCTGGAACGCATTCAGGAGATGCCCTACACC 917
Qy 475 GATTATGTAGCTACGAGATGTCACGAGCTCCTGAACCTCTGTGGGAGATACCTCAGTAT 534
Db 918 GATTATGTAGCTACGAGATGTCACGAGCTCCTGAACCTCTGTGGGAGATACCTCAGTAT 977
Qy 535 GGTTCTTTCAGTCGATATATGGGCTATTTGGTTGTGTTTTTGCAGAGCTCCTGACAGGCCAG 594
Db 978 GGTTCTTTCAGTCGATATATGGGCTATTTGGTTGTGTTTTTGCAGAGCTCCTGACAGGCCAG 1037
Qy 595 CCAGTGGCCTGGAAAAATCAGATGTGGACCAACTTTTATCTGATTAATCAGAACACT----- 650
Db 1038 CCAGTGGCCTGGAAAAATCAGATGTGGACCAACTTTTATCTGATTAATCAGAACACTAGTA 1097
Qy 651 ----- 650
Db 1098 GAGACGGGGTTTGCCTATGTTGACCAGGTGGTCTCGAACTCTTGACGTCAAGTGATCCA 1157
Qy 651 -----AGGAAAAATTAATCCCAAGACATCAATCA 678
Db 1158 CCTGCCGTAGCTCCTCAAGAGTGTGGAAATTACAGGAAAAATTAATCCCAAGACATCAATCA 1217
Qy 679 ATCTTTAAAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAA 738
Db 1218 ATCTTTAAAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATGGAA 1277
Qy 739 ACTCTTCAGGAAAGTTCTCAGATGTTTCATCCTGTGGCTCTGAACTTTCATCAAGGGGTGT 798
Db 1278 ACTCTTCAGGAAAGTTCTCAGATGTTTCATCCTGTGGCTCTGAACTTTCATCAAGGGGTGT 1337
Qy 799 CTGAAGATGAATCCAGATGACAGATTAACTGTTTCCCAACTCTCTGGAGAGCTCCTACTTTT 858
Db 1338 CTGAAGATGAATCCAGATGACAGATTAACTGTTTCCCAACTCTCTGGAGAGCTCCTACTTTT 1397
Qy 859 GATTCTTTTCAAGAGGCCCAAAATTAAGAAAAAGCACTGATGAAGGAAGAAACAGAGA 918
Db 1398 GATTCTTTTCAAGAGGCCCAAAATTAAGAAAAAGCACTGATGAAGGAAGAAACAGAGA 1457
Qy 919 CGCCAACAGGT 929
Db 1458 CGCCAACAGGT 1468

```

; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10/766,691
; CURRENT FILING DATE: 2004-01-28
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 561
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-1

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Query Match      48.1%; Score 454.4; DB 19; Length 561;
Best Local Similarity 99.8%; Pred. No. 3.9e-109;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGAAGATGATGAAAAATAGCTAAGACTGAGAGAGGCTCTTATGGGGTTGTAATCAA 60
DB 1 ATGGAAGATGATGAAAAATAGCTAAGACTGAGAGAGGCTCTTATGGGGTTGTAATCAA 60
QY 61 TGCAGAAACAAACCTCTGGAACAAGTAGCTGTTTAAAAAATTTGTGGAATCTGAAGAT 120
DB 61 TGCAGAAACAAACCTCTGGAACAAGTAGCTGTTTAAAAAATTTGTGGAATCTGAAGAT 120
QY 121 GATCCTGTTGTTAAGAAATAGCCTAAGACTGAGAGAGGCTCTTATGGGGTTGTAATCAA 180
DB 121 GATCCTGTTGTTAAGAAATAGCCTAAGACTGAGAGAGGCTCTTATGGGGTTGTAATCAA 180
QY 181 CCAATCTGTGAACTCTGGAACAAGTAGCTGTTTAAAAAATTTGTGGAATCTGAAGAT 240
DB 181 CCAATCTGTGAACTCTGGAACAAGTAGCTGTTTAAAAAATTTGTGGAATCTGAAGAT 240
QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
DB 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
QY 301 GGAGTGATCAAAAGCGTATTATGCAACACACTTCAAGCTCTTAAATTTCTGCTATATACAT 360
DB 301 GGAGTGATCAAAAGCGTATTATGCAACACACTTCAAGCTCTTAAATTTCTGCTATATACAT 360
QY 361 AACTGTTATTCACAGAGATATAAAACCTGAAATATTTCTTAATACTAAGCAAGGAATAATC 420
DB 361 AACTGTTATTCACAGAGATATAAAACCTGAAATATTTCTTAATACTAAGCAAGGAATAATC 420
QY 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATT 456
DB 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATT 456

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RESULT 11
US-10-766-691-7
; Sequence 7, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and

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```

; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10/766,691
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-766-691-7

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Query Match      48.1%; Score 454.4; DB 19; Length 594;
Best Local Similarity 99.8%; Pred. No. 4e-109;
Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGGAAGATGATGAAAAATAGCTAAGACTGAGAGAGGCTCTTATGGGGTTGTAATCAA 60
DB 1 ATGGAAGATGATGAAAAATAGCTAAGACTGAGAGAGGCTCTTATGGGGTTGTAATCAA 60
QY 61 TGCAGAAACAAACCTCTGGAACAAGTAGCTGTTTAAAAAATTTGTGGAATCTGAAGAT 120
DB 61 TGCAGAAACAAACCTCTGGAACAAGTAGCTGTTTAAAAAATTTGTGGAATCTGAAGAT 120
QY 121 GATCCTGTTGTTAAGAAATAGCCTAAGACTGAGAGAGGCTCTTATGGGGTTGTAATCAA 180
DB 121 GATCCTGTTGTTAAGAAATAGCCTAAGACTGAGAGAGGCTCTTATGGGGTTGTAATCAA 180
QY 181 CCAATCTGTGAACTCTGGAACAAGTAGCTGTTTAAAAAATTTGTGGAATCTGAAGAT 240
DB 181 CCAATCTGTGAACTCTGGAACAAGTAGCTGTTTAAAAAATTTGTGGAATCTGAAGAT 240
QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
DB 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
QY 301 GGAGTGATCAAAAGCGTATTATGCAACACACTTCAAGCTCTTAAATTTCTGCTATATACAT 360
DB 301 GGAGTGATCAAAAGCGTATTATGCAACACACTTCAAGCTCTTAAATTTCTGCTATATACAT 360
QY 361 AACTGTTATTCACAGAGATATAAAACCTGAAATATTTCTTAATACTAAGCAAGGAATAATC 420
DB 361 AACTGTTATTCACAGAGATATAAAACCTGAAATATTTCTTAATACTAAGCAAGGAATAATC 420
QY 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATT 456
DB 421 AAGATTGTGACTTCGGGTTTGCAAAATTTCTGATT 456

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RESULT 12
US-10-363-616-146
; Sequence 146, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 146
; LENGTH: 1612
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (463)..(1539)

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US-10-363-616-146

Query Match 44.0%; Score 415.4; DB 17; Length 1612;
Best Local Similarity 66.7%; Pred. No. 1.3e-98;
Matches 609; Conservative 0; Mismatches 301; Indels 3; Gaps 1;
Qy 1 ATGGAAAGATGAAAAATTAGCTTAAGCTGAGAGGGTCTTATGGGTTGTATTCAA 60
Db 466 ATGGAGAAGTATGAAAAAATGGGAAATTTGGAGAAGGATCCTATGGAGTTGTTTCAA 525
Qy 61 TGCAGAAACAAACCTCTGGACAAGTAGTACTGTGTTAAAAAATTTGGGAATCTGAAGAT 120
Db 526 TGTAGAAACAGGACACGGGTGAGTTGTGCCATCAAGAAGTTCTTGGATCAGAAGAT 585
Qy 121 GATCCTGTGTTAAGAAATAGCACTAAGAGAAATAGTATGTTGGAAGCAATTAACACAT 180
Db 586 GACCTGTGTCATAAAGAAAAATGCGCTTCGGGAAATCCGAATGCTCAAGCAACTCAAGCAT 645
Qy 181 CCAATCTGTGAACCTCATCGAGGTGTTACGGAGAAAGAAAGAAATGCTATTGTTT 240
Db 646 CCCAACCTTGTAACTTCTCCATGAGTTGACAGATACCAAGAGGGTACAGAA 765
Qy 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAAGTTGCTGAT 300
Db 706 GAATATTGTGACCAACACAGTTCTCCATGAGTTGACAGATACCAAGAGGGTACAGAA 765
Qy 301 GGAGTGATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTGATATACAT 360
Db 766 CATCTCGTGAAGAGCATAACTTGCAGACACTGCAAGCTGTAATTTTGGCATAAACAAC 825
Qy 361 AACTGTATTACAGAGATATAAACCCTGAAATATCTAATACATAGCAAGGAATATC 420
Db 826 AATTGTCATACATAGAGACGTGAAGCCAGAAATATCTCATACAGAAACATTTCCGTGAT 885
Qy 421 AAGATTGTGACTTCCGTTTGGCAAAATCTCGATT---CCAGAGAGATGCTACACCGAT 477
Db 886 AAGCTTTGTGACTTTGGAATTTGCTCGGCTTTTGACTGACCGAGTACTACTATACAGAC 945
Qy 478 TATGAGTACGAGATGGTACCGAGCTCTGAACTTCTGTGGGAGATACCTCAGTATGGT 537
Db 946 TAGTGCTACCGAGTGTACCGCTCCCTGAGCTGCTGTGGGGGACACGCGTACGGC 1005
Qy 538 TCTTCAGTCGATATATGGCTATTTGGTTGTTTGGAGAGCTCTGACAGGCGACGCA 597
Db 1006 CCCCCTGGATGTTTGGGCAATTTGGCTGTCTTGTGCTGAGCTGCTGTGAGGAGTGCCT 1065
Qy 598 CTGTGCTCGAATAACAGATGTGCAACCACTTTATCTGATAATCAGAACACTAGGAAA 657
Db 1066 CTGTGGCCAGGAAATCGATGTGGATCAGCTGTATCTGATTAGGAAGACCTTGGGGAT 1125
Qy 658 TTAATCCCAAGACATCAATCAATCTTTAAAGTAACCGGTTTTTCCATGGCATCAGTATA 717
Db 1126 CTCATTCCTAGGCCACGAGAGTGTATTAGCAAGAAATCAGTACTTTCAGTGGAGTGAAT 1185
Qy 718 CTTGAGCCAGAGACATGGAACCTCTTGAGGAAAGTTCTCAGATGTTCACTCTGTGCT 777
Db 1186 CCAGACCTCGAAGATATGGAACCACTTTGAATTAATAATTTCCAAACATCTCTTATCTGCC 1245
Qy 778 CTGAATCTTCATGAAGGGGTGCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCAA 837
Db 1246 CTGGGGCTCTTAAGGGGTGCTCCACATGACCTTACTGAAGGCTGACATGTAACAG 1305
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Db 1306 CTGTTGATCACCACATATTTTGAACAATCAGAGAAATAGAGGATTTGGCAAGAAACAC 1365
Qy 898 AATGAAGGAAGAA 910
Db 1366 AACAAACCAACAA 1378

RESULT 13
US-09-960-706-1079

; Sequence 1079, Application US/09960706
; Publication No. US20030134280A1
; GENERAL INFORMATION:
; APPLICANT: Munger, William E.
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
; TITLE OF INVENTION: Gene Expression Profiles
; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960,706
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 09/873,319
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1079
; LENGTH: 1363
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 X66358
US-09-960-706-1079

Query Match 43.8%; Score 413.8; DB 10; Length 1363;
Best Local Similarity 66.6%; Pred. No. 3e-98;
Matches 608; Conservative 0; Mismatches 302; Indels 3; Gaps 1;
Qy 1 ATGGAAAGATGAAAAAATTAGCTTAAGCTGGAAGGGTCTTATGGGTTGTATTCAA 60
Db 217 ATGGAGAAGTATGAAAAAATGGGAAATTTGGAGAAGGATCCTATGGAGTTGTTTCAA 276
Qy 61 TGCAGAAACAAACCTCTGGAACAAGTAGTACTGTTAAAAAATTTGGGAATCTGAAGAT 120
Db 277 TGTAGAAACAGGGACACGGGTGAGTTGTGCCATCAAGAAGTTCTTGGAAATCAGAAGAT 336
Qy 121 GATCCTGTTCTTGAAGAAATAGCACTAAGAGAAATAGTATGTTGAGCAATTAACAT 180
Db 337 GACCTGTCTATAAGAAAAATTTGCCCTTCGGGAAATCCGAATGCTCAAGCAACTCAAGAT 396
Qy 181 CCAATCTCTGTAACCTCATCGAGGTGTTGAGGAAAAAGAAAAATGCAATTTAGTTT 240
Db 397 CCCAACCTTGTTAACCTCTTGGAGTCTTCAAGAGGAAACGGAGGCTTCCACCTGTT 456
Qy 241 GAATATCTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAAGTTGCTGAT 300
Db 457 GAATATTGTGACACACAGTTCTCCTGAGTTGGACAGATACCAAGAGGGGTACCAGAA 516
Qy 301 GGAGTGAATCAAAGCGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
Db 517 CATCTCTGTAAGAGCATAACTTGGCAGACACTGCAAGCTGTAAATTTTGGCATAAACAAC 576
Qy 361 AACTGTATTCCAGAGATATAAAACCTGAAAAATTTCTAATACTAAGCAAGGAATATC 420
Db 577 AATTGCATACATAGACAGCTGAAGCCAGAAATATCTCATCAGAAACATTCCTGTT 636
Qy 421 AAGATTGTGACTTCCGTTTGGCAAAATTTCTGATT---CCAGAGATGCTACACCGAT 477
Db 637 AAGCTTTGTGACTTTGGATTGCTCGGCTTTTGAAGCCGAGTCTGCTGAGCTGCTGAGTACAGAC 696
Qy 478 TATGAGTACGAGATGGTACCGAGCTCTGAACTTCTTCTGGGAGATACCTCAGTATGGT 537
Db 697 TAGCTGGCTACCAAGGTGGTACCGCTCCCTGAGCTGCTGTTGGGGGACACGCGTACGGC 756
Qy 538 TCTTCAGTCGATATATGGGCTATTGGTTGTTGTTTTCAGAGCTCTCTGACAGGCGCAGCA 597
Db 757 CCCCCGTGATGTTTGGGCAATTTGGCTGTCTTCTGCTGAGCTGCTGTCAGGAGTGCCT 816
Qy 598 CTGTGGCCTGGAAAAATCAGATGTGGACCAACTTTTATCTGATTAATCAGAACACTAGGAAA 657
Db 817 CTGTGGCCAGGAAAAATCGGATGTGGATCAGCTGTATCTGATTAGGAAGACCTTGGGGAT 876
Qy 658 TTAATCCCAAGACATCAATCAATCTTTAAAGTAACCGGTTTTTCCATGGCATCAGTATA 717

Db 877 CTATCTCTGACGACCAAGTGTGTTAGCAGCAATCAGTACTTCTAGTGGAGTGAATTT 936
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 Db 937 CCAGACCTGAAGATATGGAACCACTTGAATTAATAATTCCTCAACATCTCTTATCTGCT 996
 Qy 778 CTGAACCTTCAATGAAGGGTGTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAA 837
 Db 997 CTGGGGCTCTAAAGGCTCTCTCCACATGGACCTTACTGAAAGGCTGACATGTGAACAG 1056
 Qy 838 CTCTGGAGAGCTCTTACTTTGATTTCTTTTCAAGAGGCCCAATTAAGAAAGAACACCT 897
 Db 1057 CTGTGATCACCCTATTTTGAACATCAGAGAAATAGAGGATTTGGCAAAAGAACAC 1116
 Qy 898 AATGAAGGAAGAA 910
 Db 1117 GACAAACCAACAA 1129

RESULT 14
 US-10-357-930-24573
 ; Sequence 24573, Application US/10357930
 ; Publication No. US20040259086A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schlegel, Robert
 ; APPLICANT: Endege, Wilson
 ; APPLICANT: Monahan, John
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
 ; IDENTIFICATION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
 ; TITLE OF INVENTION: HUMAN PROSTATE CANCER
 ; FILE REFERENCE: MRI-007BCN
 ; CURRENT APPLICATION NUMBER: US/10/357,930
 ; CURRENT FILING DATE: 2003-02-04
 ; PRIOR APPLICATION NUMBER: 09/785,276
 ; PRIOR FILING DATE: 2003-02-16
 ; PRIOR APPLICATION NUMBER: 60/183,319
 ; PRIOR FILING DATE: 2000-02-17
 ; PRIOR APPLICATION NUMBER: 60/189,862
 ; PRIOR FILING DATE: 2000-03-16
 ; PRIOR APPLICATION NUMBER: 60/207,454
 ; PRIOR FILING DATE: 2000-05-25
 ; PRIOR APPLICATION NUMBER: 60/211,314
 ; PRIOR FILING DATE: 2000-06-09
 ; PRIOR APPLICATION NUMBER: 60/219,007
 ; PRIOR FILING DATE: 2000-07-18
 ; PRIOR APPLICATION NUMBER: 60/255,281
 ; PRIOR FILING DATE: 2000-12-13
 ; NUMBER OF SEQ ID NOS: 62232
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 24573
 ; LENGTH: 2944
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; LOCATION: 1, 2, 3, 2940, 2941, 2942, 2943, 2944
 ; OTHER INFORMATION: n = A,T,C or G
 US-10-357-930-24573

Query Match 43.8%; Score 413.8; DB 18; Length 2944;
 Best Local Similarity 66.6%; Pred. No. 4.5e-98;
 Matches 608; Conservative 0; Mismatches 302; Indels 3; Gaps 1;
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 Db 829 ATGGAAGATATCAAAATAGCTAGAGCTGGAGAGGCTTATGGGTTGATTCAAA 888
 Qy 61 TGAGAAACAAACCTCTGGACAAGTAGTGTGTTAAAAAATTTGTGGAATCTGAAGAT 120
 Db 889 TGAGAAACAGGACACGGGTGAGATTTGGCCATCAAGAAGTTCTTGAATCAGAGAT 948
 Qy 121 GATCTCTGTTTGAAGAAATAGCACTAAGAGAAATAGTGTGTAAGCAATTAACAT 180

Db 949 GACCCCTGTATATAAGAAATTTGCCCTTCGGGAATCCGAATGCTCAAGCACTCAAGCAT 1008
 Qy 181 CCAATCTTTGTGAACCTCATCGAGGTGTTTCAAGGAGAAAGAAATGCAATTTAGTTTTT 240
 Db 1009 CCCAACCTTGTAACTCTCTGGAAGTCTTCAAGGAGGAAACGGAGCTTCACTGCTGTTT 1068
 Qy 241 GAATATCTGTATCATACATCTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 300
 Db 1069 GAATATCTGTACCAACACAGTTCTCCATGAGTTGAGCAGATACCAAGAGGGGTACCGAA 1128
 Qy 301 GGAGTGATCAAAACGGTATTATGCAAAACACTTCAAGCTCTTAAATTTCTCTCATATACAT 360
 Db 1129 CATCTCTGTGAGAGACATAAATGCGACACACTGCAAGCTGTAATTTTTCCTATAAACAC 1188
 Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGAAATATC 420
 Db 1189 AATTGCATACATAGAGACGTGAAGCCAGAAATATCTCATACGAAACATTCGGTGAT 1248
 Qy 421 AAGATTTGTGACTTTCGGGTTTGCACAAATTTCTGATT---CCAGGAGATGCTACACCGAT 477
 Db 1249 AAGCTTTGTGACTTTGGATTTGCTCGGCTTTTGAACCTGGACCGAGTCACTATACAGAC 1308
 Qy 478 TATGTAGCTACGAGATGCTACCGAGCTCCTGAACTTTCTTGTGGGAGATCTCAATATGTT 537
 Db 1309 TAGTGGCTACAGAGTGTGACCTCCCTGAGCTGCTGCTGGGGGACACGAGTACGGC 1368
 Qy 538 TCTTCAAGTATATGCGCTATTGCTTTGTTTTCAGAGCTCCTGACAGAGCTCCTGACAGCC 597
 Db 1369 CCCCGGTGGATGTTTGGGCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1428
 Qy 598 CTGTGGCTGGAATACAGATGAGCAACTTTATCTGATTAATCAGAACATCAGGAAA 657
 Db 1429 CTGTGGCTGGAATACAGATGAGCAACTTTATCTGATTTAGGAAGACCTTTGGGGAT 1488
 Qy 658 TTAATCCCAAGACATCAATCAATCTTTAAAGTAAAGGTTTTCATGGCATCAGTATA 717
 Db 1489 CTCAATCTAGGACACAGCAAGTTTACGACGATCAGTACTTCACTGAGTGAATTT 1548
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 Qy 778 CTGAACCTTCAAGAGGGTGTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAA 837
 Db 1609 CTGGGGCTCTAAAGGGCTGCTCCACATGACCTTACTGAAAGCTGACATGTGAACAG 1668
 Qy 838 CTCTGGAGAGCTCTCTCTTTGATTTCTTTCAAGAGGCCCAATTTAAAGAAAGAACAGT 897
 Db 1669 CTGTTGCTATCACCCTATTTTGAACATCAGAGAAATAGAGGATTTGGCAAAAGAACAC 1728
 Qy 898 AATGAAGGAAGAA 910
 Db 1729 GACAAACCAACAA 1741

RESULT 15
 US-10-174-794-5
 ; Sequence 5, Application US/10174794
 ; Publication No. US20030166220A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Southern California
 ; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
 ; FILE REFERENCE: 13761-707
 ; CURRENT APPLICATION NUMBER: US/10/174,794
 ; CURRENT FILING DATE: 2002-06-18
 ; PRIOR APPLICATION NUMBER: US/09/411,628
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: US 60/102,906
 ; PRIOR FILING DATE: 1998-10-02
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 5

; LENGTH: 1701
 ; TYPE: DNA
 ; ORGANISM: Orcytolagus cuniculus
 US-10-174-794-5

Query Match	30.4%	Score 287	DB 16	Length 1701
Best Local Similarity	59.1%	Pred. No. 8.7e-65		
Matches 510	Conservative 0	Mismatches 350	Indels 3	Gaps 1

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Db	1	ATGGAAGAATGATGAAATTAAGCTAAGACTGAGAGAGGGCTCTATATGGGGTTGTATTCAAA	60
Qy	61	TGCAGAAACAAACCTCTGGGCAAGTAGTAGCTGTGTTAAAAAATTTGTGGAATCTGAAGAT	120
Db	61	TGTAGGAATAAAGATAGTGGGAAGAAATTTGTGCCATCAAGAAAGTTCTTAGAAAGTGATGAT	120
Qy	121	GATCCTGTGTTAAGAAATAGCAATAGCAATACGTATGTTGAAGCAATTAACACAT	180
Db	121	GACAAATGGTTAAAAAATTTGCTATGCGAAGAAATCAAGTTACTAAAGCAACTGAGGCAT	180
Qy	181	CCAAATCTTGTGAACCTCATCGAGGTGTTTCAGAGAGAAAGAAATGCAATTTAGTTTTT	240
Db	181	GAAATTTGGTGAATCTGTTGGAGGTGTAAABAAAACGATGCTAGTCTTT	240
Qy	241	GAATACGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT	300
Db	241	GAAATTTGTGACCAACAGATCTTGTATGACATTTGGAACCTCTTTCCAAATGGACTAGATGAC	300
Qy	301	GGAGTGATCAAAAGGGTATTATGCAACACACTCAAGCTCTTAATTTCTGTCATATACAT	360
Db	301	CAAGTAGTTCAAAAGTATTTCTTTTCAGATTAATTAAGAAATGGATTTTGTACAGTCCAC	360
Qy	361	AACGTGATTTACAGAGATATAAAACCTGAAATATTTCTAATAACTAAGCAAGGAATAATC	420
Db	361	AATATCATACATAGATATTAAGCCAGAGATATATTTGGTCTCCAGTCTGGCGTTGTC	420
Qy	421	AAGATTTGTGACTTCGGGTTTGCACAAATCTG---ATTCCAGAGAGATGCCTACACCGAT	477
Db	421	AAGTTATGTGATTTTGGATTTTGCACGGACACTGGCAGCTCCCGGAGAGGTTTACACTGAT	480
Qy	478	TATGTAGCTACAGATGATGATCCGAGCTCTGAACTTTCTTGTGGGAGATACCTCAGTATGGT	537
Db	481	TATGTGCACTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	540
Qy	538	TCCTTCAGTCGATATATGGGCTATTGGTGTGTTTTCAGAGCTCTGACAGGCGCAGCCA	597
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Qy	598	CTGTGGCTTGGAAATCAGATGTGGACCAACTTTTATCTGATTAATCAGAAACATAGGAAA	657
Db	601	CTGTTTCTGGAGACTCTGATATTTGATCAGCTTTTATTAATAAATCCTGTTGTGGAGTAAGGTTG	660
Qy	658	TTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATA	717
Db	661	CTAATTTCCAGACACACAGGAGCTTTTATTAATAAATCCTGTTGTGGAGTAAGGTTG	720
Qy	718	CCTGAGCCAGAAAGACATGGAACCTCTGAGGAAAGTTCTCAGATGTTTCATCTCTGTGGCT	777
Db	721	CCTGAATCAAGGAATCAGAACCTTTGAAAGACGCTATCCCAAGCTCTCAGAAGTTGTG	780
Qy	778	CTGAATCTTGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATTAACTGTGTTCCAA	837
Db	781	ATAGATTTAGCAAGAAATGCTTACATGTTGACCCAGACAAAAGGCCCTCTGTGCTGAG	840
Qy	838	CTCCTGGAGAGCTCTACTTTGA	860
Db	841	CTCCTACACCATGATTTCTTTCA	863

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OM nucleic - nucleic search, using sw model

Run on: April 21, 2005, 20:27:40 ; Search time 178.912 Seconds
(without alignments)
8642.674 Million cell updates/sec

Title: US-10-766-691-11

Perfect score: 945

Sequence: 1 atgaaaagtatgaaaaatt.....aggtaacttcgctcaaaagt 945

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	929	98.3	972	4	US-09-671-050-5	Sequence 5, Appl
3	839	88.8	1041	4	US-09-671-050-9	Sequence 9, Appl
4	823	87.1	1068	4	US-09-671-050-3	Sequence 3, Appl
5	507	53.7	1819	4	US-09-671-050-13	Sequence 13, Appl
6	454.4	48.1	561	4	US-09-671-050-1	Sequence 1, Appl
7	454.4	48.1	594	4	US-09-671-050-7	Sequence 7, Appl
8	415.4	44.0	1177	4	US-09-949-016-1681	Sequence 1681, Ap
9	287	30.4	1701	3	US-09-411-628-5	Sequence 5, Appl
10	287	30.4	1701	4	US-10-174-794-5	Sequence 5, Appl
11	287	30.4	3080	3	US-09-411-628-3	Sequence 3, Appl
12	287	30.4	3080	4	US-10-174-794-3	Sequence 3, Appl
13	283.8	30.0	1794	4	US-09-949-016-2083	Sequence 2083, Ap
14	171.8	18.2	903	2	US-08-874-347-9	Sequence 9, Appl
15	171.8	18.2	903	3	US-09-093-522-9	Sequence 9, Appl
16	163.4	17.3	1476	2	US-08-969-106-1	Sequence 1, Appl
17	163.4	17.3	1476	4	US-09-338-125-1	Sequence 1, Appl
18	163.4	17.3	1476	4	US-09-266-225D-13	Sequence 13, Appl
19	163.4	17.3	1635	4	US-09-417-197-112	Sequence 112, App
20	163.4	17.3	1635	4	US-09-417-197-114	Sequence 114, App
21	161.8	17.1	1296	4	US-09-949-016-2154	Sequence 2154, Ap
22	161.8	17.1	2213	4	US-09-023-655-1037	Sequence 1037, Ap
23	155.6	16.5	1050	4	US-09-220-132-3	Sequence 3, Appl
24	155.6	16.5	1825	4	US-09-919-039-115	Sequence 115, App
25	152.4	16.1	1042	4	US-09-949-016-4802	Sequence 4802, Ap
26	146.8	15.5	3823	4	US-09-949-016-4276	Sequence 4276, Ap
27	136.6	14.5	1158	4	US-09-949-016-4906	Sequence 4906, Ap

28 136.6 14.5 1161 4 US-09-023-655-1373 Sequence 1373, Ap
29 136.6 14.5 1161 4 US-09-949-016-181 Sequence 181, App
30 136.6 14.5 1825 4 US-09-620-312D-313 Sequence 313, App
31 134.6 14.2 987 4 US-09-949-016-5854 Sequence 5854, Ap
32 134.6 14.2 1089 1 US-08-154-915-1 Sequence 1, Appli
33 134.6 14.2 1089 2 US-08-464-517-37 Sequence 37, Appl
34 134.6 14.2 1089 2 US-08-246-361A-37 Sequence 37, Appl
35 134.6 14.2 1089 3 US-08-463-772-37 Sequence 37, Appl
36 134.6 14.2 1089 5 PCT-US93-09945-1 Sequence 1, Appli
37 131 13.9 993 4 US-09-248-796A-4323 Sequence 4323, Ap
38 131 13.9 1002 1 US-08-463-090B-3 Sequence 3, Appli
39 120.4 12.7 1044 4 US-09-248-796A-4325 Sequence 4325, Ap
40 117.2 12.4 1070 1 US-08-463-090B-5 Sequence 5, Appli
41 112.4 11.9 69909 4 US-09-949-016-13423 Sequence 13423, A
42 112 11.9 1308 4 US-09-801-861-4 Sequence 4, Appli
43 112 11.9 1308 4 US-10-224-562-4 Sequence 4, Appli
44 112 11.9 2203 4 US-09-801-861-1 Sequence 1, Appli
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ALIGNMENTS

RESULT 1

US-09-671-050-11

; Sequence 11, Application US/09671050

; Patent No. 6716616

; GENERAL INFORMATION:

; APPLICANT: Donoho, Gregory

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Nehls, Michael

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and

; FILE REFERENCE: LEX-0046-USA

; CURRENT APPLICATION NUMBER: US/09/671.050

; CURRENT FILING DATE: 2001-06-11

; PRIOR APPLICATION NUMBER: US 60/156,511

; PRIOR FILING DATE: 1999-09-28

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11

; LENGTH: 945

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-671-050-11

Query Match 100.0%; Score 945; DB 4; Length 945;

Best Local Similarity 100.0%; Pred. No. 6.8e-258;

Matches 945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCAAAAGTATGAAAAATTTAGCTTAAGACTGAGAGGGTCTTATGGGGTTGTATTTCAA 60
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Qy 61 TGCAGAAACAAAACCTCTGGACAAAGTAGTACTGTAAAAAATTTTGTGGAATCTCGAAGAT 120
Db 61 TGCAGAAACAAAACCTCTGGACAAAGTAGTACTGTAAAAAATTTTGTGGAATCTCGAAGAT 120
Qy 121 GATCCTGTGTAAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATATAAACAAT 180
Db 121 GATCCTGTGTAAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATATAAACAAT 180
Qy 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAAAGAAAATGCATTTAGTTT 240
Db 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAAAGAAAATGCATTTAGTTT 240
Qy 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAGAAAACCCAAATGGAGTGTCTCAT 300
Db 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAGAAAACCCAAATGGAGTGTCTCAT 300

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Qy      |||
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541 TCAGTTCGATATATGGGTATTTGGTTGTTTTCAGAGCTCTGCAAGGCCAGCCACTG 600
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601 TGGCTTGAAATCAGATGTGGACCACTTTATCTGTAATCAGAACACTAGGAAATTA 660
Qy      |||
661 ATCCCAAGACATCAATCAATCTTTAAAGTAAACGGTCTTTCCATGGCATCAGTATACCT 720
Db      |||
661 ATCCCAAGACATCAATCAATCTTTAAAGTAAACGGTCTTTCCATGGCATCAGTATACCT 720
Qy      |||
721 GAGTCAGAGATGGAACCTTTGAGGAAAGTTCTCAGATGTTCACTGTTGGCTCTG 780
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721 GAGTCAGAGATGGAACCTTTGAGGAAAGTTCTCAGATGTTCACTGTTGGCTCTG 780
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Db      |||
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841 CTGAGAGCTCCTACTTTGATTTCTTTTCAAGAGGCCCAAAATTAAGAAAGACGATTAAT 900
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841 CTGAGAGCTCCTACTTTGATTTCTTTTCAAGAGGCCCAAAATTAAGAAAGACGATTAAT 900
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901 GAAGGAAGAACAGAGACGCAACGCTACTTCCGCTCAAAAGT 945
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RESULT 2

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US-09-671-050-5
; Sequence 5, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 972
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-671-050-5

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Query Match 98.3%; Score 929; DB 4; Length 972;
Best Local Similarity 100.0%; Pred. No. 2.4e-253;

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Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 ATGAAAGATATGAAAAATTTAGCTAAGACTGAGAGAGGGCTTATGCGGTGTGATTCAAA 60
Db      |||
Qy      1 ATGAAAGATATGAAAAATTTAGCTAAGACTGAGAGAGGGCTTATGCGGTGTGATTCAAA 60
Db      |||
Qy      61 TGCAGAAACAAAACCTCTGGACAGTAGTAGCTGTTAAAAAATTTTGGAAATCTGGAAGAT 120
Db      |||
Qy      61 TGCAGAAACAAAACCTCTGGACAGTAGTAGCTGTTAAAAAATTTTGGAAATCTGGAAGAT 120
Db      |||
Qy      121 GATCCTGTGTTAAGAAAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACACAT 180
Db      |||
Qy      121 GATCCTGTGTTAAGAAAAATAGCACTAAGAGAAATAGCTATGTTGAAGCAATTAACACAT 180
Db      |||
Qy      181 CCAATCTTGTGAACCTCATCGAGTGTTCAGAGAGAAAAAGGAAAAATGCAATTTAGTTT 240
Db      |||
Qy      181 CCAATCTTGTGAACCTCATCGAGTGTTCAGAGAGAAAAAGGAAAAATGCAATTTAGTTT 240
Db      |||
Qy      241 GAATACCTGATCATACACATTTTAAATGAGCTGGAAGAAACCCCAATGGAGTTGCTGAT 300
Db      |||
Qy      241 GAATACCTGATCATACACATTTTAAATGAGCTGGAAGAAACCCCAATGGAGTTGCTGAT 300
Db      |||
Qy      301 GGAGTGATCAAAAGCGTATTATGCAAACTTCAAGCTCTTAATTTCTGTCATATACAT 360
Db      |||
Qy      301 GGAGTGATCAAAAGCGTATTATGCAAACTTCAAGCTCTTAATTTCTGTCATATACAT 360
Db      |||
Qy      361 AACTGTATTACAGAGATATAAAACCTGAAAAATTTCTAATACTAAGCAAGGAATAATC 420
Db      |||
Qy      361 AACTGTATTACAGAGATATAAAACCTGAAAAATTTCTAATACTAAGCAAGGAATAATC 420
Db      |||
Qy      421 AAGATTCTGACTTCGGGTTCGCAAAATCTGATTCAGAGAGATGCTTACACCGATTAT 480
Db      |||
Qy      421 AAGATTCTGACTTCGGGTTCGCAAAATCTGATTCAGAGAGATGCTTACACCGATTAT 480
Db      |||
Qy      481 GTAGTACGAGATGGTACCGAGCTCTGAACTTTCTGTTGGGAGATATCTAGTATGGTTCT 540
Db      |||
Qy      481 GTAGTACGAGATGGTACCGAGCTCTGAACTTTCTGTTGGGAGATATCTAGTATGGTTCT 540
Db      |||
Qy      541 TCAGTTCGATATATGGGTATTTGGTTGTTTTCAGAGAGCTCTGAGGCCAGCCACTG 600
Db      |||
Qy      541 TCAGTTCGATATATGGGTATTTGGTTGTTTTCAGAGAGCTCTGAGGCCAGCCACTG 600
Db      |||
Qy      601 TGGCTTGAAATCAGATGTGGACCACTTTATCTGTAATCAGAACACTAGGAAATTA 660
Db      |||
Qy      601 TGGCTTGAAATCAGATGTGGACCACTTTATCTGTAATCAGAACACTAGGAAATTA 660
Db      |||
Qy      661 ATCCCAAGACATCAATCAATCTTTAAAGTAAACGGTCTTTCCATGGCATCAGTATACCT 720
Db      |||
Qy      661 ATCCCAAGACATCAATCAATCTTTAAAGTAAACGGTCTTTCCATGGCATCAGTATACCT 720
Db      |||
Qy      721 GAGTCAGAGATGGAACCTTTGAGGAAAGTTCTCAGATGTTCACTGTTGGCTCTG 780
Db      |||
Qy      721 GAGTCAGAGATGGAACCTTTGAGGAAAGTTCTCAGATGTTCACTGTTGGCTCTG 780
Db      |||
Qy      781 AACTTCATGAAGGGTGTCTGAAAGATGAATCCAGATGACGATTAACTGTTCCCAACTC 840
Db      |||
Qy      781 AACTTCATGAAGGGTGTCTGAAAGATGAATCCAGATGACGATTAACTGTTCCCAACTC 840
Db      |||
Qy      841 CTGAGAGCTCCTACTTTGATTTCTTTTCAAGAGGCCCAAAATTAAGAAAGACGATTAAT 900
Db      |||
Qy      841 CTGAGAGCTCCTACTTTGATTTCTTTTCAAGAGGCCCAAAATTAAGAAAGACGATTAAT 900
Db      |||
Qy      901 GAAGGAAGAACAGAGAGCGCCAAACAGGT 929
Db      |||
Qy      901 GAAGGAAGAACAGAGAGCGCCAAACAGGT 929
Db      |||

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RESULT 3
US-09-671-050-9
; Sequence 9, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory

```
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671,050
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1041
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-671-050-9

Query Match      88.8%; Score 839; DB 4; Length 1041;
Best Local Similarity 90.8%; Pred. No. 8.3e-228;
Matches 945; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

Qy 1 ATGGAAGAAGTATGAAAATAGCTTAAGACTGAGAAAGGCTCTATGGGTTGTATTCAA 60
Db 1 ATGGAAGAAGTATGAAAATAGCTTAAGACTGAGAAAGGCTCTATGGGTTGTATTCAA 60
Qy 61 TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTAAAGAAATTTGTGGAATCTGAAGAT 120
Db 61 TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTAAAGAAATTTGTGGAATCTGAAGAT 120
Qy 121 GATCCTGTGTAAAGAAATAGCACTAAGAGAAATACGTATGTTGGAAGCAATTAACACAT 180
Db 121 GATCCTGTGTAAAGAAATAGCACTAAGAGAAATACGTATGTTGGAAGCAATTAACACAT 180
Qy 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAGGAAATGCATTAGTTTTT 240
Db 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAGGAAATGCATTAGTTTTT 240
Qy 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
Db 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
Qy 301 GGAGTGATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
Qy 361 AACTGTATTACAGAGATATAAACCCTGAAATATTTCTAATACTAAGCAAGGAATATC 420
Db 361 AACTGTATTACAGAGATATAAACCCTGAAATATTTCTAATACTAAGCAAGGAATATC 420
Qy 421 AAGATTGTGACTTCGGGTTTGCAAAATCTGATTCAGGAGATGCTACACCGATTAT 480
Db 421 AAGATTGTGACTTCGGGTTTGCAAAATCTGATTCAGGAGATGCTACACCGATTAT 480
Qy 481 GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGAGATACCTCAGTATGGTTCT 540
Db 481 GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGAGATACCTCAGTATGGTTCT 540
Qy 541 TCAGTCAGATATATGGGCTATTTGGTTGTTTTTTCGAGAGCTTCCTGACAGGCGAGCCACTG 600
Db 541 TCAGTCAGATATATGGGCTATTTGGTTGTTTTTTCGAGAGCTTCCTGACAGGCGAGCCACTG 600
Qy 601 TGGCTCGAAATCAGATGTGGACCAACTTTATCTGATTAATCAACAACAT 650
Db 601 TGGCTCGAAATCAGATGTGGACCAACTTTATCTGATTAATCAACAACAT 650
Qy 651 -----AGGAAAAATTAATCCCAAGACATCAATCAATCTTT 684
Db 651 -----AGGAAAAATTAATCCCAAGACATCAATCAATCTTT 684
Qy 661 GGGTTTCGCCATGTTGACCAGGCTGGTCTCGAACTCTTTGAGCTCAAGTGATCCACCTGCC 720
Db 661 GGGTTTCGCCATGTTGACCAGGCTGGTCTCGAACTCTTTGAGCTCAAGTGATCCACCTGCC 720
Qy 651 -----AGGAAAAATTAATCCCAAGACATCAATCAATCTTT 684
Db 651 -----AGGAAAAATTAATCCCAAGACATCAATCAATCTTT 684
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Db 721 GTAGCCTCTCAAAGTGTGGAATTAAGGAAAAATTAATCCCAAGACATCAATCAATCTTT 780
Qy 685 AAAAGTAAACGGGTTTTTCCATGCGATCAGTATACCTGAGCCAGAGACATCGAAACTCTT 744
Db 781 AAAAGTAAACGGGTTTTTCCATGCGATCAGTATACCTGAGCCAGAGACATCGAAACTCTT 840
Qy 745 GAGGAAAAATTTCTCAGATGTTTCATCTCTGGCTCTGAACTTCATGAAGGGGTGCTGAAG 804
Db 841 GAGGAAAAATTTCTCAGATGTTTCATCTCTGGCTCTGAACTTCATGAAGGGGTGCTGAAG 900
Qy 805 ATGAATCCAGATGACAGATTAACCTGTTCCAACTCTCGAGAGCTCTCTACTTTGATTCT 864
Db 901 ATGAATCCAGATGACAGATTAACCTGTTCCAACTCTCGAGAGCTCTCTACTTTGATTCT 960
Qy 865 TTTCAAGAGGCCCCAAATTTAAAGAAAAAGCAGTAAATGAAGGAAAGAAACAGAGACGCCAA 924
Db 961 TTTCAAGAGGCCCCAAATTTAAAGAAAAAGCAGTAAATGAAGGAAAGAAACAGAGACGCCAA 1020
Qy 925 CAGGTACTTCCGCTCAAAAGT 945
Db 1021 CAGGTACTTCCGCTCAAAAGT 1041

RESULT 4
US-09-671-050-3
; Sequence 3, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Doncho, Gregory
; APPLICANT: Turfer, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671,050
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1068
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-671-050-3
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Query Match      87.1%; Score 823; DB 4; Length 1068;
Best Local Similarity 90.6%; Pred. No. 2.9e-223;
Matches 929; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

Qy 1 ATGGAAGAAGTATGAAAATAGCTTAAGACTGAGAAAGGCTCTTATGGGTTGTATTCAA 60
Db 1 ATGGAAGAAGTATGAAAATAGCTTAAGACTGAGAAAGGCTCTTATGGGTTGTATTCAA 60
Qy 61 TGCAGAAACAAAACCTCTGGAACAAGTAGTAGCTGTAAAGAAATTTGTGGAATCTGAAGAT 120
Db 61 TGCAGAAACAAAACCTCTGGAACAAGTAGTAGCTGTAAAGAAATTTGTGGAATCTGAAGAT 120
Qy 121 GATCCTGTGTAAAGAAATAGCACTAAGAGAAATACGTATGTTGGAAGCAATTAACACAT 180
Db 121 GATCCTGTGTAAAGAAATAGCACTAAGAGAAATACGTATGTTGGAAGCAATTAACACAT 180
Qy 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAGGAAATGCATTAGTTTTT 240
Db 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGGAGAAAGGAAATGCATTAGTTTTT 240
Qy 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
Db 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
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QY 301 GGAGTGATCAAAAGCGTATTATGGCAACACATTCAGCTCTTAATTTCTGTCATATACAT 360
Db 301 GGAGTGATCAAAAGCGTATTATGGCAACACATTCAGCTCTTAATTTCTGTCATATACAT 360
QY 361 AACTGTATTTCAGAGATATAAAACCTGAAATATTTCTAATAACTTAAGCAAGGAATAATC 420
Db 361 AACTGTATTTCAGAGATATAAAACCTGAAATATTTCTAATAACTTAAGCAAGGAATAATC 420
QY 421 AAGATTGTGACTTCGGGTTTGGCAAAATTCGTATTCAGGAGATGCCTACACCGATTAT 480
Db 421 AAGATTGTGACTTCGGGTTTGGCAAAATTCGTATTCAGGAGATGCCTACACCGATTAT 480
QY 481 GTAGCTACGAGATGTCAGGCTCTGAACTTCTTGTGGGAGATACCTACATATGTTCT 540
Db 481 GTAGCTACGAGATGTCAGGCTCTGAACTTCTTGTGGGAGATACCTACATATGTTCT 540
QY 541 TCAGTTCGATATATGGGCTATTGGTTGTTTGTGAGAGCTCTGACAGGCGAGCACTG 600
Db 541 TCAGTTCGATATATGGGCTATTGGTTGTTTGTGAGAGCTCTGACAGGCGAGCACTG 600
QY 601 TGGCTTGAAATCAGATGTGGACCACTTTATCTGATAATCAGAACACTAGTAGAGAG 660
Db 601 TGGCTTGAAATCAGATGTGGACCACTTTATCTGATAATCAGAACACTAGTAGAGAG 660
QY 651 ----- 650
Db 651 ----- 650
QY 661 GGGTTTGGCCATGTTGACAGGCTGTCTCGAATCTTTGAGCTCAAGTGATCCACCTGCC 720
QY 651 -----AGAAAAATTAATCCCAAGACATCAATCAATCTTT 684
Db 721 GTAGCCTCTCAAAGTCTGGAATACAGGAAAAATTAATCCCAAGACATCAATCAATCTTT 780
QY 685 AAAAGTAACGGGTTTCCATGGCATCAGTATACCTGACGAGCTCTGACAGGAGGTTCTGAAG 900
Db 781 AAAAGTAACGGGTTTCCATGGCATCAGTATACCTGACGAGGAGGTTCTGAAG 900
QY 745 GAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTTCATGAAGGGTGTCTGAAG 804
Db 841 GAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTTCATGAAGGGTGTCTGAAG 900
QY 805 ATGAATCCAGATGACAGATTAACCTGTTCCTGCAATCTCTGAGAGCTCTTACTTTGATTCT 864
Db 901 ATGAATCCAGATGACAGATTAACCTGTTCCTGCAATCTCTGAGAGCTCTTACTTTGATTCT 960
QY 865 TTTCAAGAGGCCCAATTAAGAAAGCAAGTAAAGGAGAAACAGAGAGGCGCAA 924
Db 961 TTTCAAGAGGCCCAATTAAGAAAGCAAGTAAAGGAGAAACAGAGAGGCGCAA 1020
QY 925 CAGGT 929
Db 1021 CAGGT 1025
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RESULT 5

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US-09-671-050-13
; Sequence 13, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671,050
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
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; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13

; LENGTH: 1819

; TYPE: DNA

; ORGANISM: homo sapiens

US-09-671-050-13

Query Match 53.7%; Score 507; DB 4; Length 1819;

Best Local Similarity 69.8%; Pred. No. 1.6e-133;

Matches 929; Conservative 0; Mismatches 0; Indels 402; Gaps 2;

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QY 1 ATGCAAAAGATGATAAAATTAAGCTTAACACTGGAGAAGGCTCTTATGGGTGTTGTTATTTCAA 60
Db 138 ATGCAAAAGATGATAAAATTAAGCTTAACACTGGAGAAGGCTCTTATGGGTGTTGTTATTTCAA 197
QY 61 TGCAGAAACAAAACCTCTCGACAAAGTAGTAGCTGTTAAAAAATTTGTGGAAATCTGAAGAT 120
Db 198 TGCAGAAACAAAACCTCTCGACAAAGTAGTAGCTGTTAAAAAATTTGTGGAAATCTGAAGAT 257
QY 121 GATCCTGTTTAAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTTAAACAT 180
Db 258 GATCCTGTTTAAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTTAAACAT 317
QY 181 CCAAACTCTGTAACCTCATCGAGGCTTCCAGAGAAAAAGGAAAAATGCAATTTAGTTTTT 240
Db 318 CCAAACTCTGTAACCTCATCGAGGCTTCCAGAGAAAAAGGAAAAATGCAATTTAGTTTTT 377
QY 241 GAATACCTGTCATACACATTTTAAATGAGCTCGAAAGAAACCCAAATGGAGTTGCTGAT 300
Db 378 GAATACCTGTCATACACATTTTAAATGAGCTCGAAAGAAACCCAAATGGAGTTGCTGAT 437
QY 301 GGAGTGATCAAAAGCGTATTATGGCAACACATTCAGCTCTTAATTTCTGTCATATACAT 360
Db 438 GGAGTGATCAAAAGCGTATTATGGCAACACATTCAGCTCTTAATTTCTGTCATATACAT 497
QY 361 AACTGTATTTCAGAGATATAAAACCTGAAAAATTTCTAATAACTTAAGCAAGGAATAATC 420
Db 498 AACTGTATTTCAGAGATATAAAACCTGAAAAATTTCTAATAACTTAAGCAAGGAATAATC 557
QY 421 AAGATTGTGACTTCGGGTTTGGCAAAATTTCTG----- 453
Db 558 AAGATTGTGACTTCGGGTTTGGCAAAATTTCTGAGTTGGACTTCATCTTCTCTGGTGCC 617
QY 454 ----- 453
Db 618 TCCTTGATTGGCTTAATAGTTGACCTTCTGAAATCTTTTTCTGCCAATTCAGAGATTTT 677
QY 454 ----- 453
Db 678 CTCCTGGCTTGGATCCATTGCTGACACAGTGTTTCCACATGGGGCCCGCTCATCTCGA 737
QY 454 ----- 453
Db 738 ACTTCTGGCCTCAAGTGATCCTTCCACCTCGGCTCCCAAGTGTCTGGATTGCAAGTG 797
QY 454 ----- 453
Db 798 AGCCACGGTCCCGCCAGATTTTTCAAAACAATACTACTGAGAGCTCAAGAGTTGTTT 857
QY 454 -----ATTCCAGGAGATGCTTACACC 474
Db 858 TTAGTGGGAACAACAATTTCGAACAAATTTCTTGAGAACGCAATCCAGAGATGCTTACACC 917
QY 475 GATTATGTAGCTACGAGATGTTACCGAGCTCTTGAACTTCTTGTGGGAGATACCTAGTAT 534
Db 918 GATTATGTAGCTACGAGATGTTACCGAGCTCTTGAACTTCTTGTGGGAGATACCTAGTAT 977
QY 535 GGTTCTTTCAGTCGATATATGGGCTATTGGTTGTTTGTGAGAGCTCTTCAGAGGCCAG 594
Db 978 GGTTCTTTCAGTCGATATATGGGCTATTGGTTGTTTGTGAGAGCTCTTCAGAGGCCAG 1037
QY 595 CCACCTGCGCTGGAAAAATCAGATGTGGACCAATTTATCTGATAATCAGAACACT----- 650
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Db 1038 CCACTGTGGCTGGAAAAATCAGATGTGGACCAACTTTTATCTGATATCAGAACACTAGTA 1097
 Qy 651 ----- 650
 Db 1098 GAGACGGGTTTCGCCATGTTGACCGGTGGTCTCGAACTCTTGACGTCAAAGTGATCCA 1157
 Qy 651 -----AGGAAATTAATCCCAAGACATCA 678
 Db 1158 CTTGCCGTAGCTCTCAAAGTGTGSGAATTACAGGAAAAATTAATCCCAAGACATCA 1217
 Qy 679 ATCTTTAAAGTAAACCGGTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATCGAA 738
 Db 1218 ATCTTTAAAGTAAACCGGTTTTCCATGGCATCAGTATACCTGAGCCAGAGACATCGAA 1277
 Qy 739 ACTCTTGAGAAAGTTCTCAGATGTTTCATCCTGTGTGCTCTGAACTTCATGAAGGGGTGT 798
 Db 1278 ACTCTTGAGAAAGTTCTCAGATGTTTCATCCTGTGTGCTCTGAACTTCATGAAGGGGTGT 1337
 Qy 799 CTGAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTCTCTGGAGAGCTCTACTTT 858
 Db 1338 CTGAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTCTCTGGAGAGCTCTACTTT 1397
 Qy 859 GATCTTTTTCAAGAGGCCCAAAATTAAGAAAGCACTAATGAAGCAAGAAACAGAGA 918
 Db 1398 GATCTTTTTCAAGAGGCCCAAAATTAAGAAAGCACTAATGAAGCAAGAAACAGAGA 1457
 Qy 919 CGCCAAACAGGT 929
 Db 1458 CGCCAAACAGGT 1468

RESULT 6

US-09-671-050-1
 ; Sequence 1, Application US/09671050
 ; Patent No. 6716616
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
 ; TITLE OF INVENTION: Polynucleotides Encoding the Same
 ; FILE REFERENCE: LEX-0046-USA
 ; CURRENT APPLICATION NUMBER: US/09/671.050
 ; CURRENT FILING DATE: 2001-06-11
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 561
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-09-671-050-1

Query Match 48.1%; Score 454.4; DB 4; Length 561;
 Best Local Similarity 99.8%; Pred. No. 7.5e-119;
 Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 ATGGAAGAATGAAAAAATTAGCTTAAGACTGGAGAAGGGTCTTATGGGGTTGTATCAAA 60
 Db 1 ATGGAAGAATGAAAAAATTAGCTTAAGACTGGAGAAGGGTCTTATGGGGTTGTATCAAA 60
 Qy 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTCTTAAAAAATTTGGAATCTGAAGAT 120
 Db 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTCTTAAAAAATTTGGAATCTGAAGAT 120
 Qy 121 GATCCTGTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGGAAGCAATTAACAT 180
 Db 121 GATCCTGTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGGAAGCAATTAACAT 180

Qy 181 CCAATCTTGTGAACCTCATCGAGGTGTTTCAGGAGAAAAAGGAAAAATGCATTTAGTTTTT 240
 Db 181 CCAATCTTGTGAACCTCATCGAGGTGTTTCAGGAGAAAAAGGAAAAATGCATTTAGTTTTT 240
 Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAAAACCCAAATGGAAGTTGCTGAT 300
 Db 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAAAACCCAAATGGAAGTTGCTGAT 300
 Qy 301 GGAAGTGAATCAAAAGCGTATTATGGAACAACCTTCAAGCTCTTAAATTTCTGTATATACAT 360
 Db 301 GGAAGTGAATCAAAAGCGTATTATGGAACAACCTTCAAGCTCTTAAATTTCTGTATATACAT 360
 Qy 361 AACTGTATTACAGAGATATAAAACCTGGAATAATTTCTAATACTAAGCAAGGAATAATC 420
 Db 361 AACTGTATTACAGAGATATAAAACCTGGAATAATTTCTAATACTAAGCAAGGAATAATC 420
 Qy 421 AAGATTGTGACTTCGGGTTTGCACAAATTTCTGATT 456
 Db 421 AAGATTGTGACTTCGGGTTTGCACAAATTTCTGATT 456

RESULT 7

US-09-671-050-7
 ; Sequence 7, Application US/09671050
 ; Patent No. 6716616
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
 ; TITLE OF INVENTION: Polynucleotides Encoding the Same
 ; FILE REFERENCE: LEX-0046-USA
 ; CURRENT APPLICATION NUMBER: US/09/671.050
 ; CURRENT FILING DATE: 2001-06-11
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 594
 ; TYPE: DNA
 ; ORGANISM: homo sapiens
 US-09-671-050-7

Query Match 48.1%; Score 454.4; DB 4; Length 594;
 Best Local Similarity 99.8%; Pred. No. 7.8e-119;
 Matches 455; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 ATGGAAGAATGAAAAAATTAGCTTAAGACTGGAGAAGGGTCTTATGGGGTTGTATCAAA 60
 Db 1 ATGGAAGAATGAAAAAATTAGCTTAAGACTGGAGAAGGGTCTTATGGGGTTGTATCAAA 60
 Qy 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTCTTAAAAAATTTGGAATCTGAAGAT 120
 Db 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTCTTAAAAAATTTGGAATCTGAAGAT 120
 Qy 121 GATCCTGTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGGAAGCAATTAACAT 180
 Db 121 GATCCTGTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGGAAGCAATTAACAT 180
 Qy 181 CCAATCTTGTGAACCTCATCGAGGTGTTTCAGGAGAAAAAGGAAAAATGCATTTAGTTTTT 240
 Db 181 CCAATCTTGTGAACCTCATCGAGGTGTTTCAGGAGAAAAAGGAAAAATGCATTTAGTTTTT 240
 Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAAAACCCAAATGGAAGTTGCTGAT 300
 Db 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAAAACCCAAATGGAAGTTGCTGAT 300
 Qy 301 GGAAGTGAATCAAAAGCGTATTATGGAACAACCTTCAAGCTCTTAAATTTCTGTATATACAT 360

Db 301 GGAGTGATCAAAAGCGTATTATGGCAAAACACTTCAAGCTCTTAATTTCTGTCAATACAT 360
QY 361 AACTGTATTACAGAGATATAAACTGAATATTTCTAATACTTAAGCAAGGATATAC 420
Db 361 AACTGTATTACAGAGATATAAACTGAATATTTCTAATACTTAAGCAAGGATATAC 420
QY 421 AAGATTCTGACTTCGGGTTTGCAAAATTTCTGATT 456
Db 421 AAGATTCTGACTTCGGGTTTGCAAAATTTCTGATT 456

RESULT 8

US-09-949-016-1681
; Sequence 1681, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1681
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1681

Query Match 44.0%; Score 415.4; DB 4; Length 1177;
Best Local Similarity 66.7%; Pred. No. 1.3e-107;
Matches 609; Conservative 0; Mismatches 301; Indels 3; Gaps 1;
QY 1 ATGGAAGATGAAATTAAGCTTAAGCTGGAGAGGGCTTATGGGTTGATTCAAA 60
Db 32 ATGGAAGATGAAATTAAGCTTAAGCTGGAGAGGGCTTATGGGTTGATTCAAA 91
QY 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTCTTAAATAATTTGGGAATCTGAAGAT 120
Db 92 TGTAGAACAGGACACGGGTGAGTTGTGCCATCAAGAGTTCTTGAATCAGAGAT 151
QY 121 GATCCTGTTTAAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
Db 152 GACCTGTCTATAAGAAATTTGCCCTTTCGGGAATCGGAATGCTCAAGCAACTCAAGCAT 211
QY 181 CCAATCTGTGACCTCATCGAGTCTTCCAGGAAAGAAAGAAATGCAATTTAGTTT 240
Db 212 CCAATCTGTGACCTCATCGAGTCTTCCAGGAAAGAAAGAAATGCAATTTAGTTT 271
QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 300
Db 272 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 331
QY 301 GAGTGTATCAAAAGCGTATTATGCAAAACCTTCAAGCTCTTAATTTCTGTCAATACAT 360
Db 332 CATCTCGTGAAGAGCATAACTTGGCAGACACTGCAAGCTGAAATTTTGGCAATAAACAC 391
QY 361 AACTGTATTACAGAGATATAAACTGAATATTTCTAATACTTAAGCAAGGATATAC 420
Db 392 AATGTATATAGACGTGAGCCGAGAAATATCTCTATCAGAAACATTCCTGATT 451
QY 421 AAGATTCTGACTTCGGGTTTGCAAAATTTCTGATT---CCAGGAGATGCTTACACCGAT 477
Db 452 AAGCTTTGTGACTTTGGATTGCTCGGCTTTTGACTGACCGAGTACTACTATACAGAC 511
QY 478 TATGTAGTACAGAGATGGTACCGAGCTCTGAACTTCTTGTGGAGATACCTAGTATGGT 537

Db 512 TACGTGCTACAGGTGTATCCGCTCCCTGAGCTGCTGTGGGGGACACCGCAGTAGCGC 571
QY 538 TCTTCACTGCATATATCGGCTATTGGTGTGTTTTTGCAGAGCTCTTGACAGGCCAGCCA 597
Db 572 CCCCCTGTGATGTTGGCAATTTGGCTGTCTTTGCTGAGCTGCTGTGAGGAGTGCCT 631
QY 598 CTGTGGCTGGAAATCAGATGTGGACCAACTTTATCTGATATCAGAACACTAGGAAA 657
Db 632 CTGTGGCCAGGAAATCGGATGTGGATCAGCTGTATCTGATTAGGAAGACCTTGGGGGAT 691
QY 658 TTAATCCAAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATA 717
Db 692 CTCAATCTTAGGACACGAGAGTGTGTAGCAGCATCAGTACTTTCAGTGAAGTGAAT 751
QY 718 CTTGAGCCAGAACATGGAACCTCTTGAGGAAAGTTCTCAGATGTTCACTCTGTGCT 777
Db 752 CCAGACCTCAAGATATGGAACCACTTGAATTTAAATTTCCAAACATCTCTTATCTGCC 811
QY 778 CTGAACCTCATGAGGGTCTCTGAAGATGAATCCAGATCAGACATTAACCTGTTCCAA 837
Db 812 CTGGGGCTCTTAAAGGGCTGTCTCCACATGAGCCCTACTGAAAGGCTGACATGTGAACAG 871
QY 838 CTCCTGGAGAGCTCTTACTTCTTCTTCAAGAGCCCAAAATTAAGAAAGAACACGT 897
Db 872 CTGTGATCACCACATATTTTGAACATCAGAGAAATAGAGGATTTGGCAGAAAGACAC 931
QY 898 AATGAAGAAAGAA 910
Db 932 AACAAACCAACAA 944

RESULT 9

US-09-411-628-5
; Sequence 5, Application US/09411628
; Patent No. 6428994
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/09/411,628
; EARLIER FILING DATE: 1999-10-01
; EARLIER FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1701
; TYPE: DNA
; ORGANISM: Orcytolagus cuniculus
US-09-411-628-5

Query Match 30.4%; Score 287; DB 3; Length 1701;
Best Local Similarity 59.1%; Pred. No. 4e-71;
Matches 510; Conservative 0; Mismatches 350; Indels 3; Gaps 1;
QY 1 ATGGAAGATGCAAAATTAAGCTTAAGCTGGAGAGGGCTTATCGGGTTGATTCAAA 60
Db 1 ATGGAAGATGCAAAATTAAGCTTAAGCTGGAGAGGGCTTATCGGGTTGATTCAAA 60
QY 61 TGCAGAAACAAACCTCTGCAAGTAGTAGCTGTTTAAATAATTTTGGAACTCTGAAGAT 120
Db 61 TGTAGGAATTAAGATAGTAGTGAAGATTTGTGCCATCAAGAGTTCTTAGAAGTATGAT 120
QY 121 GATCTGTTGTTAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
Db 121 GACAAATGTTTAAATAATTTGCTATCGAGAAATCAAGTTACTTAAAGCAACTGAGCAT 180
QY 181 CCAATCTGTGAACTCATCGAGGTTTTCAGGAGAAAGGAAATGCAATTTAGTTTTT 240
Db 181 GAAATTTGTGTAATCTGTTGGAGGTTGTAAATAAAAAACGATGGTATCTTAGTCTTT 240


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Oy 598 CTGTGGCTGGAATCAGATGTGGACCACTTTATCTGTAATCAGAACACTAGGAAA 657
Db 849 CTGTTTCTGTGAGACTCTGATATTGATCAGCTTTTATCTTATTATGAGGTGTTAGTAA 908
Oy 658 TTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTCCATGGCATCAGTATA 717
Db 909 CTAATTCCAAGACACAGGAGCTTTTATTAATAATCTCTGTTTGTGAGTAAGTTG 968
Oy 718 CCTGAGCCAGAGACATGGAACTCTTGAGGAAAAGTTCTCAGATGTTCAFCCTGTGCT 777
Db 969 CCTGAAATCAAGGAATCAGAACCTCTTGAAAGACGCTATCCAGCTCTCAGAAAGTTGTG 1028
Oy 778 CTGAACCTCATGAGGGGTCTGAGATGAATCCAGATGACAGATTAACCTGTTCCAA 837
Db 1029 ATAGATTAGCAAGAAATGCTTACATGTTGACCCAGACAAAAGGCCCTCTGTGCTGAG 1088
Oy 838 CTCCTGGAGAGCTCCTACTTTGA 860
Db 1089 CTCCTACCATGATTTCTTTCA 1111

RESULT 13
US-09-949-016-2083
; Sequence 2083, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012.
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2083
; LENGTH: 1794
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2083

Query Match 30.0%; Score 283.8; DB 4; Length 1794;
Best Local Similarity 58.9%; Pred. No. 3.3e-70;
Matches 508; Conservative 0; Mismatches 352; Indels 3; Gaps 1;

Oy 1 ATGGAAAGTATGAAAAATTAGCTAAGACTGGAGAGGGTCTTATGGGGTTGTATTCAA 60
Db 376 ATGGAAAAATGAAAACCTGGTTTGGTTGAGAGGGAGTTATGGAATGGTATGAG 435
Oy 61 TGCAGAAACAAACCTCTGGACAGTAGTAGCTGTAAAAAATTTGGGAATCTGAAGAT 120
Db 436 TGTAGGAATAAGATACTGGAAGAATTTGGCCATAAAGAAGTTCTTAGAAAGTGACGAT 495
Oy 121 GATCCTGTGTTAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
Db 496 GACAAAATGGTTAAAAAGATTGCAATGCGAGAAATCAAGTTACTAAAGCAACTTAGGCAT 555
Oy 181 CCAATCTGTGAACCTCATCGAGTGTTCAGGAGAAAAGGAAAATGCAATTTAGTTT 240
Db 556 GAAAACCTGGTGAATCTCTTGGAGTGTGAAGAAAAAACAACGATGGTACCTAGTCTT 615
Oy 241 GAATCATCTGTATACATACACTTTTAAATGAGTGGAAAGAAACCAAAATGGAGTTGCTGAT 300
Db 616 GAAATTTGTTGACCAACAATCTTGTATGACTTTGGAGCTCTTCCAAATGGAGTAGACTAC 675
Oy 301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTGCATATACAT 360
Db 676 CAAGTAGTTCAAAAAGTATTTGTTTTCAGATTATTAATGAATTTGATTTTGTGCAGTCA 735
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Oy 361 AACTGTATTACAGAGATATAAAACCTGAAAAATATCTTAATACTAAGCAAGGAATATC 420
Db 736 AATATCATACACAGAGATATAAAGCCAGAGAAATATATTAGTCTCCAGTCTGGGGTTGTC 795
Oy 421 AAGATTGTGACTTCGGGTTTGCAAAATCTG---ATTCCAGGAGATGCCCTACACCGAT 477
Db 796 AAGCTATGCGAATTTGGATTTGCGCGAAACATTTGGCAGCTCCTGGGAGGTTTATACTGAT 855
Oy 478 TATGTAGCTACGAGATGGTACCCGAGCTCCTGAACTTCTTGTGGGAGACTACTCAGTATGGT 537
Db 856 TATGTGCAACCCGATGGTACAGAGCTCCAGAACTATTGGTTGGTGTCAAGTATGSC 915
Oy 538 TCTTCAGTCATATATGGCTATTGGTTGTGTTTTTGGCAGAGCTCTCGAAGGCCAGCCA 597
Db 916 AAGGCTCTGTATGTGTGGCCATTGGTTGTCTGTAACCTGAAATGTTTCATGGGGGAACCC 975
Oy 598 CTGTGGCTCGAAAAATCAGATGTGGACCAACTTTTATCTGATAATCAGAACACTAGGAAA 657
Db 976 CTATTTCTGGAGATTTCTGATATTGATCAGCTATATCATATTATGATGTGTTTAGTAA 1035
Oy 658 TTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATA 717
Db 1036 CTAATTCAGGCACTCAGGAGCTTTTAAATAAAATCTCTGTGTTGCTGGAGTAAGTTG 1095
Oy 718 CCTGAGCCAGAAACATGGAACCTCTTTGAGGAAAAAGTTCTCAGATGTTTCATCTGTGCT 777
Db 1096 CCTGAAATCAAGGAAAGAGAAACCTCTTTGAAAGAGCGCTATCTTAAGCTCTCTGAAAGTGGTG 1155
Oy 778 CTGACTTCATGAGGGGTCTGAGATGAATCCAGATGACAGATTAACCTGTTTCCAA 837
Db 1156 ATAGATTAGCAAAAGAAATGCTTACATATTGACCCGACAAAGACCCCTTCTGTGCTGAG 1215
Oy 838 CTCCTGGAGAGCTCCTACTTTGA 860
Db 1216 CTCCTACCATGATTTCTTTCA 1238

RESULT 14
US-08-874-347-9
; Sequence 9, Application US/08874347
; Patent No. 5863741
; GENERAL INFORMATION:
; APPLICANT: Limper, Andrew H.
; APPLICANT: Leof, Edward B.
; APPLICANT: Thomas, Charles F.
; APPLICANT: Gustafson, Michael P.
; TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C., P.A.
; STREET: 60 South Sixth Street, Suite 3300
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/874,347
; FILING DATE: 13-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellinger, Mark S.
; REGISTRATION NUMBER: 34,812
; REFERENCE/DOCKET NUMBER: 07039/055001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-335-5070
; TELEFAX: 612-288-9696
```

TELEX:
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 903 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cdna
 FEATURE:
 NAME/KEY: Coding Sequence
 LOCATION: 1...900
 OTHER INFORMATION:
 US-08-874-347-9

Query Match 18.2%; Score 171.8; DB 2; Length 903;
 Best Local Similarity 52.3%; Pred. No. 1.4e-38;
 Matches 458; Conservative 0; Mismatches 402; Indels 15; Gaps 3;

QY 1 ATGGAAAGTATGAAAAATTAGCTAAGACTGGAGAGGCTCTTATGGGGTTGTATTCAA 60
 DB 1 ATGGAGCAATATCAGAGGTAGAGAGATTGGAGAGGAACTTATGGAGTTGTTATAA 60
 QY 61 TGCAGAAACAAACCTCTGACAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
 DB 61 GCAAGAGATCTTGAAAGTGGTACAAATTTAGTCTCTTAAGAAAAATCCGATTAGAACGAGAA 120
 QY 121 GATCCTGTGTTAAAGAAATAGCAATAGCAATAGCAATAGCAATAGCAATAGCAAT 180
 DB 121 GATCCTGTGTTAAAGAAATAGCAATAGCAATAGCAATAGCAATAGCAATAGCAAT 180
 QY 181 CCAATCTGTGAACCTCATCGAGTGTTCAGGAGAAAGAAATGCAATTTAGTGTGTTT 240
 DB 181 GATAATGTTGAAGACTTTTGAATATAATTCATCAAGAGTCACGTTTATATCTGTTT 240
 QY 241 GAATCTGTGATCATACATTTTAAATGAGTGAAGAAACCAATG-----GAGTT 294
 DB 241 GAATCTGTGATCATACATTTTAAATGAGTGAAGAAACCAATG-----GAGTT 294
 QY 295 GCTGATGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCAT 354
 DB 301 GGTGAGAAATGATTAAAGTTTATGTCAACACTTGTATCAGGTGTTAATATTGTCAT 360
 QY 355 ATACATACTGATATCAGAGATATAAAGCTGAAATATTTCTAATACTAAGCAAGGA 414
 DB 361 TCTCATCGTATTCTTCATCGTACTTGAAACCAACAAATCTCTTATAGATCGAAGAGGA 420
 QY 415 ATAAATCAAGATTTCGCTCGGCTTTGCA---CAAATTCGATTCAGGAGATCGCTAC 471
 DB 421 AATCTTAATAGCAGATTTTGGCTTGCAGGGCGTTGGTGTCCATTTGGTGGTTAT 480
 QY 472 ACCGATTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 531
 DB 481 ACTCATGAAGTTGTTACACTTTGATGATGATGATGATGATGATGATGATGATGATGAT 540
 QY 532 TATGGTTCTTCAGTCGATATATGGCTATTTGGTGTGTTTGGTGTGTTTGGTGTGTTTGG 591
 DB 541 TATGCAACAGCGCTTGATATATGAGCAATTTGATGATGATGATGATGATGATGATGATGAT 600
 QY 592 CAGCACTGTGGCTGGAATATCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 651
 DB 601 AAGCCATATTTCCAGTGATTCGAAATTTGATGATGATGATGATGATGATGATGATGATGAT 660
 QY 652 GGAATAATTAATCCAGACATCAATCAATCTTTAAAGATGAACGGGTTTTTCCATGGCATC 711
 DB 661 GGGACTCCAGATGAAATTTCTGGCTGTTATACATCTTATCCGATTTTAAGGCAACT 720
 QY 712 AGTATACCTGAGCAGAGATGGAATCTTTGAGGAAAGTTCTTCAGATGTTCACTCT 771
 DB 721 TTTCCAAATGGTCACCA-----AAAAATCTTGGAGAAATTAATTAAGCAATTTGATGAT 774
 QY 772 GTGGCTCTGAATCTCATGAAGGGGTGTCTGAAGATGAATCAATCCAGATGACGATTAACCTGT 831
 DB 775 GATGGAATAGATTTATTACAGAAATGTTCTAGATATTATCTCTGCTGAACGATATGCGCT 834

QY 832 TCCCAACTCTCGAGAGCTCTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 866
 DB 835 AAAAAAGCTCTCGATCATCTTATTTTGTGATGATTT 869

RESULT 15
 US-09-093-522-9
 ; Sequence 9, Application US/09093522
 ; Patent No. 6015700
 ; GENERAL INFORMATION:
 ; APPLICANT: Limber, Andrew H.
 ; APPLICANT: Leof, Edward B.
 ; APPLICANT: Thomas, Charles F.
 ; APPLICANT: Gustafson, Michael P.
 ; TITLE OF INVENTION: CDC2 PROTEIN KINASE FROM PNEUMOCYSTIS
 ; TITLE OF INVENTION: CARINII
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fish & Richardson P.C., P.A.
 ; STREET: 60 South Sixth Street, Suite 3300
 ; CITY: Minneapolis
 ; STATE: MN
 ; COUNTRY: USA
 ; ZIP: 55402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/093,522
 ; FILING DATE: 08-JUN-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/874,347
 ; FILING DATE: 13-JUN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ellinger, Mark S.
 ; REGISTRATION NUMBER: 34,812
 ; REFERENCE/DOCKET NUMBER: 07039/055002
 ; TELEPHONE: 612-335-5070
 ; TELEFAX: 612-288-9696
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 903 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cdna
 ; FEATURE:
 ; NAME/KEY: Coding Sequence
 ; LOCATION: 1...900
 ; OTHER INFORMATION:
 ; US-09-093-522-9

Query Match 18.2%; Score 171.8; DB 3; Length 903;
 Best Local Similarity 52.3%; Pred. No. 1.4e-38;
 Matches 458; Conservative 0; Mismatches 402; Indels 15; Gaps 3;

QY 1 ATGGAAAGTATGAAAAATTAGCTAAGACTGGAGAGGCTCTTATGGGGTTGTATTCAA 60
 DB 1 ATGGAGCAATATCAGAGGTAGAGAGATTGGAGAGGAACTTATGGAGTTGTTATAA 60
 QY 61 TGCAGAAACAAACCTCTGACAGTAGTAGCTGTTAAAAAATTTGTGGAATCTGAAGAT 120
 DB 61 GCAAGAGATCTTGAAAGTGGTACAAATTTAGTCTCTTAAGAAAAATCCGATTAGAACGAGAA 120
 QY 121 GATCCTGTGTTAAAGAAATAGCAATAGCAATAGCAATAGCAATAGCAATAGCAAT 180
 DB 121 GATCCTGTGTTAAAGAAATAGCAATAGCAATAGCAATAGCAATAGCAATAGCAAT 180

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Qy 181 CCAATCTTGTGAACCTCATCGAGGTGTTCAAGGAGAAAAGGAAATGCCATTTAGTTTTT 240
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
181 GATAATGTTGAAGACTTTTGAATATAATTTCATCAAGAGTCACGTTTATATCTTGTGTTTT 240
Qy 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATG-----GAGTT 294
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
241 GAATTTCTTGATCTTGATTTAAATAAGTATATGATATGTATTCAAAGGACATGATGCTT 300
Qy 295 GCTGATGAGTGATCAAAAGCGTATTATGGCAACACCTTCAAGCTCTTAAATTTCTGTGCAT 354
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
301 GGTGAGAAATGATTAAAGTTTATGTGCACAACTTGTATCAGGTGTTAAATATTGTCAT 360
Qy 355 ATACATACTGTATTCACAGAGATATAAAACCTGAAATATTTCTAATAACTTAAGCAAGGA 414
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
361 TCTCATCGTATTCTTCATCGTGACTTGAACACCAAAATCTTATATAGATCGAGAAGGA 420
Qy 415 ATAAATCAAGATTTGCTCGGCTTTGCA---CAAATTCCTGATCCAGGAGATGCGCTAC 471
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
421 AATCTTAAATTAGCAGATTTTGGGCTTGCAGAGGGGTTTGGTGTTCATTCGGTGGTTAT 480
Qy 472 ACCGATTTATGTAGCTACGAGATGGTACCGAGCTCTGAACTTCTTGTGGGAGATACCTCAG 531
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
481 ACTCATGAGTGTGTACACTTGGTATCGTCTCCAGAGTTCCTTTAGGTGGTCGACAA 540
Qy 532 TATGGTTCTTCAGTCGATATATGGGCTATTTGGTGTGTTTTTGCAGAGCTCCTCACAGGC 591
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
541 TATGCAACAGCGCTTGATATATGAGCATTTGGATGTATTTTGCAGAAATGGCTACAAA 600
Qy 592 CAGCCACTGTGGCTTGGAAATCAGATGTGACCAACTTTATCTGATAATCAGAACACTA 651
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
601 AAGCCATTTATTCAGGTGATTTGAAATTCGATAATTTAGAAATATTAGAAATTTAGAAATTA 660
Qy 652 GGAATAATTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATC 711
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
661 GGGACTCCAGATGAAATTTCTTGGCCTGGTATTACATCTTATCCGGATTTTAAGGCAACT 720
Qy 712 AGTATACCTGAGCCAGAGACATGGAACTCTTGAGGAAAGTTCTCAGATGTTTCATCCT 771
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
721 TTTCCAAAATGGTCACCA-----AAAAATCTTGAGAAATTAATTACAGAACTTCATAGT 774
Qy 772 GTGGCTCTGAACTTCATGAAGGGGTGCTGAAGATGATCCAGATGACAGATTAACTGT 831
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
775 GATGGAATAGATTTATTACAGAAATGCTTAGATATTATCTCTGCTGAACGTTAGCGCT 834
Qy 832 TCCCAACTCCTGGAGAGCTCCTACTTTGATTCCTT 866
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
835 AAAAAAGCTCTCGATCATCCTTATTTTGTGATTT 869

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Search completed: April 22, 2005, 01:29:34
Job time : 183.912 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 21, 2005, 20:23:24 ; Search time 517.228 Seconds
(without alignments)
10815.645 Million cell updates/sec

Title: US-10-766-691-11

Perfect score: 945
Sequence: 1 atggaaaagtatgaaaatt.....aggtaacttcgctcaaaagt 945

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	945	100.0	945	4	AAD03817 Human kin
2	929	98.3	972	4	AAD03814 Human kin
3	927	98.1	1790	6	AAD30557 Human kin
4	868.8	91.9	1678	10	ABX08936 cDNA enco
5	863	91.3	1083	4	AA06725 Polynucle
6	839	88.8	1041	4	AAD03816 Human kin
7	823	87.1	1068	4	AAD03813 Human kin
8	808	85.5	1266	12	ADK71927 Human kin
9	704.4	74.5	1429	12	ADI40928 Human kin
10	645.4	68.3	882	6	AAI64248 Human kin
11	643	68.0	911	4	AAF44669 Novel pro
12	643	68.0	911	12	ADI29367 Human MAR
13	559.2	59.2	2615	4	AAF44670 Novel pro
14	559.2	59.2	2615	12	ADI29368 Mouse MAR
15	543.2	57.5	1281	8	ABX34679 Human mdd
16	507	53.7	1819	4	AAD03818 Human kin
17	501	53.0	1086	10	ABZ77165 Human pro
18	454.4	48.1	561	4	AAD03812 Human kin
19	454.4	48.1	594	4	AAD03815 Human kin
20	415.4	44.0	1612	6	ABQ93433 Human CDN

21	413.8	43.8	1175	12	ADO01536	Ado01536 Human cys
22	413.8	43.8	1178	12	ADO01535	Ado01535 Human cys
23	413.8	43.8	2944	5	ABV24584	Abv24584 Human pro
24	287	30.4	1698	3	AAA29746	Aaa29746 Rabbit KK
25	287	30.4	3080	3	AAA29745	Aaa29745 Rabbit KK
26	283.8	30.0	2095	10	ADC77658	Adc77658 Human 162
27	283.8	30.0	2095	13	ADQ89155	Adq89155 Human uro
28	274	29.0	1179	4	ADQ89155	Adq89155 Human uro
29	227.4	24.1	1513	3	ABL12603	Ab112603 Drosophil
30	227.4	24.1	1513	3	AAZ51208	Aaz51208 Human los
31	227.4	24.1	1773	4	ADI57213	Adi57213 Human NKI
32	218.4	23.1	3297	4	AA06724	Aa06724 Polynucle
33	215.8	22.8	2503	13	ACN42574	Acn42574 Human dia
34	211.4	22.4	1667	3	AAZ51207	Aaz51207 Rat lost
35	211.4	22.4	1738	3	AAZ51206	Aaz51206 Rat lost
36	177.4	18.8	1158	5	AA070329	Aa070329 DNA enco
37	175.8	18.6	1866	4	AAF44672	Aaf44672 Novel pro
38	175.8	18.6	1866	12	ADI29370	Adi29370 Human MAR
39	171.8	18.2	903	2	AA07476	Aa07476 Pneumocys
40	171.4	18.1	2982	12	ADO01537	Ado01537 Human cys
41	163.4	17.3	1476	3	AAZ37835	Aaz37835 Cyclin-de
42	163.4	17.3	1635	2	AAV71074	Aav71074 Green flu
43	163.4	17.3	1635	2	AAV71073	Aav71073 CDK2-gree
44	163	17.2	1024	10	ABZ83372	Abz83372 Toxicolog
45	163	17.2	1297	6	ABQ60787	Abq60787 Human 10C

ALIGNMENTS

RESULT 1
AAD03817
ID AAD03817 standard; CDNA; 945 BP.
XX
AC AAD03817;
XX
DT 19-JUN-2001 (first entry)
XX
DE Human kinase CDNA #6.
XX
KW Human; kinase; gene therapy; bioreactor; mental disorder;
KW biological disorder; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..945
FT /product= "Human kinase #6"
FT /note= "The coding region does not include stop codon"
FT /partial
XX
XX WO200123579-A1.
XX
XX PD 05-APR-2001.
XX
XX PF 27-SEP-2000; 2000WO-US026621.
XX
XX PR 28-SEP-1999; 99US-0156511P.
XX
XX PA (LEXI-) LEXICON GENETICS INC.
XX
XX PI Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
XX PI Sands AT;
XX
XX DR WPI; 2001-266166/27.
XX
XX DR P-ESDS; AAE00495.
XX
XX PT New isolated human kinase polynucleotide useful for generating
XX PT antibodies, as reagents in diagnostic assays and for screening for
XX PT compounds useful for treating mental, biological or medical diseases.
XX
XX PS Claim 3; Page 33; 38pp; English.

The present sequence is a cDNA encoding novel human protein (NHP) known as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression.

Sequence 945 BP; 323 A; 165 C; 202 G; 255 T; 0 U; 0 Other;

Query Match 100.0%; Score 945; DB 4; Length 945;
 Best Local Similarity 100.0%; Pred. No. 3.3e-244;
 Matches 945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGAAAGTATGAAATTAAGCTAGCTAGCTGAGAGGGCTTATGGGTGTTATCAAA 60
 DB 1 ATGGAAAGTATGAAATTAAGCTAGCTAGCTGAGAGGGCTTATGGGTGTTATCAAA 60
 QY 61 TGCAGAAACAAACCTCTGGACAAAGTAGCTAGCTGTTAAATAATTTGGGAATCTGAAGAT 120
 DB 61 TGCAGAAACAAACCTCTGGACAAAGTAGCTAGCTGTTAAATAATTTGGGAATCTGAAGAT 120
 QY 121 GATCTGTGTTAGAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACACAT 180
 DB 121 GATCTGTGTTAGAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACACAT 180
 QY 181 CCAATCTTGTGAACCTCATCGAGGTGTTAGGAGAAAGGAAATGCAATTTAGTTTTT 240
 DB 181 CCAATCTTGTGAACCTCATCGAGGTGTTAGGAGAAAGGAAATGCAATTTAGTTTTT 240
 QY 241 GAATCTGTGATACATACATTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 300
 DB 241 GAATCTGTGATACATACATTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 300
 QY 301 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAATTTCTGCTATATACAT 360
 DB 301 GGAGTGATCAAAAGCGTATTATGCAACACTTCAAGCTCTTAATTTCTGCTATATACAT 360
 QY 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGCAATATC 420
 DB 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGCAATATC 420
 QY 421 AAGATTGTGACTTGGGTTTGCACAAATCTGATTCAGAGATGCTACACCGATTAT 480
 DB 421 AAGATTGTGACTTGGGTTTGCACAAATCTGATTCAGAGATGCTACACCGATTAT 480
 QY 481 GTAGCTACGAGATGTTACCGAGCTCTGAACTCTTGTGGGAGATACAGTATGTTCT 540
 DB 481 GTAGCTACGAGATGTTACCGAGCTCTGAACTCTTGTGGGAGATACAGTATGTTCT 540
 QY 541 TCAGTCGATATATGGGCTATTTGGTTGTTTTTTCAGAGCTCTCTGACAGCCAGCCACTG 600
 DB 541 TCAGTCGATATATGGGCTATTTGGTTGTTTTTTCAGAGCTCTCTGACAGCCAGCCACTG 600
 QY 601 TGGCCTGGAAATCAGATGTTGGAACCACTTATCTGATTAATCAGAACACTAGGAAATTA 660
 DB 601 TGGCCTGGAAATCAGATGTTGGAACCACTTATCTGATTAATCAGAACACTAGGAAATTA 660
 QY 661 ATCCCAAGACATCAATCAATCTTTAAAGAAAGTACCGGGTTTTTCCATGGCATCATACCT 720

DB 661 ATCCCAAGACATCAATCAATCTTTAAAGTAAACGGTTTTTCCATGGCATCAGTATACCT 720
 QY 721 GAGCCAGAGACATCGAAACTCTTTGAGGAAAGTTCTCAGATGTTCACTCTGCTGCTG 780
 DB 721 GAGCCAGAGACATCGAAACTCTTTGAGGAAAGTTCTCAGATGTTCACTCTGCTGCTG 780
 QY 781 AACTTCATGAAGGGGTCTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTC 840
 DB 781 AACTTCATGAAGGGGTCTCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCCAACTC 840
 QY 841 CTGAGAGCTCTCTACTTTGATCTTTTCAAGAGGCCCAATTAAGGAAAGACGTAAT 900
 DB 841 CTGAGAGCTCTCTACTTTGATCTTTTCAAGAGGCCCAATTAAGGAAAGACGTAAT 900
 QY 901 GAAGGAAAGAACAGAGACGCCCAACAGGTACTTCCGCTCAAAAGT 945
 DB 901 GAAGGAAAGAACAGAGACGCCCAACAGGTACTTCCGCTCAAAAGT 945

RESULT 2
 AAD03814
 ID AAD03814 standard; cDNA; 972 BP.
 AC AAD03814;
 XX 19-JUN-2001 (first entry)
 XX Human kinase cDNA #3.
 DE Human; kinase; gene therapy; bioreactor; mental disorder;
 XX Human; kinase; gene therapy; bioreactor; mental disorder;
 KW biological disorder; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..972
 FT /tag= a
 FT /product= "Human kinase #3"
 FT /note= "The coding region does not include stop codon"
 FT /partial
 XX MO200123579-A1.
 XX 05-APR-2001.
 XX 27-SEP-2000; 2000MO-US026621.
 XX 28-SEP-1999; 99US-0156511P.
 XX (LEXI-) LEXICON GENETICS INC.
 XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
 PI Sands AT;
 XX WPI; 2001-266166/27.
 DR P-PSDB; AAE00492.
 XX New isolated human kinase polynucleotide useful for generating
 PT antibodies, as reagents in diagnostic assays and for screening for
 PT compounds useful for treating mental, biological or medical diseases.
 XX Disclosure; Page 29-30; 38pp; English.
 XX The present sequence is a cDNA encoding novel human protein (NHP) known
 CC as human kinase. The human kinases share structural similarity with
 CC animal kinases, more particularly serine or threonine protein kinases.
 CC Human kinase cDNA is useful for the detection of mutant human kinase for
 CC the diagnosis of disease, and also as a therapeutic. It is useful for
 CC screening drugs effective in the treatment of symptomatic or phenotypic
 CC manifestations perturbing the normal function of NHP in the body. The NHP
 CC nucleotide sequences are useful for generation of antibodies, as reagents
 CC in diagnostic assays, for the identification of other cellular gene
 CC products related to human kinases, and as reagents in assays for
 CC screening compounds that are useful for treating mental, biological or
 CC medical disorders. NHP oligonucleotides are used as probes. The labelled
 CC NHP probes are useful for screening human genomic library for identifying
 CC polymorphisms and as primers in amplification assays to detect mutations
 CC within the exons, introns and splice sites that can be used in
 CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP
 CC products are used to genetically engineer cells in vivo that functions as
 CC bioreactors in the body delivering a continuous supply of NHP to the
 CC body. Nucleotide constructs encoding functional NHPs are used in gene
 CC therapy for the modulation of NHP expression.

CC products related to human kinases, and as reagents in assays for
 CC screening compounds that are useful for treating mental, biological or
 CC medical disorders. NHP oligonucleotides are used as probes. The labelled
 CC NHP probes are useful for screening human genomic library for identifying
 CC polymorphisms and as primers in amplification assays to detect mutations
 CC within the exons, introns and splice sites that can be used in
 CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP
 CC products are used to genetically engineer cells in vivo that functions as
 CC bioreactors in the body delivering a continuous supply of NHP to the
 CC body. Nucleotide constructs encoding functional NHPs are used in gene
 CC therapy for the modulation of NHP expression
 XX
 SQ

Sequence 972 BP; 323 A; 172 C; 214 G; 263 T; 0 U; 0 Other;

Query Match 98.3%; Score 929; DB 4; Length 972;

Best Local Similarity 100.0%; Pred. No. 6.8e-240;

Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCAAAAGTATGAAAATTAGCTTAAGCTCGAGAGGGTCTTATGGGTTGTATTCAAA 60
 Db |||||
 Qy 1 ATGCAAAAGTATGAAAATTAGCTTAAGCTCGAGAGGGTCTTATGGGTTGTATTCAAA 60
 Db |||||
 Qy 61 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTGTAAAAAATTTGGGAATCTGAAGAT 120
 Db |||||
 Qy 61 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTGTAAAAAATTTGGGAATCTGAAGAT 120
 Db |||||
 Qy 121 GATCCTGTGTAAAGAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACAT 180
 Db |||||
 Qy 121 GATCCTGTGTAAAGAAATAGCACTAAGAGAAATAGTATGTTGAAGCAATTAACAT 180
 Db |||||
 Qy 181 CCAATCTTGTGACCTCATCGAGTGTTCAGGAGAAAGAAATGCAATTTAGTTTT 240
 Db |||||
 Qy 181 CCAATCTTGTGACCTCATCGAGTGTTCAGGAGAAAGAAATGCAATTTAGTTTT 240
 Db |||||
 Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
 Db |||||
 Qy 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300
 Db |||||
 Qy 301 GGAGTGATCAAAAGCGTATTAATGCAAAACACTTCAAGCTCTTAATTTCTGTATATACAT 360
 Db |||||
 Qy 301 GGAGTGATCAAAAGCGTATTAATGCAAAACACTTCAAGCTCTTAATTTCTGTATATACAT 360
 Db |||||
 Qy 361 AACTGTATTCACAGATATATAACCTGAAATATTTCTAATACCTAGCAAGGAATATC 420
 Db |||||
 Qy 361 AACTGTATTCACAGATATATAACCTGAAATATTTCTAATACCTAGCAAGGAATATC 420
 Db |||||
 Qy 421 AAGATTTGTGACTTTCGGTTTGCACAAATCTCGATTCAGGAGATGCTACACCGATTAT 480
 Db |||||
 Qy 421 AAGATTTGTGACTTTCGGTTTGCACAAATCTCGATTCAGGAGATGCTACACCGATTAT 480
 Db |||||
 Qy 481 GTAGTACGAGATGGTACCGAGCTCCTGAACCTTCTTGTGGGAGATACCTAGTATGGTTCT 540
 Db |||||
 Qy 481 GTAGTACGAGATGGTACCGAGCTCCTGAACCTTCTTGTGGGAGATACCTAGTATGGTTCT 540
 Db |||||
 Qy 541 TCAGTCATATATGGCTATTTGGTTGTTTTCAGAGCTCTTCGACAGCCAGCCACTG 600
 Db |||||
 Qy 541 TCAGTCATATATGGCTATTTGGTTGTTTTCGAGAGCTCTTCGACAGCCAGCCACTG 600
 Db |||||
 Qy 601 TGGCTCGAAAATCAGATGTGCAACCACTTTATCTGATTAATCAGAACACTAGGAAATTA 660
 Db |||||
 Qy 601 TGGCTCGAAAATCAGATGTGCAACCACTTTATCTGATTAATCAGAACACTAGGAAATTA 660
 Db |||||
 Qy 661 ATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATACCT 720
 Db |||||
 Qy 661 ATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCATGGCATCAGTATACCT 720
 Db |||||
 Qy 721 GAGCCAGACATGGAACCTTTGAGGAAAGTTCTCAGATGTTTCATCTGGGCTCTG 780
 Db |||||
 Qy 721 GAGCCAGACATGGAACCTTTGAGGAAAGTTCTCAGATGTTTCATCTGGGCTCTG 780
 Db |||||
 Qy 781 AACTTCATGAGGGGTCTGTAAGATGAATCCAGATGACGATTAACCTGTTCCCACTC 840
 Db |||||
 Qy 781 AACTTCATGAGGGGTCTGTAAGATGAATCCAGATGACGATTAACCTGTTCCCACTC 840
 Db |||||

Qy 841 CTGAGAGCTCTTACTTCTTGTGATTTTCAAGAGGCCCAAAATTAAGAAAGACGCTAAT 900
 Db |||||
 Qy 841 CTGAGAGCTCTTACTTCTTGTGATTTTCAAGAGGCCCAAAATTAAGAAAGACGCTAAT 900
 Db |||||
 Qy 901 GAACGAGAAACAGAACGACGCAACAGT 929
 Db |||||
 Qy 901 GAACGAGAAACAGAACGACGCAACAGT 929
 Db |||||
 RESULT 3
 AAD30557
 ID AAD30557 standard; cDNA; 1790 BP.
 AC AAD30557;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Human kinase polypeptide (PKIN-10) cDNA.
 XX
 KW Human; kinase polypeptide; PKIN-10; gene therapy; Addison's disease;
 KW leukaemia; immune disorder; lymphoma; melanoma; developmental disorder;
 KW acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension;
 KW asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis;
 KW cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer;
 KW cholestasis; cardiant; cardiovascular disorder; Niemann-Pick's disease;
 KW lipid disorder; fatty liver; Gaucher's disease; myocardial infarction;
 KW drug screening; transgenic animal; antiinflammatory; hepatotropic;
 KW hypotensive; anti-HIV; enzyme; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 239..1267
 FT /*tag= a
 FT /product= "Human PKIN-10"
 XX
 FN WO200208399-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 20-JUL-2001; 2001WO-US023092.
 XX
 PR 21-JUL-2000; 2000US-0220038P.
 PR 28-JUL-2000; 2000US-022112P.
 PR 04-AUG-2000; 2000US-022831P.
 PR 11-AUG-2000; 2000US-0224729P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 PA (THOR/) THORNTON M.
 XX
 PI Thornton M, Yue H, Khan FA, Gururajan R, Hafalia AJA, Wallia NK;
 PI Patterson C, Ramkumar J, Gandhi AR, Policky JL, Baughn MR;
 PI Tribouley CM, Bandman O, Nguyen DB, Lu Y, Burford N, Lal P, Ding L;
 PI Yao MG, Elliott VS, Recipon SA, Kearney L, Lu DAW, Greenwald SR;
 PI Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL;
 XX
 DR WPI; 2002-206083/26.
 DR P-PSDB; AAE19152.
 XX
 FT New human kinase polypeptide, useful in diagnosis, prevention and
 FT treatment of cancer, immune disorder, growth and developmental disorder,
 FT cardiovascular disorder and lipid disorder.
 XX
 PS Claim 5; Page 183; 196pp; English.
 XX
 CC The present invention relates to an isolated human kinase polypeptide
 CC (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is
 CC useful for diagnosing, treating and preventing cancer (e.g., leukaemia,
 CC lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency
 CC syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's
 CC disease, rheumatoid arthritis), a growth and developmental disorder (e.g.
 CC bursitis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a

CC cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial
 CC infarction), and a lipid disorder (e.g., fatty liver, cholestasis,
 CC Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of
 CC drug screening techniques and to analyse the proteome of a tissue or cell
 CC type. PKIN is useful for creating knockin humanised animals or transgenic
 CC animals to model human diseases, in somatic or germline gene therapy, to
 CC generate a transcript image of a tissue or cell type, for detecting
 CC differences in the chromosomal location due to translocation, inversion,
 CC etc., among normal, carrier or affected individuals, and as hybridisation
 CC probes for mapping naturally occurring genomic sequences. PKIN is useful
 CC in southern or northern analysis, dot blot or other membrane-based
 CC technologies, in PCR technologies, in dipstick, pin, microformat enzyme
 CC linked immunosorbent (ELISA)-like assays and in microarrays utilising
 CC fluids or tissues from patients to detect altered PKIN expression. The
 CC present sequence is human PKIN-10 cDNA
 XX

SQ Sequence 1790 BP; 581 A; 328 C; 366 G; 515 T; 0 U; 0 Other;

Query Match 98.1%; Score 927; DB 6; Length 1790;
 Best Local Similarity 100.0%; Pred. No. 3e-239;
 Matches 927; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGAAAGATGATAAAATAGCTAGAGCTGAGAGGGTCTTATGGGGTGTGATTTCAA	60
DB	239	ATGGAAAGATGATAAAATAGCTAGAGCTGAGAGGGTCTTATGGGGTGTGATTTCAA	298
QY	61	TGAGAAACAAACCTCTGACAGTAGTAGCTGTTAAAAATTTGTGAATCTGAAGAT	120
DB	299	TGAGAAACAAACCTCTGACAGTAGTAGCTGTTAAAAATTTGTGAATCTGAAGAT	358
QY	121	GATCTCTGTTTAAAGAAATAGCATTAGAGAAATACGTATGTGAACAAATTAACAT	180
DB	359	GATCTCTGTTTAAAGAAATAGCATTAGAGAAATACGTATGTGAACAAATTAACAT	418
QY	181	CCAAATCTTGTGAACCTCATCGAGTGTTTCAGGAGAAAGAAATGCTTTAGTTT	240
DB	419	CCAAATCTTGTGAACCTCATCGAGTGTTTCAGGAGAAAGAAATGCTTTAGTTT	478
QY	241	GAATAGCTGTATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT	300
DB	479	GAATAGCTGTATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTTGCTGAT	538
QY	301	GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT	360
DB	539	GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT	598
QY	361	AACGTATTCACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGAAATATC	420
DB	599	AACGTATTCACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGAAATATC	658
QY	421	AAGATTTGTGACTTCGGGTTTGGCAAAATTCGATTCAGAGAGTCCCTACACCGATTAT	480
DB	659	AAGATTTGTGACTTCGGGTTTGGCAAAATTCGATTCAGAGAGTCCCTACACCGATTAT	718
QY	481	GTAGCTACGAGATGGTACCGAGCTCCCTGAATCTTCTGCGAGATACCTAGTATGTTCT	540
DB	719	GTAGCTACGAGATGGTACCGAGCTCCCTGAATCTTCTGCGAGATACCTAGTATGTTCT	778
QY	541	TCAGTGCATATATGGCTATGTTGTTGTTTTCAGAGCTCTCTGACAGCCAGCCACTG	600
DB	779	TCAGTGCATATATGGCTATGTTGTTGTTTTCAGAGCTCTCTGACAGCCAGCCACTG	838
QY	601	TGGCTCTGAAATCAGATGTGGACCACTTTATCTGATATACAGACACTAGGAAATTA	660
DB	839	TGGCTCTGAAATCAGATGTGGACCACTTTATCTGATATACAGACACTAGGAAATTA	998
QY	661	ATCCCAAGACATCAATCAATCTTTAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCT	720
DB	999	ATCCCAAGACATCAATCAATCTTTAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCT	958
QY	721	GAGCCAGACATGGAACCTCTTGGAGAAAGTTCTCAGATGTTTATCTGTCGCTCG	780
DB	959	GAGCCAGACATGGAACCTCTTGGAGAAAGTTCTCAGATGTTTATCTGTCGCTCG	1018

QY	781	AACCTTCATGAAGGGGTGCTCAAGATGAATCCAGATGACAGTAACTGTTCCCACTC	840
DB	1019	AACCTTCATGAAGGGGTGCTCAAGATGAATCCAGATGACAGTAACTGTTCCCACTC	1078
QY	841	CTGAGAGCTCTCTATTGATCTTTTCAAGAGCCCAAAATTAAGAAAGACAGCTAAT	900
DB	1079	CTGAGAGCTCTCTATTGATCTTTTCAAGAGCCCAAAATTAAGAAAGACAGCTAAT	1138
QY	901	GAAGGAGAAACACAGACGCGCCACAG	927
DB	1139	GAAGGAGAAACACAGACGCGCCACAG	1165

RESULT 4

ABX08936
 ID ABX08936 standard; cDNA; 1678 BP.
 XX
 AC ABX08936;
 XX
 DT 21-JAN-2003 (first entry)
 XX
 DE cDNA encoding human DITHP protein #6.

Human; ss; gene; diagnostic and therapeutic; DITHP; cancer;
 arteriosclerosis atherosclerosis; psoriasis; primary thrombocytopenia;
 autoimmune; inflammatory; anaemia; asthma; autoimmune thyroiditis;
 Crohn's disease; diabetes mellitus; glomerulonephritis; gout; stroke;
 multiple sclerosis; rheumatoid arthritis; uveitis; AIDS; allergy;
 acquired immunodeficiency disease; neurological disorder; epilepsy;
 Alzheimer's disease; dementia; mental retardation; gastrointestinal;
 Parkinson's disease; ulcer; cirrhosis; reproductive; infertility;
 endometriosis; endocrine disorder; hyperparathyroidism; hyperlipidemia;
 hypercholesterolemia; hypoglycaemia; obesity; Reiter's syndrome;
 connective tissue disorder; osteoporosis; infection.

Homo sapiens.

XX WO200279473-A2.
 XX 10-OCT-2002.
 XX 09-JAN-2002; 2002WO-US001009.
 XX 12-JAN-2001; 2001US-0261622P.
 XX 16-JAN-2001; 2001US-0261864P.
 XX 16-JAN-2001; 2001US-0261865P.
 XX 17-JAN-2001; 2001US-0262164P.
 XX 17-JAN-2001; 2001US-0262207P.
 XX 17-JAN-2001; 2001US-0262208P.
 XX 17-JAN-2001; 2001US-0262209P.
 XX 18-JAN-2001; 2001US-0262215P.
 XX 18-JAN-2001; 2001US-0263102P.
 XX 19-JAN-2001; 2001US-0262599P.
 XX 19-JAN-2001; 2001US-0262662P.
 XX 19-JAN-2001; 2001US-0262760P.
 XX 19-JAN-2001; 2001US-0263063P.
 XX 19-JAN-2001; 2001US-0263064P.
 XX 19-JAN-2001; 2001US-0263065P.
 XX 19-JAN-2001; 2001US-0263069P.
 XX 19-JAN-2001; 2001US-0263077P.
 XX 19-JAN-2001; 2001US-0263329P.
 XX 19-JAN-2001; 2001US-0263330P.

(INCY-) INCYTE GENOMICS INC.

XX Panzer SR, Lincoln SE, Altus CM, Dufour GE, Hillman JL, Jones AL;
 PI Dam TC, Liu TF, Harris B, Flores V, Daffo A, Marwaha R, Chen AJ;
 PI Chang SC, Gerstin EH, Peralta CH, David MH, Lewis SA;
 XX WPI; 2003-040680/03.
 DR P-PSDB; ABU05290.
 XX

PT New human diagnostic and therapeutic (DITHP) polynucleotides and
 PT polypeptides, useful for diagnosing, preventing or treating diseases,
 PT e.g. cancer, AIDS, Parkinson's disease, or autoimmune/inflammatory
 PT diseases.
 XX
 XX
 PS Claim 1; Page 267; 331pp; English.
 PS
 XX
 CC This invention relates to the cDNA and protein sequences of fifty six
 CC polynucleotides for diagnostic and therapeutic (DITHP). The human DITHP
 CC polynucleotides and polypeptides are useful for diagnosing, preventing or
 CC treating diseases associated with, as well as effects of exogenous
 CC compounds, on the expression of human molecules, such as cell
 CC proliferative diseases (e.g. cancer, arteriosclerosis atherosclerosis,
 CC psoriasis, primary thrombocytopenia), autoimmune/inflammatory diseases
 CC (e.g. anaphylaxis, asthma, autoimmune thyroiditis, Crohn's disease, diabetes
 CC mellitus, glomerulonephritis, gout, multiple sclerosis, rheumatoid
 CC arthritis, uveitis, acquired immunodeficiency disease; AIDS; allergies;
 CC neurological disorders (e.g. stroke, Alzheimer's disease, dementia;
 CC mental retardation, Parkinson's disease, epilepsy), gastrointestinal
 CC (e.g. ulcer, cirrhosis), reproductive (e.g. infertility, endometriosis),
 CC endocrine disorders (e.g. hyperparathyroidism, hypercholesterolemia,
 CC hypoglycaemia, hyperlipidemia, obesity), connective tissue disorders
 CC (e.g. osteoporosis, Reiter's syndrome), or infections (e.g. bacterial,
 CC viral, fungal, parasitic, protozoal). The DITHP sequences may be used to
 CC generate hybridisation probes useful in chromosomal mapping of naturally
 CC occurring genomic sequences. They are also useful in designing probes
 CC useful in diagnostic assays. The polynucleotides are useful as molecular
 CC weight markers, or as antigen to elicit an immune response. The present
 CC sequence represents a human diagnostics and therapeutics (DITHP) cDNA
 CC sequence of the invention
 XX
 SQ Sequence 1678 BP; 541 A; 308 C; 336 G; 493 T; 0 U; 0 Other;
 Query Match 91.9%; Score 868.8; DB 10; Length 1678;
 Best Local Similarity 99.2%; Pred. No. 1.4e-223;
 Matches 925; Conservative 0; Mismatches 2; Indels 5; Gaps 5;
 Qy 1 ATGGAAGAGTATGAAAAATTAGCTAAGACTGAGAGAGGCTTTATGGGTTGTATTCAA 60
 Db 131 ATGGAAGAGTATGAAAAATTAGCTAAGACTGAGAGAGGCTTTATGGGTTGTATTCAA 190
 Qy 61 TGCAGA-AACAAAACCTCTGCACAGTAGTAGCTGTTAAATAATTTGGGAATCTGAGA 119
 Db 191 TGCAGATAACAAAACCTCTGCACAGTAGTAGCTGTTAAATAATTTGGGAATCTGAGA 250
 Qy 120 TGATCCTCTGTTAAGAAAATAGCACTAAGAAATACGTA-TGTTGAAGCAATTTAAAC 178
 Db 251 TGATCCTCTGTTAAGAAAATAGCACTAAGAAATACGTA-TGTTGAAGCAATTTAAAC 310
 Qy 179 ATCCAAATCTTGTGAACCTCATCGAGGTGTTTCAGAGAAAAGGAAATATGATTAGTTT 238
 Db 311 ATCCAAATCTTGTGAACCTCATCGAGGTGTTTCAGAGAAAAGGAAATATGATTAGTTT 370
 Qy 239 TTGATATCTGTCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTCGT 298
 Db 371 TTGATATCTGTCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTCGT 430
 Qy 299 ATGAGTGCATCAAAAGCGTATTATGGCAACACACTTCAAGCTCTTAATTTCTGTCATATAC 358
 Db 431 ATGAGTGCATCAAAAGCGTATTATGGCAACACACTTCAAGCTCTTAATTTCTGTCATATAC 490
 Qy 359 ATAATCTGTTTACAGAGATATAAAACCTGAAATATTTCTTAATAACCAAGCAAGTAAT 418
 Db 491 ATAATCTGTTTACAGAGATATAAAACCTGAAATATTTCTTAATAACCAAGCAAGTAAT 550
 Qy 419 TCAAGATTTGACCTTCGGGTTTGCACAAATCTGATTCAGGAGATGCTTACACCGATT 478
 Db 551 TCAAGATTTGACCTTCGGGTTTGCACAAATCTGATTCAGGAGATGCTTACACCGATT 610
 Qy 479 ATGTAGCTA-CGAGATGTCACCGAGCT-CCTGAACTCTTCTGGGAGATCT-CAGTATG 535
 Db 611 ATGTAGCTA-CGAGATGTCACCGAGCT-CCTGAACTCTTCTGGGAGATCT-CAGTATG 670

Qy 536 GTTCTTCAGTCGATATATGGGCTATTGGTTGTTTTTTCAGAGCTCTTCAGAGCCAGC 595
 Db 671 GTTCTTCAGTCGATATATGGGCTATTGGTTGTTTTTTCAGAGCTCTTCAGAGCCAGC 730
 Qy 596 CACTGTGGCCCTGGAAATATCAGATGTGGACCAACTTTATCTGATATCAGAACTAGGAA 655
 Db 731 CACTGTGGCCCTGGAAATATCAGATGTGGACCAACTTTATCTGATATCAGAACTAGGAA 790
 Qy 656 AATTAATCCCAAGACATCAATCAATCTTTTAAAGTAACGGGTTTTTCCATGGCATCAGTA 715
 Db 791 AATTAATCCCAAGACATCAATCAATCTTTTAAAGTAACGGGTTTTTCCATGGCATCAGTA 850
 Qy 716 TACCTGAGCCAGACAGACATGAAACTCTTGGAGGAAAGTTCTCAGATCTTTCATCTGTTGG 775
 Db 851 TACCTGAGCCAGACAGACATGAAACTCTTGGAGGAAAGTTCTCAGATCTTTCATCTGTTGG 910
 Qy 776 CTCTGAACTTTCATGAAGGGGTGCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCC 835
 Db 911 CTCTGAACTTTCATGAAGGGGTGCTGAAGATGAATCCAGATGACAGATTAACCTGTTCCC 970
 Qy 836 AACTCTGAGAGCTCTCTTACTTTTGAATCTTTTCAAGAGGCCCAATTAAGAAAGAACAC 895
 Db 971 AACTCTGAGAGCTCTCTTACTTTTGAATCTTTTCAAGAGGCCCAATTAAGAAAGAACAC 1030
 Qy 896 GTAATGAGGAGGAGAAACAGAGAGCCCAACAG 927
 Db 1031 GTAATGAGGAGGAGAAACAGAGAGCCCAACAG 1062
 RESULT 5
 AAS06725
 ID AAS06725 standard; cDNA; 1083 BP.
 XX AC AAS06725;
 XX DT 12-SEP-2001 (first entry)
 XX DE Polynucleotide sequence encoding human protein kinase #25.
 XX KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
 KW metabolic disorder; immune related disease; neurological disorder;
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;
 KW reproductive disorder; gene therapy; ss.
 XX OS Homo sapiens.
 XX PN WO200138503-A2.
 XX PD 31-MAY-2001.
 XX PF 22-NOV-2000; 2000WO-US032085.
 XX PR 24-NOV-1999; 99US-0167482P.
 XX PA (SUGE-) SUGEN INC.
 XX PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
 PI Flanagan P, Clary D;
 XX WPI; 2001-343950/36.
 DR P-PSDB; AAU03525.
 XX Nucleic acids encoding human kinase polypeptides, useful for preventing
 PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
 PT neuronal-associated diseases, and microbial infections.
 XX Example 1; Fig 1; 433pp; English.
 PS AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel
 CC protein kinases have been identified as members of the tyrosine or
 CC serine/threonine kinase (PTK and STK) families. The polynucleotides
 CC encoding protein kinases and the polypeptides may be used in the
 CC prevention, diagnosis and treatment of diseases associated with

inappropriate kinase expression. For example, they may be used to treat cancers (especially cancers of haematopoietic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), immune related diseases (e.g. rheumatoid arthritis), neurological disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. Parkinson's disease), inflammatory disorders (e.g. asthma), infectious disease (e.g. HIV) and reproductive disorders (e.g. infertility). Additionally, polynucleotides encoding protein kinases may be used for gene therapy and as DNA probes in diagnostic assays. The protein kinase polypeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify modulators of protein kinase expression and activity.

1	ATGGAAGAGTATGAAATATAGCTTAAGACATGGAGAGGCTCTATATCGGGTGTGATTCAA	60
1	ATGGAAGAGTATGAAATATAGCTTAAGACATGGAGAGGCTCTATATCGGGTGTGATTCAA	60
61	TGCAGAAACAAACCTCTGGACAAGTAGTAGCTGTGTAAAAATTTGTGGAATCTGAAGAT	120
61	TGCAGAAACAAACCTCTGGACAAGTAGTAGCTGTGTAAAAATTTGTGGAATCTGAAGAT	120
121	GATCTGCTGTTTAAAGAAAATAGCACATAAGAGAAAATACGTATCTGTCAAGCAATTAACAAT	180
121	GATCTGCTGTTTAAAGAAAATAGCACATAAGAGAAAATACGTATCTGTCAAGCAATTAACAAT	180
181	CCAAATCTTGTGAACCTCATCGAGAGTGTTCAGGAGAAAAAGGAAATGCATTAGTATTTT	240
181	CCAAATCTTGTGAACCTCATCGAGAGTGTTCAGGAGAAAAAGGAAATGCATTAGTATTTT	240
241	GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTGTCTGAT	300
241	GAATACCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTGTCTGAT	300
301	GGAGTGTATCAAAAGCGTATATGGCAAAACACTTCAAGCTCTTAATTTCTGTCTATATACAT	360
301	GGAGTGTATCAAAAGCGTATATGGCAAAACACTTCAAGCTCTTAATTTCTGTCTATATACAT	360
361	AACCTGTATTACAGAGATATAAACTGGAATATTTCTAATACTAGCAAGGAATATC	420
361	AACCTGTATTACAGAGATATAAACTGGAATATTTCTAATACTAGCAAGGAATATC	420
421	AGATTGTGCACTTCGGGTTTGCAAAATTCGA	454
421	AGATTGTGCACTTCGGGTTTGCAAAATTCGA	454
455	-----TTCCAGAGATGCTTACACCGATTATGTAGCT	486
455	-----TTCCAGAGATGCTTACACCGATTATGTAGCT	486
481	TTACCTGATCTGATGATGCAATTCGAGTTCAGGAGATGCTTACACCGATTATGTAGCT	540
481	TTACCTGATCTGATGATGCAATTCGAGTTCAGGAGATGCTTACACCGATTATGTAGCT	540
487	ACGAGATGATACGAGCTCTGAACTTCTTGTGGAGATACCTCAGTATGTTCTTCAGTCT	546
487	ACGAGATGATACGAGCTCTGAACTTCTTGTGGAGATACCTCAGTATGTTCTTCAGTCT	546
541	ACGAGATGATACGAGCTCTGAACTTCTTGTGGAGATACCTCAGTATGTTCTTCAGTCT	600
541	ACGAGATGATACGAGCTCTGAACTTCTTGTGGAGATACCTCAGTATGTTCTTCAGTCT	600
547	GATATATGGCTATTGTTGTTTTCAGAGCTCTCTGACAGCCAGCCATCTGAGGCT	606
547	GATATATGGCTATTGTTGTTTTCAGAGCTCTCTGACAGCCAGCCATCTGAGGCT	606
601	GATATATGGCTATTGTTGTTTTCAGAGCTCTCTGACAGCCAGCCATCTGAGGCT	660
601	GATATATGGCTATTGTTGTTTTCAGAGCTCTCTGACAGCCAGCCATCTGAGGCT	660
607	GGAAATCAGATGTGGAACAACTTTATCTGATTAATCAGAAACACTAGGAAAAATTAATCCCA	666
607	GGAAATCAGATGTGGAACAACTTTATCTGATTAATCAGAAACACTAGGAAAAATTAATCCCA	666
661	GGAAATCAGATGTGGAACAACTTTATCTGATTAATCAGAAACACTAGGAAAAATTAATCCCA	720
661	GGAAATCAGATGTGGAACAACTTTATCTGATTAATCAGAAACACTAGGAAAAATTAATCCCA	720
667	AGACATCAATCAATCTTTAAAGTAAACGGGTTTTTCATGGCATCAGTATACCTGAGCCA	726
667	AGACATCAATCAATCTTTAAAGTAAACGGGTTTTTCATGGCATCAGTATACCTGAGCCA	726
721	AGACATCAATCAATCTTTAAAGTAAACGGGTTTTTCATGGCATCAGTATACCTGAGCCA	780
721	AGACATCAATCAATCTTTAAAGTAAACGGGTTTTTCATGGCATCAGTATACCTGAGCCA	780
727	GAAGACATGGAAACTCTTTGAGGAAAAAGTTCTCAGATGTTTCATCTGTGCTCTGAACCTTC	786
727	GAAGACATGGAAACTCTTTGAGGAAAAAGTTCTCAGATGTTTCATCTGTGCTCTGAACCTTC	786

CC products are used to genetically engineer cells in vivo that functions as
CC bioreactors in the body delivering a continuous supply of NHP to the
CC body. Nucleotide constructs encoding functional NHPs are used in gene
CC therapy for the modulation of NHP expression
XX
SQ Sequence 1068 BP; 344 A; 197 C; 240 G; 287 T; 0 U; 0 Other;

Query Match 87.1%; Score 823; DB 4; Length 1068;
Best Local Similarity 90.6%; Pred. No. 2.6e-211;
Matches 929; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

QY 1 ATGGAAGATGATGAAATATAGCTAAGACTGGAGAGGCTCTTATGGGTTCTATTCAAA 60
DB |||||
QY 1 ATGGAAGATGATGAAATATAGCTAAGACTGGAGAGGCTCTTATGGGTTCTATTCAAA 60
DB |||||
QY 61 TGCAGAAACAAACCTCTGGCAAGCTAGTAGCTGTATATAAAATTTGTGAATCTGAAGAT 120
DB |||||
QY 61 TGCAGAAACAAACCTCTGGCAAGCTAGTAGCTGTATATAAAATTTGTGAATCTGAAGAT 120
DB |||||
QY 121 GATCTCTGTTGTTAAGAAATAGCACTTAAGAGAAATACGTATGTTCAAGCAATTAACAT 180
DB |||||
QY 121 GATCTCTGTTGTTAAGAAATAGCACTTAAGAGAAATACGTATGTTCAAGCAATTAACAT 180
DB |||||
QY 181 CCAATCTCTGCACTCATCGAGTGTTCAGAGAAAGAAATGCNTTTAGTTTTT 240
DB |||||
QY 181 CCAATCTCTGCACTCATCGAGTGTTCAGAGAAAGAAATGCNTTTAGTTTTT 240
DB |||||
QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAGAAACCCAAATGGAGTTCGTAT 300
DB |||||
QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAGAAACCCAAATGGAGTTCGTAT 300
DB |||||
QY 301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
DB |||||
QY 301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCATATACAT 360
DB |||||
QY 361 AACTGTATTTCAGAGATATAAACCCTGAAATATTTCTAATTAACCTAAGCAAGAAATATC 420
DB |||||
QY 361 AACTGTATTTCAGAGATATAAACCCTGAAATATTTCTAATTAACCTAAGCAAGAAATATC 420
DB |||||
QY 421 AAGATTTGTGACTTCGGGTTTGCAAAATTCGATTCAGAGATGCTTACACCGATTAT 480
DB |||||
QY 421 AAGATTTGTGACTTCGGGTTTGCAAAATTCGATTCAGAGATGCTTACACCGATTAT 480
DB |||||
QY 481 GTAGTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGAGATATCTAGTATGGTTCT 540
DB |||||
QY 481 GTAGTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGAGATATCTAGTATGGTTCT 540
DB |||||
QY 541 TCAGTTCGATATATGGGCTATTGGTGTGTTTTCAGAGCTCTTCAGAGCCAGCCACTG 600
DB |||||
QY 541 TCAGTTCGATATATGGGCTATTGGTGTGTTTTCAGAGCTCTTCAGAGCCAGCCACTG 600
DB |||||
QY 601 TGGCTCGAAATCAGATGTGGACCACTTTATCTGATATATCGAAACACT- 650
DB |||||
QY 601 TGGCTCGAAATCAGATGTGGACCACTTTATCTGATATATCGAAACACTTAGTAGAGC 660
DB |||||
QY 651 ----- 650
DB |||||
QY 661 GGGTTTCGCCATGTTGACCGGCTGTCTCGAACTCTTGACGTCAAGTGATCCACCTGCC 720
DB |||||
QY 651 -----AGGAAATTAATCCCAAGACATCAATCAATCTTT 684
DB |||||
QY 721 GTAGCTCTCAAAAGTGTGGAATTAACAGGAAATTAATCCCAAGACATCAATCAATCTTT 780
DB |||||
QY 685 AAAAGTAACGGGTTTTCATGGATCAGTATACCTGAGCCAGAGACATGGAACCTCTT 744
DB |||||
QY 781 AAAAGTAACGGGTTTTCATGGATCAGTATACCTGAGCCAGAGACATGGAACCTCTT 840
DB |||||
QY 745 GAGGAAAGTTCTCAGATGTTTCACTCTGCTGCTCACTTCAATGAAGGGTCTCGAAG 804
DB |||||
QY 841 GAGGAAAGTTCTCAGATGTTTCACTCTGCTGCTCACTTCAATGAAGGGTCTCGAAG 900
DB |||||
QY 805 ATGAATCCAGATGACAGATTAACCTGTTCCCACTCTCGAGAGCTCTTACTTGAATCT 864
DB |||||

Db 901 ATGAATCCAGATGACAGATTAACTGTTCCCAACTCTCGAGAGCTCTACTTTGATTCT 960
QY 865 TTTCAAGAGGCCCAAAATTTAAAGAAAGACGTAATGAAGCAAGAAACAGAGACGCCAA 924
DB |||||
Db 961 TTTCAAGAGGCCCAAAATTTAAAGAAAGACGTAATGAAGCAAGAAACAGAGACGCCAA 1020
QY 925 CAGGT 929
DB |||||
Db 1021 CAGGT 1025
DB |||||

RESULT 8
ADK71927

ID ADK71927 standard; cDNA; 1266 BP.

XX ADK71927;

XX 20-MAY-2004 (first entry)

XX Human kinase and phosphatase KPP-45 cDNA.

XX human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic;
XX hypotensive; vasotropic; antiinflammatory; antiangiinal; anti-HIV;
XX antiallergic; antiasthmatic; immunosuppressive; antithyroid;
XX dermatological; antidiabetic; nephrotropic; antitumor; gastrointestinal;
XX neuroprotective; osteopathic; antirheumatic; antiparasitic;
XX antipneumatic; haemostatic; cytotactic; antiparasitic; hepatotropic;
XX antiparasitic; haemostatic; cytotactic; antiparasitic; hepatotropic;
XX antihelminthic; antibacterial; virucide; protozoicidal; fungicide;
XX cardiovascular disease; immune system; neurological; growth; development;
XX cell proliferation; viral; bacterial; fungal; parasitic; protozoan;
XX helminthic infection; transgenic; gene therapy; ss; gene.

XX Homo sapiens.

XX WO2004018641-A2.

XX 04-MAR-2004.

XX 25-AUG-2003; 2003WO-US026635.

XX 26-AUG-2002; 2002US-0406172P.

XX 25-SEP-2002; 2002US-0413910P.

XX 27-SEP-2002; 2002US-0414296P.

XX 11-OCT-2002; 2002US-0417821P.

XX (INCY-) INCYTE CORP.

XX Baughn MR, Richardson TW, Marquis JP, Swarnakar A, Tang YT;
XX Becha SD, Emerling BM, Jin P, Wilson AD, Yue H, Gietzen KJ;
XX Chang H, Yang YG, Lee SY, Khare R, Elliott VS, Hafalia AJA;
XX Chawla NK, Ramkumar J, Gururajan R, Tribouley CM, Chien D, Tran UK;
XX Mursage J;

XX WPI; 2004-226830/21.

XX P-PSDB; ADK71868.

XX New human kinases and phosphatases, useful for diagnosing, treating or
XX preventing atherosclerosis, hypertension, AIDS, allergy, multiple
XX sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
XX or hepatitis.

XX Claim 5; SEQ ID NO 104; 347pp; English.

XX The invention relates to a novel isolated polypeptide which is a human
XX kinase and phosphatase (KPP). The polypeptide of the invention
XX demonstrates cardiovascular, antiarteriosclerotic, hypotensive,
XX vasotropic, antiinflammatory, antiangiinal, anti-HIV, antiallergic,
XX antidiabetic, immunosuppressive, antithyroid, dermatological,
XX antidiabetic, nephrotropic, antitumor, gastrointestinal, neuroprotective,
XX osteopathic, antirheumatic, uropathic, ophthalmological, antipneumatic,
XX antiparkinsonian, neurotropic, anticonvulsant, hepatotropic, antipsoriatic,
XX haemostatic, cytotactic, antiparasitic, antiparasitic, antihelminthic,

XX SD ...

Claim 5; SEQ ID NO 94; 330pp; English.

The present sequence encodes a human kinase and phosphatase (kpp) protein. Kpp sequences have cardiovascular, antiarteriosclerotic, hypotensive, vasotropic, antiinflammatory, antiangiinal, anti-HIV, antiallergic, antialsthmatic, immunosuppressive, antithyroid, dermatological, antidabetic, nephrotropic, antitumor, neuroprotective, osteopathic, antiarthritic, antiparasitic, antirheumatic, anteparkinsonian, antipruritic, antigout, gastrointestinal, CNS, antipsoriatic, haemostatic, cytostatic, anticonvulsant, hepatotropic, antihelmintic, antibacterial, virucide, antipneumant, antiparasitic activities, and can be used in gene therapy, and as kinase modulators and phosphatase modulators. Kpp proteins, polynucleotides, agonists and antagonists can be used for diagnosing, treating or preventing disorders associated with aberrant expression of kpp, such as cardiovascular diseases (e.g. atherosclerosis, hypertension, vasculitis, angina pectoris or congestive heart failure), immune system disorders (e.g. AIDS, allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease, diabetes mellitus, glomerulonephritis, multiple sclerosis, osteoarthritis, gout, irritable bowel syndrome, multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid arthritis, Sjogren's syndrome or uveitis), neurological diseases (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, dementia or epilepsy), disorders affecting growth and development (e.g. cirrhosis, hepatitis, mixed connective tissue disease, psoriasis or primary thrombocytopoenia), cell proliferative disorders (e.g. hypercholesterolaemia, hyperlipidaemia or cancer), or viral, bacterial, fungal, parasitic, protozoan or helminthic infections. The kpp and polynucleotides are also useful in assessing the effects of exogenous compounds on the expression of nucleic acids and kinases and phosphatases, or for facilitating the drug discovery process, including determination of efficacy, dosage, toxicity and pharmacology. The polynucleotides encoding kpp are useful for creating transgenic animals to model human disease.

Sequence 1429 BP; 466 A; 286 C; 294 G; 383 T; 0 U; 0 Other;

Query Match	Score 704.4;	DB 12;	Length 1429;
Best Local Similarity	74.5%		

Best local similarity 82.2%; Pred. No. 2.7e-179;
Matches 924; Conservative 0; Mismatches 1; Indels 199; Gaps 2;

1 ATGAAAGATGATGAAAAATTAGCTAAGACTGGAGAGGTCCTATCGGGTCTGTATTCAAA 60
|||||
70 ATGAAAGATGATGAAAAATTAGCTAAGACTGGAGAGGTCCTATCGGGTCTGTATTCAAA 129

61 TGCAGAAACAAAACCTCTGGACAGTAGCTGTTAAAAATTTCTGGAATCTGAAGAT 120

130 TGCAGAAACAAACCTCTGGCAAGTAGCTGTAAAAAATTTGTGGAATCTGAAGAT 189.

121 GATCCTGTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTTAAACAT 180

190 GATCCTGTTGTTAAGAAAAATAGCATTAGAGAAATACGTATGTTGAAGCAATTTAAACAT 249

181 CCAATCTTGTGAACCTCATCGAGGTCTTCAGGAGAAAAGGAAAATGCATTTAGTTTTT 240

250 CCAATCTTGTGAACTCATCGAGGTTCAGGAGAAAAGGAAAATGCATTAGTTTT 309

241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 300

310 GAATACTGTGATCATACACTTTTAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 369

301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTGATATACAT 360

370 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTCTGTGTCATATACAT 429

361 AACCTGATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAGGAATAATC 420

430 AACGTATTCCAGAGATATAAACCTGAAATATTCTAATAACTAAGCAGGAATAATC 489

421 AAGATTGTGACTTCGGGTTTGACAAATTCTG-----453

490 AAGATTTGTGACTTCGGGTTTGCAAAATTCGAAACACAGTGTTTCACCATGGGGCCGAG 549

Qy	454	-----	453
Db	550	GCTCATCTCGAACTCTTGGCCTCAAGTGATCTTCCACCTCGGCCTCCCAAAGTCTGGA	609
Qy	454	-----	453
Db	610	TTACAAGTGTGAGCCACCGTCCCGCCAGCCAGATTTTTCAAACAATAACTACTGAGAGCTCA	669
Qy	454	-----ATTCCAGGAG	463
Db	670	CAAGATTGTTTTTATGTGGGAACAATAATTGGAACAATCTTGTGAGAAGCCATTCAGGAG	729
Qy	464	ATGCCTACACCGAATATGTAGTACGAGATGGTACCGAGCTCCTGGAACCTTCTTGTGGGAG	523
Db	730	ATGCCTACACCGAATGTGTAGTACGAGATGGTACCGAGCTCCTGGAACCTTCTTGTGGGAG	789
Qy	524	ATACTCAGTATGGTCTTTCAGTCAATATATGGGCTATTTGGTTGTTTTTGCAGAGCTCC	583
Db	790	ATACTCAGTATGGTCTTTCAGTCAATATATGGGCTATTTGGTTGTTTTTGCAGAGCTCC	847
Qy	584	TGACAGGCCAGCCACTGTGGCCTGGAAAAATCAGATGTGGACCAACTTTATCTGATAATCA	643
Db	848	TGACAGGCCAGCCACTGTGGCCTGGAAAAATCAGATGTGGACCAACTTTATCTGATAATCA	907
Qy	644	GAACACTAGGAAAAATTAATCCCAAGACATCAATCAATCTTTAAAGTAAACGGGTTTTTCC	703
Db	908	GAACACTAGGAAAAATTAATCCCAAGACATCAATCAATCTTTAAAGTAAACGGGTTTTTCC	967
Qy	704	ATGGCATCAGTATACCTGAGCCAGAGACATGGAAAATCTTTGAGGAAAAAGTTCTCAGATG	763
Db	968	ATGGCATCAGTATACCTGAGCCAGAGACATGGAAAATCTTTGAGGAAAAAGTTCTCAGATG	1027
Qy	764	TTCAATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGAT	823
Db	1028	TTCAATCCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGAT	1087
Qy	824	TAACTGTGTTCCCAACTCCTGGAGAGCTCCTACTTTTGATTTCTTTTCAAGAGGCCAAATTA	883
Db	1088	TAACTGTGTTCCCAACTCCTGGAGAGCTCCTACTTTTGATTTCTTTTCAAGAGGCCAAATTA	1147
Qy	884	AAAGAAAACAGCTAATGAAGGAAGAAAACAGAAAGCGCCAAACAG	927
Db	1148	AAAGAAAACAGCTAATGAAGGAAGAAAACAGAAAGCGCCAAACAG	1191

RESULT 10

AAI64248

ID AAI64248 standard; cDNA; 882 bp.

XX 5

AC
YY
AAI6.

DT 08-MAR-2003 (first contact)

XX
2007-2011
TJTB 15111)

DE Human kinase 14257 cDNA.

Protein kinase; enzyme; cytostatic; osteopathic; hepatotropic; antidiabetic; neuroprotective; antiarthritic; dermatological; immunosuppressive; antiinflammatory; antithyroid; antiproliferative; ophthalmological; antiallergic; antiasthmatic; antihistoclerotic; hypertensive; vasotropic; antiarrhythmic; virucide; anorectic; immunomodulator; analgesic; cellular proliferative disorder; cancer; acute lymphoblastic leukaemia; Hodgkin's disease; bone metabolism disorder; osteoporosis; immune system disorder; inflammatory; diabetes mellitus; osteoarthritis; asthma; cardiovascular disorder; hypertension; coronary artery disease; endothelial cell disorder; psoriasis; ss.

Homo sapiens.

Key	Location/Qualifiers
5/11/1960	5/11/1960

```

1: .128
/*tag=

```

FT CDS 129..815
 FT /*tag= b
 FT /product= "Protein kinase 14275"
 FT 816..882
 FT /*tag= c
 XX
 PN WO200179488-A2.
 XX
 PD 25-OCT-2001.
 XX
 XX 13-APR-2001; 2001WO-US012188.
 XX
 PR 13-APR-2000; 2000US-0196910P.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX Kapeller-Libermann R;
 XX
 XX WPI; 2002-034355/04.
 DR P-PSDB; AAG78547.
 XX
 XX New 14257 polypeptides (protein kinases), useful as diagnostic targets
 PT and therapeutic agents for controlling cellular proliferative and/or
 PT differentiative disorder, bone disorders, immune disorders and
 PT cardiovascular disorders.
 XX
 XX Claim 2; Fig 1A; 98pp; English.
 XX
 XX The invention relates to an isolated 14257 polypeptide and nucleic acid
 CC encoding it. The 14257 protein is a protein kinase that acts as a
 CC modulating agent in regulating a variety of cellular processes, including
 CC cell proliferation, differentiation, growth and division. The activity of
 CC the protein of the invention may be described as; cytoskeletal; osteopathic
 CC ; hepatotropic; antidiabetic; neuroprotective; antiarthritic;
 CC dermatological; immunosuppressive; antiinflammatory; antithyroid;
 CC antipsoriatic; ophthalmological; antiallergic; antiasthmatic;
 CC antiatherosclerotic; hypotensive; vasotropic; antiarrhythmic; virucide;
 CC anorectic; metabolic; immunomodulator and analgesic. The protein of the
 CC invention may act as a novel diagnostic target or therapeutic agent
 CC controlling certain disorders, for example kinase-associated or other
 CC 14257-associated disorders. These may include cellular proliferative
 CC disorders such as cancers e.g. acute lymphoblastic leukemia or Hodgkin's
 CC disease. Other disorders include bone metabolism disorders such as
 CC osteoporosis, disorders of the immune system, e.g. inflammatory,
 CC diabetes mellitus, osteoarthritis and asthma. Proteins of the invention
 CC may also be of use as therapeutic agents in cardiovascular disorders such
 CC as hypertension and coronary artery disease, and some endothelial cell
 CC disorders, including psoriasis. The current sequence represents a human
 CC kinase 14257 cDNA
 XX
 SQ Sequence 882 BP; 288 A; 150 C; 198 G; 245 T; 0 U; 1 Other;

Query Match 68.3%; Score 645.4; DB 6; Length 882;
 Best Local Similarity 99.1%; Pred. No. 1.8e-163;
 Matches 649; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ATGGAAAGTATGAAATAGCTAAGACTGAGAGGGTCTTATGGGGTTGATTCAAA 60
 DB 129 ATGGGAAGTATGAAATAGCTAAGACTGAGAGGGTCTTATGGGGTTGATTCAAA 188
 QY 61 TGCAGAAACAAACCTCTGGCAAGTAGTAGCTGTAAAAAATTTGGGAATCTGAAGAT 120
 DB 189 TGCAGAAACAAACCTCTGGCABCTAGTAGCTGTAAAAAATTTGGGAATCTGAAGAT 248
 QY 121 GATCCTGTGTAGAAATAGCTAGAGAAATACGTATGTGACCAATTAACAT 180
 DB 249 GATCCTATTTAGAAATAGCTAGAGAAATACGTATGTGACCAATTAACAT 308
 QY 181 CCAATCTGTGAACCTCATCCAGTGTTCAGGAGAAAAAGAAATGCAATTTAGTTT 240
 DB 309 CCAATCTGTGAACCTCATCCAGTGTTCAGGAGAAAAAGAAATGCAATTTAGTTT 368
 QY 241 GAATACTGTGATCATACACTTTTAAATGAGCTGGAAAGAAACCCAAATGGAGTGTCTGAT 300

Db 369 GAATACTGTGATCATGCACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT 428
 QY 301 GGAGTGATCAAAAGCGTATTATGGCAAAACACTTCAAGAGCTCTTAATTTTGTTCATATACAT 360
 Db 429 GGAGTGATCAAAAGCGTATTATGGCAAAACACTTCAAGAGCTCTTAATTTTGTTCATATACAT 488
 QY 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATAATC 420
 Db 489 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATAATC 548
 QY 421 AAGATTGTGACTTCGGGTTTGCAAAATCTGATTCAGGAGATGCTACACCGATTAT 480
 Db 549 AAGATTGTGACTTCGGGTTTGCAAAATCTGATTCAGGAGATGCTACACCGATTAT 608
 QY 481 GTAGTACGAGATGGTACCGAGCTCTCGAACTTCTTGTGGGAGATATCTCAGTATGGTTCT 540
 Db 609 GTAGTACGAGATGGTACCGAGCTCTCGAACTTCTTGTGGGAGATATCTCAGTATGGTTCT 668
 QY 541 TCAGTCAATATATGGGCTATTGGTTGGTTTTTTCAGAGCTCTTCGACAGGCCAGCCACTG 600
 Db 669 TCAGTCAATATATGGGCTATTGGTTGGTTTTTTCAGAGCTCTTCGACAGGCCAGCCACTG 728
 QY 601 TGGCCTGAAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACTAGGAA 655
 Db 729 TGGCCTGAAAAATCAGATGTGGACCAACTTTATCTGATAATCAGAACTAGGTA 783

RESULT 11
 AAF44669
 ID AAF44669 standard; cDNA; 911 BP.
 AC AAF44669;
 XX
 DT 27-MAR-2001 (first entry)
 DE Novel protein kinase cDNA, SEQ ID NO: 49.
 KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;
 KW dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.
 OS Homo sapiens.
 PN WO200073469-A2.
 PD 07-DEC-2000.
 PF 26-MAY-2000; 2000WO-US014842.
 PR 28-MAY-1999; 99US-0136503P.
 XX (SUGE-) SUGEN INC.
 PI Plowman GD, Martinez R, Whyte D, Sudersanam S;
 DR WPI; 2001-032161/04.
 DR P-PSDB; AAB65642.
 PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 PT neurodegenerative diseases and/or cancers.
 XX Example 4; Fig 2; 310pp; English.
 XX The present sequence encodes a novel protein kinase. The nucleic acids
 CC and the protein kinases they encode may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and

complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase expression and activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive disorders

Sequence 911 BP; 293 A; 182 C; 178 G; 258 T; 0 U; 0 Other;

Query Match 68.0%; Score 643; DB 4; Length 911;

Best Local Similarity 100.0%; Pred. No. 7.9e-163; Matches 643; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

285 AAATGGAGTTCCTGATGAGTATCAAAAGCGTATTATGCGAAACACTTCAAGCTCTTAA 344
 1 AAATGGAGTTCCTGATGAGTATCAAAAGCGTATTATGCGAAACACTTCAAGCTCTTAA 60
 345 TTCTCTCATATACATAAATCAATCTTACAGAGATATAAAACCTGAAATATTCTATATAC 404
 61 TTCTCTCATATACATAAATCAATCTTACAGAGATATAAAACCTGAAATATTCTATATAC 120
 405 TAAGCAAGGAATAATCAAGATTGTGACTTCGGGTTTGCAAAATCTGATTCACAGGAGA 464
 121 TAAGCAAGGAATAATCAAGATTGTGACTTCGGGTTTGCAAAATCTGATTCACAGGAGA 180
 465 TGCTTACACCGATTATGTAGTACGAGATGTACCGAGTCTCTGAACTTTTGTGGGAGA 524
 181 TGCTTACACCGATTATGTAGTACGAGATGTACCGAGTCTCTGAACTTTTGTGGGAGA 240
 525 TACTCAGTATGTTCTTCAGTTCAGATATATGGCTATTTGTTGTTTTCAGAGCTCCT 584
 241 TACTCAGTATGTTCTTCAGTTCAGATATATGGCTATTTGTTGTTTTCAGAGCTCCT 300
 585 GACAGCCAGCCAGTGTGGCTTGGAAATCAGATGTGACCAACTTTATCTGATAATCAG 644
 301 GACAGCCAGCCAGTGTGGCTTGGAAATCAGATGTGACCAACTTTATCTGATAATCAG 360
 645 AACCTTAGGAAATTAATCCCAAGACATCAATCAATCTTTAAAGTAAACGGGTTTTTCCA 704
 361 AACCTTAGGAAATTAATCCCAAGACATCAATCAATCTTTAAAGTAAACGGGTTTTTCCA 420
 705 TGGCATCAGTATACCTGAGCCAGACAGATCGAACTTTGAGGAAAGTTCTCAGATGT 764
 421 TGGCATCAGTATACCTGAGCCAGACAGATCGAACTTTGAGGAAAGTTCTCAGATGT 480
 765 TCATCCTGTGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATCAGATT 824
 481 TCATCCTGTGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATCAGATT 540
 825 AACCTGTTCCTCAACTCTGAGAGCTCTTACTTTGATTTTCAAGAGGCCCAATTA 884
 541 AACCTGTTCCTCAACTCTGAGAGCTCTTACTTTGATTTTCAAGAGGCCCAATTA 600
 885 AAGAAAAGCAGTAAATCAAGGAAGAAACAGAGAGCCACAG 927
 601 AAGAAAAGCAGTAAATCAAGGAAGAAACAGAGAGCCACAG 643

RESULT 12

AD129367

ID AD129367 standard; cDNA; 911 BP.

XX AD129367;

AC AD129367;

XX 22-APR-2004 (first entry)

DT Human MARK3-associated cDNA #37.

DE

XX Human; ss; antisense gene therapy; MARK3;
 KW MAP/microtubule affinity-regulating kinase 3; cancer;
 KW Alzheimer's disease; neurodegenerative disorder;
 KW hyperproliferative disorder; cytostatic.
 XX Homo sapiens.
 XX US2003232771-A1.
 XX 18-DEC-2003.
 XX 17-JUN-2002; 2002US-00174319.
 XX 17-JUN-2002; 2002US-00174319.
 XX (ISIS-) ISIS PHARM INC.
 XX Ward DT, Freier SM, Dobie KW;
 XX WPI; 2004-052188/05.
 XX P-PSDB; ADI29249.
 XX New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3), useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.
 XX Disclosure; Fig 2; 233pp; English.
 XX The invention relates to a compound comprising a sequence comprising 8-80 base pairs (bp) targeted to a nucleic acid encoding MARK3 (MAP/microtubule affinity-regulating kinase 3), that specifically hybridizes with the nucleic acid encoding MARK3 and inhibits expression of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a composition comprising the compound and a carrier or diluent, inhibiting the expression of MARK3 in cells or tissues, treating an animal having or suspected of having a disease or condition associated with MARK3 and screening for an antisense compound. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder, particularly cancer and neurodegenerative diseases e.g. Alzheimer's disease. The present sequence is a MARK3 associated cDNA included in the figures but not mentioned anywhere else in the specification.

Query Match 68.0%; Score 643; DB 12; Length 911;

Best Local Similarity 100.0%; Pred. No. 7.9e-163; Matches 643; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

285 AAATGGAGTTCCTGATGAGTATCAAAAGCGTATTATGCGAAACACTTCAAGCTCTTAA 344
 1 AAATGGAGTTCCTGATGAGTATCAAAAGCGTATTATGCGAAACACTTCAAGCTCTTAA 60
 345 TTCTCTCATATACATAAATCAATCTTACAGAGATATAAAACCTGAAATATTCTATATAC 404
 61 TTCTCTCATATACATAAATCAATCTTACAGAGATATAAAACCTGAAATATTCTATATAC 120
 405 TAAGCAAGGAATAATCAAGATTGTGACTTCGGGTTTGCAAAATCTGATTCACAGAGA 464
 121 TAAGCAAGGAATAATCAAGATTGTGACTTCGGGTTTGCAAAATCTGATTCACAGAGA 180
 465 TGCCTACACCGATTATGTAGTACGAGATGTACCGAGTCTCTGAACTTTTGTGGGAGA 524
 181 TGCCTACACCGATTATGTAGTACGAGATGTACCGAGTCTCTGAACTTTTGTGGGAGA 240
 525 TACTCAGTATGTTCTTCAGTTCAGATATATGGCTATTTGTTGTTTTCAGAGCTCCT 584
 241 TACTCAGTATGTTCTTCAGTTCAGATATATGGCTATTTGTTGTTTTCAGAGCTCCT 300
 585 GACAGCCAGCCAGTGTGGCTTGGAAATCAGATGTGACCAACTTTATCTGATAATCAG 644
 301 GACAGCCAGCCAGTGTGGCTTGGAAATCAGATGTGACCAACTTTATCTGATAATCAG 360

Qy 645 AACACTAGGAAATTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCA 704
 Db 361 AACACTAGGAAATTAATCCCAAGACATCAATCAATCTTTAAAGTAACGGGTTTTTCCA 420
 Qy 705 TGGCATCAGTATACCTGAGCCAGAGACATCGAAACTCTTCAGGAAAGTTCTCAGATGT 764
 Db 421 TGGCATCAGTATACCTGAGCCAGAGACATCGAAACTCTTCAGGAAAGTTCTCAGATGT 480
 Qy 765 TCATCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT 824
 Db 481 TCATCTGTGGCTCTGAACTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT 540
 Qy 825 AACCTGTTCCCACTCTCGAGAGCTCTACTTTGATCTTTTCAAGAGGCCCAAAATAA 884
 Db 541 AACCTGTTCCCACTCTCGAGAGCTCTACTTTGATCTTTTCAAGAGGCCCAAAATAA 600
 Qy 885 AAGAAAGCAGTAAATGAAGCAAGAAACAGAGAGCGCCAAACAG 927
 Db 601 AAGAAAGCAGTAAATGAAGCAAGAAACAGAGAGCGCCAAACAG 643

RESULT 13

AAFA4670
 ID AAF4670 standard; cDNA; 2615 BP.

XX
 AC AAF4670;

XX
 DT 27-MAR-2001 (first entry)

XX
 DE Novel protein kinase cDNA, SEQ ID NO: 50.

XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
 KW immunosuppressive; cardiac; renal; antiinflammatory; antiaesthetic;
 KW dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
 KW immune disorder; cardiovascular disease; neurodegenerative disease;
 KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
 KW inflammatory pelvic disease; multiple sclerosis; psoriasis; ss.

XX Mus musculus.

XX W0200073469-A2.

XX
 PD 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US014842.

XX 28-MAY-1999; 99US-0136503P.

XX (SUGE-) SUGEN INC.

XX Plowman GD, Martinez R, Whyte D, Sudersanam S;

XX WPI; 2001-032161/04.

XX P-PSDB; AAB65643.

PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
 PT treating immune-related diseases and disorders, cardiovascular disease,
 PT neurodegenerative diseases and/or cancers.

XX Disclosure; Fig 2; 310pp; English.

XX The present sequence encodes a novel protein kinase. The nucleic acids
 CC and the protein kinases they encode may be used in the treatment and
 CC diagnosis of diseases associated with inappropriate kinase expression
 CC such as immune-related diseases and disorders, cardiovascular disease,
 CC neurodegenerative diseases and/or cancers. The nucleic acids and
 CC complementary sequences may also be used as DNA probes in diagnostic
 CC assays. The kinase polypeptides may be used as antigens in the production
 CC of antibodies of kinase expression and activity. Anti-kinase antibodies
 CC and kinase antagonists may also be used to down regulate kinase
 CC expression and activity. Diseases related to kinase expression and
 CC activity include rheumatoid arthritis, atherosclerosis, autoimmune

CC disorders, complications of organ transplantation, myocardial infarction,
 CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
 CC stress related disorders, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
 CC disorders
 XX
 SQ Sequence 2615 BP; 742 A; 580 C; 585 G; 708 T; 0 U; 0 Other;

Query Match 59.2%; Score 559.2; DB 4; Length 2615;
 Best Local Similarity 81.8%; Pred. No. 4.6e-140;
 Matches 658; Conservative 0; Mismatches 143; Indels 3; Gaps 1;

Qy 135 GAAATAGACACTAAGAGAAATACGTATGTTGAAGCAATTAAGAAATCAAAATCTTTGAA 194
 Db 1 GAAATAGACCTCGCGGAAATCCGTATGCTGAAG---TTGAAACACCAAACTCTGTA 57
 Qy 195 CCTCATCGAGGTGTTCAAGAGAAAGAAATGCAATTTAGTTTTCGAATCTCTGATCA 254
 Db 58 CCTCATCGAGGTGTTCAAGAGAAAGAAAGATGCAATTTAGTTTTCGAATCTCTGATCA 117
 Qy 255 TACACTTTTAAATGAGCTGGAAAGAAACCAAAATGGAGTTGCTGATGGAGTGATCAAAAG 314
 Db 118 CACACTGTTAAACGAGCTGGAGAGAAACCAACGGAGTTTCTGATGGAGTGATTAAG 177
 Qy 315 CGTATTATGGAAACACTTCAAGCTCTTAATTTCTGCATATACATTAATCTGTATTTCAG 374
 Db 178 TGTGCTATGGCAAACTTCAAGCCCTTAACCTTCTGTCAAGCACAATTTGATTTCATCG 237
 Qy 375 AGATATAAACCTCGAAATATTTCTAATACTAAGCAGGATTAATCAAGTTTCTGACTT 434
 Db 238 GGAATATAAACCTCGAAACATCTTAATAACCAAGCAGGATTAATAAGATTTTGTACTT 297
 Qy 435 CGGTTTTCACAAATCTGATTCAGGAGATGCTTACACCGATTTATCTAGCTACGAGATG 494
 Db 298 TGAATTTGACGAATTTCTAATTCAGAGAGAGCTTACACAGACTATGTTGCCACAGGTG 357
 Qy 495 GTACCGAGCTCTGAACTTCTTGTGGGAGATATCTAGTATGGTTTCTTCAGTCGATATATG 554
 Db 358 GTACCGAGCTCTGAACTTCTTGTGGGAGATATCTAGTATGGTTTCTTCGTAGACGTGTG 417
 Qy 555 GGCATTATGGTTGTTTTCAGAGCTCTTCAAGAGCCAGCCACTGTGGCTCGGAAATC 614
 Db 418 GGCCTGCGGCTGTGTTTTCAGAGCTCTTCAAGAGCTCTGAGCGGTGAGCCACTTGGCGGAAATC 477
 Qy 615 AGATGTGACCAACTTTATCTGATAATCAGAAACATAGGAAATTAATCCCAAGACATCA 674
 Db 478 CGAGTGGACACAGCTTTACCTGATCATCAGACGTTGGGAGCTGATTCGAAGACACCA 537
 Qy 675 ATCAATCTTTAAAGTAAACGGGTTTTTCCATGGCATCAGTATACCTCAGCCAGAGACAT 734
 Db 538 GTCTATCTTTAGGAGTAAACCAAGTTTTTCCGCGGCATCAGCATACCTGAAACAGAGGACAT 597
 Qy 735 GGAACCTCTTGAGAAAGTTCTCAGATGTTTCATCTGCTGCTCTGAATCTCATGAGGG 794
 Db 598 GGAAGCTCTTTGAAAGAAATTTCTCAATGTTTCAGCTGTGGCTTTAAGTTTCATGAGGG 657
 Qy 795 GTGCTCAAGATGAATCCAGATGACAGTTAACTGTTCCCAACTCTCTGGAGAGCTCCTA 854
 Db 658 ATGCTGAAGATGAATCTGATGAGGCTGACCTGTGCCAGCTGTGACAGCTGTGCTA 717
 Qy 855 CTTTGTATTTCTTTCAAGAGGCCCAAAATTAAGAAAGCAAGCAAGTAAAGAGAAACAG 914
 Db 718 CTTTGTAGTCTTTCAAGAGGATCAATGAAGAAAGAAAGCCCGCATGAGGGGAGAGCG 777
 Qy 915 AAGACGCCAACAGGTACTTCGGCT 938
 Db 778 AAGCGCCACAGCAATCAACTGCT 801

RESULT 14

ADI29368
 ID ADI29368 standard; cDNA; 2615 BP.

XX AC ADI29368;
 XX DT 22-APR-2004 (first entry)
 XX DE Mouse MARK3-associated cDNA #12.
 XX KW Mouse; ss; antisense gene therapy; MARK3;
 KW MAP/microtubule affinity-regulating kinase 3; cancer;
 KW Alzheimer's disease; neurodegenerative disorder;
 KW hyperproliferative disorder; cytostatic.
 XX OS Mus musculus.
 XX FN US2003232771-A1.
 XX PD 18-DEC-2003.
 XX PF 17-JUN-2002; 2002US-00174319.
 XX PR 17-JUN-2002; 2002US-00174319.
 XX PA (ISIS-) ISIS PHARM INC.
 XX PI Ward DT, Freier SM, Dobie KW;
 XX DR WPI; 2004-052188/05.
 XX DR P-PSDB; ADI29250.
 XX PT New antisense compound targeted to a nucleic acid molecule encoding
 PT microtubule-affinity-regulating kinases (MARK3), useful for modulating
 PT expression of MARK3 or for treating cancer or Alzheimer's disease.
 XX PS Disclosure; Fig 2; 233pp; English.
 XX CC The invention relates to a compound comprising a sequence comprising 8-80
 CC base pairs (bp) targeted to a nucleic acid encoding MARK3
 CC (MAP/microtubule affinity-regulating kinase 3), that specifically
 CC hybridises with the nucleic acid encoding MARK3 and inhibits expression
 CC of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a
 CC composition comprising the compound and a carrier or diluent, inhibiting
 CC the expression of MARK3 in cells or tissues, treating an animal having or
 CC suspected of having a disease or condition associated with MARK3 and
 CC screening for an antisense compound. The antisense oligonucleotide is
 CC useful for preparing a composition for treating hyperproliferative
 CC disorder, particularly cancer and neurodegenerative diseases e.g.
 CC Alzheimer's disease. The present sequence is a MARK3 associated cDNA
 CC included in the figures but not mentioned anywhere else in the
 CC specification.

Query Match 59.2%; Score 559.2; DB 12; Length 2615;
 Best Local Similarity 81.8%; Pred. No. 4.6e-140;
 Matches 658; Conservative 0; Mismatches 143; Indels 3; Gaps 1;
 135 GAAATAGCTACTAAGAGAAATACGTATGTGAAGCAATTAATAATCAATCTCTGAA 194
 1 GAAATAGCTCTGGCGGAAATCGTATGTGAG--TTGAACACCCAACTCGTGA 57
 195 CCTCATCGAGTGTTCAGAGAAAGAAATGCAATTTAGTTTGTGAATCTGTGATCA 254
 58 CCTCATCGAGTGTTCAGAGAAAGAGAAAGATGCAATTTAGTTTGTGATCTGTGATCA 117
 255 TACACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGATGAGTGCATCAAG 314
 118 CACACTTTAAACGAGCTGAGAGAAACCCAAACGAGTTTCTGATGAGTGAATTAAG 177
 315 CGTATTATGCAACACTTCAAGCTCTTAATTTCTGTATATACATACTGATTTACAG 374
 178 TGTGCTATGCAACCCCTTCAAGCCCTTAATTTCTGTCAAGCAACAAATTTGATTCATCG 237
 375 AGATATAAACCTGAAATAATTTCTAATACTAAGCAAGAAATAATCAAGATTTGTGACTT 434

Db 238 GGATGTAAACCTGAAACATCTTAATAACCAAGGAGATGATAAGATTGTGACTT 297
 QY 435 CGGGTTTGACAAATTTCTGATTCAGAGAGATGCTTACACCGATTATGTAGTACGATG 494
 Db 298 TGGATTTCAGCAATTTCTAATTCAGAGAGACGCTACACAGACTATGTTGCCACAGGTG 357
 QY 495 GTACCGAGCTCTGAACCTTCTTGTGGAGATACACTAGTATGTTTCTTTCAGTATATG 554
 Db 358 GTACCGAGCCCCGAACTTCTGTTGGAGACACGAAGTACGGTTCTCTCTAGACGTGTG 417
 QY 555 GGCTATTGGTTGTGTTTTTTCAGAGCTCTTGAACAGGCGACGACTGTGGCTCGAAATC 614
 Db 418 GCGCGTGGCTGTGTTTTTTCAGAGCTCTTGAACAGGCTCTGCGGCTGAGCCACTCTGGCCGGAATC 477
 QY 615 AGATGTGAGCCAACTTTTATCTGATATATCAAGAACACTAGGAAATTAATCCAAAGACATCA 674
 Db 478 CGAGTGTGAGCCAGCTTTTACCTGATCATCAGGAGCTTGGGGAAGCTGATTCGAAGACCA 537
 QY 675 ATCAATCTTTAAAGTAACGGTTTTTCCATGTCATCAGTATACCTGAGCCAGACACAT 734
 Db 538 GTCTATCTTTAGGAGTAACCCAGTTTTTTCGCGGCATCAGCATACCTGAACAGAGACAT 597
 QY 735 GGAACCTCTTGAAGAAAGTTCTCAGATGTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 794
 Db 598 GGAGACTCTTTGAAGAAATTTCTCAATGTTTCAAGCTGTGGCTTTTAAAGTTTCAATGAGGG 657
 QY 795 GTGTCTGAAGATCAATCCAGATGACAGATTAACTGTTTCCCACTCTCCAGCTCTGAGAGCTCTTA 854
 Db 658 ATGCTTGAAGATCAATCTGATGAGAGGCTGACCTGTGCTCCAGCTGCTGAGAGTGCCTTA 717
 QY 855 CTTTGTATCTTTTCAAGAGGCTTCAATTAAGAAAGCAAGCAATTAATGAAGGAAAGAAACAG 914
 Db 718 CTTTGTATCTTTTCAAGAGGATCAATTAAGAAAGCAAGCAATTAATGAAGGAAAGAAACAG 914
 QY 915 AAGACGCCAACAGTACTTTCGCT 938
 Db 778 AAGGCGCCAGCAGATCACTGCT 801

RESULT 15
 ABX34679
 ID ABX34679 standard; cDNA; 1281 BP.
 XX ABX34679;
 XX AC
 XX DT 13-FEB-2003 (first entry)
 XX DE Human mddt cDNA SEQ ID 240.
 XX KW MDDT; human; disease detection and treatment molecule polypeptide;
 KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
 KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;
 KW gene therapy; protein replacement therapy; cell proliferative disorder;
 KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
 KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
 KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopenia;
 KW psoriasis; hepatitis; gene; ss.
 XX OS Homo sapiens.
 XX FN WO200279449-A2.
 XX PD 10-OCT-2002.
 XX PF 27-MAR-2002; 2002WO-US009944.
 XX PR 28-MAR-2001; 2001US-0279619P.
 XX PR 29-MAR-2001; 2001US-0280067P.
 XX PR 29-MAR-2001; 2001US-0280068P.
 XX PR 16-MAY-2001; 2001US-0291280P.
 XX PR 17-MAY-2001; 2001US-0291829P.
 XX PR 17-MAY-2001; 2001US-0291849P.

PR 19-JUN-2001; 2001US-0299428P.
 PR 20-JUN-2001; 2001US-029976P.
 PR 20-JUN-2001; 2001US-030001P.
 XX (INCY-) INCYTE GENOMICS INC.
 XX PA
 XX PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshay SR;
 PI Daugherty SC, Dam TC, Liu TP, Nguyen DA, Kleeefeld Y, Gerstin EH;
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
 XX
 XX WPI; 2003-058431/05.
 DR P-PSDB; ABU11689.
 XX
 XX New purified disease detection and treatment molecule proteins and
 PT polynucleotides, useful for diagnosing, treating or preventing cancers
 PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis
 PT or hepatitis.
 XX
 XX Claim 1; SEQ ID NO 240; 339pp + Sequence Listing; English.
 PS
 PS This invention describes a novel disease detection and treatment molecule
 CC polypeptide (MDPT) which has anti-inflammatory, immunosuppressive,
 CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
 CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides
 CC and the polypeptides of the invention can be used for gene therapy,
 CC protein replacement therapy and are useful for treating a variety of
 CC diseases or conditions. These polypeptides or polynucleotides are
 CC particularly useful for diagnosing, treating or preventing cell
 CC proliferative disorders (e.g. cancers including adenocarcinoma,
 CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
 CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
 CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
 CC hepatitis. ABX34440-ABX34835 encode the MDPT polypeptides represented in
 CC ABU11450-ABU11845, described in the disclosure of the invention. NOTE:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 1281 BP; 428 A; 191 C; 317 G; 345 T; 0 U; 0 Other;
 Query Match 57.5%; Score 543.2; DB 8; Length 1281;
 Best Local Similarity 99.5%; Pred. No. 7.1e-136;
 Matches 545; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 ATGCAAAAGTATGAAAAATTAGCTAAGACTGAGAGGGCTTATGGGTTGTATTCAAA 60
 DB 704 ATGAAAAGTATGAAAAATTAGCTAAGACTGAGAGGGCTTATGGGTTGTATTCAAA 763
 QY 61 TGCAGAAACAAAACCTCTGGACAAAGTAGTAGCTGTAAAAAATTTGTGGAATCTGAAGAT 120
 DB 764 TGCAGAAACAAAACCTCTGGACAAAGTAGTAGCTGTAAAAAATTTGTGGAATCTGAAGAT 823
 QY 121 GATCCTGTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 180
 DB 824 GATCCTGTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT 883
 QY 181 CCAATCTGTGACCTCATCGAGGTGTTACAGGAGAAAGAAATGCAATTTAGTTT 240
 DB 884 CCAATCTGTGACCTCATCGAGGTGTTACAGGAGAAAGAAATGCAATTTAGTTT 943
 QY 241 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTCAT 300
 DB 944 GAATCTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTCAT 1003
 QY 301 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCAATATACAT 360
 DB 1004 GGAGTGATCAAAAGCGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCAATATACAT 1063
 QY 361 AACTGTATTCCAGAGATATAAAACCTGAAATATTTCTTAATACTAAGCAGGGAATATC 420
 DB 1064 AACTGTATTCCAGAGATATAAAACCTGAAATATTTCTTAATACTAAGCAGGGAATATC 1123

QY 421 AAGATTGTGCACTTCGGGTTTGACAAATTTCTGATTCAGGAGATGCTACACCGATTAT 480
 DB 1124 AAGATTGTGCACTTCGGGTTTGACAAATTTCTGATTCAGGAGATGCTACACCGATTAT 1183
 QY 481 GTAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACCTCAGTATGGTTCT 540
 DB 1184 GCAGCTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGGAGATACCTCAGTATGGTTCT 1243
 QY 541 TCAGTCGA 548
 DB 1244 TCAGTCAA 1251

Search completed: April 21, 2005, 21:13:06
 Job time : 522.228 secs

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OM nucleic - nucleic search, using sw model

Run on: April 21, 2005, 20:25:49 ; Search time 4109.75 Seconds
(without alignments)
11141.838 Million cell updates/sec

Title: US-10-766-691-11
Perfect score: 945
Sequence: 1 atggaagaatgataaaatt.....aggtaattccgtcctcaaaagt 945

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	945	100.0	945	6 AR492170	Sequence
2	945	100.0	945	6 AX107722	Sequence
3	929	98.3	972	6 AR492167	Sequence
4	929	98.3	972	6 AX107716	Sequence
5	927	98.1	1790	6 AX746179	Sequence
6	868.8	91.9	1678	6 AX698820	Sequence
7	863	91.3	1083	6 AX166534	Sequence
8	839	88.8	1041	6 AR492169	Sequence
9	839	88.8	1041	6 AX107720	Sequence
10	823	87.1	1068	6 AR492166	Sequence
11	823	87.1	1068	6 AX107714	Sequence
12	647	68.5	687	6 AX286069	Sequence
13	647	68.5	882	6 AX286067	Sequence
14	643	68.0	911	6 AX056404	Sequence
15	559.2	59.2	2615	6 AX056405	Sequence
16	507	53.7	1819	6 AR492171	Sequence
17	507	53.7	1819	6 AX107724	Sequence
18	501	53.0	1086	6 AX803417	Sequence
19	454.4	48.1	561	6 AR492165	Sequence

20	454.4	48.1	561	6	AX107712	Sequence
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22	454.4	48.1	534	6	AX107718	Sequence
23	451.4	47.8	1525	5	BC079506	Danio rer
24	416.4	44.1	1861	10	BC081896	BC081896 Rattus no
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26	413.8	43.8	1363	9	HSSTHPKB	X66358 H sapiens m
27	413.8	43.8	2944	6	CQ492706	Sequence
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29	360.8	38.2	538	6	CQ714922	Sequence
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31	287	30.4	1701	6	AR438689	Sequence
32	287	30.4	3080	6	AR221994	Sequence
33	287	30.4	3080	6	AR438688	Sequence
34	287	30.4	3153	4	AB029045	AB029045 Oryctolag
35	283.8	30.0	1993	9	HSU35146	U35146 Homo sapien
36	280.6	29.7	1061	5	CR407462	Gallus ga
37	275.8	29.2	2132	10	BC083590	BC083590 Rattus no
38	274	29.0	1179	6	CQ588387	Sequence
39	272.6	28.8	1518	10	AB029067	AB029067 Mus muscu
40	272.6	28.8	3988	10	AB029066	AB029066 Mus muscu
41	272.6	28.8	4022	10	AB029065	AB029065 Mus muscu
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43	234.8	24.8	823	5	BX932070	BX932070 Gallus ga
44	227.4	24.1	1513	9	AF130372	AF130372 Homo sapi
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ALIGNMENTS

RESULT 1	AR492170	Sequence 11 from patent US 6716616.	945 bp	DNA	linear	PAT 15-MAY-2004
LOCUS	AR492170					
DEFINITION	Sequence 11 from patent US 6716616.					
ACCESSION	AR492170					
VERSION	AR492170.1	GI:47260680				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 945)					
AUTHORS	Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B. and Sands,A.T.					
TITLE	Human kinase proteins and polynucleotides encoding the same					
JOURNAL	Patent: US 6716616-A 11 06-APR-2004;					
FEATURES	Location/Qualifiers					
source	1..945					
	/organism="unknown"					
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ORIGIN	Query Match	100.0%;	Score 945;	DB 6;	Length 945;
	Best Local Similarity	100.0%;	Pred. No. 1.7e-205;		
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Qy	1	ATGGAAGAATGATGAAAAATTTAGTACGACTGGAGAGGGTCTTATCGGGTTGTTATTTCAA	60		
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Db	61	TGAGAAACAAAACCTCTGGACAAGTAGTAGCTGTTAAAAAATTTGGGAATCTGAAGAT	120		
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Db	121	GATCCTGTTCTTGAAGAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAACAT	180		
Qy	181	CCAAATCTTGGAACCTCATCGAGGTGTTTCAGGAGAAAAAGGAAAAATGCAATTTATTTT	240		
Db	181	CCAAATCTTGGAACCTCATCGAGGTGTTTCAGGAGAAAAAGGAAAAATGCAATTTATTTT	240		
Qy	241	GATACTGTGATCATACACTTTTAAATGAGCTGGAAGAAACCCAAATGGAGTTGCTGAT	300		

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 Db 841 CTGGAGAGCTCTACTTGTGATTTCTTTTCAAGAGGCCCAATTAAGAAAGCAAGTAAAT 900
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 Db 901 GAAGGAAGAAACAGAGAGCGCAACAGTACTTCCGCTCAAAAGT 945

RESULT 2
 AX107722 945 bp DNA linear PAT 30-APR-2001
 LOCUS Sequence 11 from Patent WO0123579.
 DEFINITION AX107722
 ACCESSION AX107722
 VERSION AX107722.1 GI:13923202
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and
 Sands, A.T.
 Human kinase proteins and polynucleotides encoding the same
 Patent: WO 0123579-A 11 05-APR-2001;
 JOURNAL Lexicon Genetics Incorporated (US)
 FEATURES
 source Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 945; DB 6; Length 945;

Best Local Similarity 100.0%; Pred. No. 1.7e-205;
 Matches 945; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 61 TGCAGAAACAAAACCTCTGGAACAAGTAGTAGCTCTTAAATAAATTTGTTGGAATCTGAGAT 120
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 Db 121 GATCCTGTTGTTAAGAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTAAGACAT 180
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 Qy 241 GAATCTGTGATCATACATCTTTTAAATGAGCTGGAAGAAACCAATGGAGTTGCTGAT 300
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 Db 301 GAGTGTATCAAAAGCGTATTATGCGAAACACTTCAAGCTCTTAAATTTCTGTATATACAT 360
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 Db 421 AAGATTGTGACTTGGGTTTGCACAAATCTGATTTCCAGGAGATGCCCTACACCGATTAT 480
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 Db 901 GAAGGAAGAAACAGAGAGCGCAACAGTACTTCCGCTCAAAAGT 945

RESULT 3

AX492167

LOCUS

DEFINITION

ACCESSION

AX492167
 Sequence 5 from patent US 6716616.
 linear PAT 15-MAY-2004
 AR492167

VERSION AR492167.1 GI:47260677
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 972)
AUTHORS Donoho, G., Turner, C.A. Jr., Nehls, M.C., Friedrich, G., Zambrowicz, B. and Sands, A.T.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: US 6716616-A 5 06-APR-2004;
FEATURES
source
1. 972
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 98.3%; Score 929; DB 6; Length 972;
Best Local Similarity 100.0%; Pred. No. 7.6e-202;
Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 901 GAAGGAAGAAACAGAGACGCCCAACAGGT 929

RESULT 4
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LOCUS AX107716 972 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 5 from Patent WO0123579.
ACCESSION AX107716
VERSION AX107716.1 GI:13923199
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Donoho, G., Turner, C.A., Nehls, M., Friedrich, G., Zambrowicz, B. and Sands, A.T.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: WO 0123579-A 5 05-APR-2001;
Lexicon Genetics Incorporated (US)
FEATURES
source
1. 972
/organism="Homo sapiens"
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ORIGIN
Query Match 98.3%; Score 929; DB 6; Length 972;
Best Local Similarity 100.0%; Pred. No. 7.6e-202;
Matches 929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGAAAGTATGAAATTAAGCTTAAGACTGGAGAGGGTCTTATGGGGTTGTATTCAA 60
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 Db 901 GAAGGAAGAAACAGAGAGCCCAACAGGT 929

RESULT 5
 AX746179
 LOCUS AX746179 1790 bp DNA linear PAT 13-JUN-2003
 DEFINITION Sequence 30 from Patent WO0208399.
 ACCESSION AX746179
 VERSION AX746179.1 GI:31746165

KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1
 AUTHORS Yue, H., Khan, F.A., Gururajan, R., Hafalia, A.J., Chawla, N.K.,
 Arvizu, C.S., Ramkumar, J., Gandhi, A.R., Policky, J.L., Baughn, M.R.,
 Tribouley, C.M., Bandman, O., Nguyen, D.B., Lu, Y., Burford, N., Lal, P.,
 Ding, L., Yao, M.G., Elliott, V.S., Recipon, S.A., Kearney, L., Lu, D.A.,
 Greenwald, S.R., Tang, Y.T., Xu, Y., Walsh, R.T., Gietzen, K.J.,
 Yang, J., Jackson, J.L. and Thornton, M.
 Human kinases
 TITLE Patent: WO 0208399-A 30 31-JAN-2002;
 JOURNAL Incyte Genomics, Inc. (US); Thornton, Michael (US)
 FEATURES Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /note="Incyte ID No: 1698381CB1"

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 Best Local Similarity 100.0%; Pred. No. 2e-201;
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 Db 239 ATGGAAAGCTATGAAATTTAGCTAGCTGGAAGAGGCTTTATCGGGTGTGATTCAAA 298
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Qy 121 GATCCTGTTGTTAAGAAATAGCACTAAGAGAAATACCTATGTTGAAGCAATTAARACAT 180
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 Db 1139 GAAGGAAGAAACAGAGAGCCCAACAG 1165

RESULT 6
 AX698820
 LOCUS AX698820 1678 bp DNA linear PAT 02-APR-2003
 DEFINITION Sequence 6 from Patent WO02079473.
 ACCESSION AX698820
 VERSION AX698820.1 GI:29499608
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1
 AUTHORS Panzer, S.R., Lincoln, S.E., Altus, C.M., Dufour, G.E., Hillman, J.L.,
 Jones, A.L., Dam, T.C., Liu, T.F., Harris, B., Flores, V., Daffo, A.,
 Marwaha, R., Chen, A.J., Chang, S.C., Gerstin, J.E., Peralta, C.H.,
 David, M.H. and Lewis, S.A.

TITLE Molecules for diagnostics and therapeutics

JOURNAL Patent: WO 02079473-A 6 10-OCT-2002;

Incyte Genomics, Inc. (US)

FEATURES Location/Qualifiers

source

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/organism="Homo sapiens"

/mol_type="unassigned DNA"

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/note="Incyte ID No: LI:058298.1:2001JAN12"

ORIGIN

Query Match 91.9%; Score 868.8; DB 6; Length 1678;

Best Local Similarity 99.2%; Pred. No. 4.1e-198;

Matches 925; Conservative 0; Mismatches 2; Indels 5; Gaps 5;

Qy 1 ATGGAAGATGATAAATAGCTAAGACTGAGAGGGCTCTATGGGTTGTATCAAA 60
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 Qy 61 TGCAGA-AACAAACCTCTGACAACTAGTAGTGTGTTAAAAATTTGTGGAATCTGAAGA 119
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 Db 251 TGATCCTGTTTAAAGAAATAGCACTAAGAGAAATAGCTA-TCTTGAAGCAATTAAC 310
 Qy 179 ATCCAAATCTTGTAACCTCATCAGAGTGTTCAGAGAGAAAGGAAATGCAATTTAGTTT 238
 Db 311 ATCCAAATCTTGTAACCTCATCAGAGTGTTCAGAGAGAAAGGAAATGCAATTTAGTTT 370
 Qy 239 TTGAATCTGTGATACATACCTTTAAATAGAGTGGAAAGAAACCCAAATGAGTGTGCTG 298
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 Db 431 ATGAGTGTCAAAAGGGTATTATGGCAACACTTCAAGCTCTTAATTTCTGTCAATATAC 490
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 Qy 479 ATGTAGCTA-CGAGATGTCAGGAGCT-CCTGAACTTCTTGGGAGATCT-CAGTATG 535
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 Qy 536 GTTCTTCAGTCGATATATGGGCTATTGGTGTGTTTTTGGCAGAGCTCTGACAGGCCAGC 595
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Qy 896 GTAATGAAG 927

Db 1031 GTAATGAAG 1062

RESULT 7

AX166534

LOCUS

DEFINITION Sequence 25 from Patent WO0138503. 1083 bp DNA linear PAT 22-JUN-2001

AX166534

AX166534.1 GI:14546879

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

AUTHORS

Flanagan, G.D., Whyte, D., Manning, G.S., Sudarsanam, S.S., Martinez, R.,

Flanagan, P. and Clary, D.S.

Novel human protein kinases and protein kinase-like enzymes

TITLE Patent: WO 0138503-A 25 31-MAY-2001;

JOURNAL Sugeh, Inc. (US)

FEATURES

source

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/db_xref="taxon:9606"

ORIGIN

Query Match 91.3%; Score 863; DB 6; Length 1083;

Best Local Similarity 94.5%; Pred. No. 9.2e-187;

Matches 927; Conservative 0; Mismatches 0; Indels 54; Gaps 1;

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 Qy 181 CCAATCTTGTGAACCTCATCGAGTGTTCAGAGAGAAAGGAAATGCAATTTAGTTTTT 240
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 Qy 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAGAGAAACCCAAATGGAGTTGCTGAT 300
 Db 241 GAATACCTGTGATCATACACTTTTAAATGAGCTGGAGAGAAACCCAAATGGAGTTGCTGAT 300
 Qy 301 GGAGTGAATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTCAATATAC 360
 Db 301 GGAGTGAATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTCAATATAC 360
 Qy 361 AACTGTATTACAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATATC 420
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 Qy 455 -----TTCCAGGAGATGCTACACCGATTATGTAGCT 486
 Db 481 TTACCTGATCTGATTGATGCAATTTGCAGTTCCAGAGATGCTACACCGATTATGTAGCT 540
 Qy 487 ACAGATGTTACCGAGCTCTCGAATCTTCTGTGGAGATACCTCAGTATGTTCTTCAGTC 546

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Db      601  GATATATGGGCTATTTGGTTGTGTTTGTGAGAGCTCTGACAGCCAGCCACTGTGGCT 660
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Qy      667  AGACATCAATCAATCTTTAAAGTAAGGTTTTCATGGGATCAGTATACCTGAGCCA 726
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Qy      787  ATGAAGGGGTGTCTGAAGATGAATCAGATGACAGATTAACCTGTTCCTGAG 846
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Qy      847  AGCTCCTACTTTGATTTCTTTCAAGAGGCCCAATTAAGAAAAGACGTAATGAAGGA 906
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Qy      907  AGAACAAGAGCGCAACAG 927
Db      961  AGAACAAGAGCGCAACAG 981

RESULT 8
AR492169
LOCUS      1041 bp
DEFINITION Sequence 9 from patent US 6716616.
ACCESSION AR492169
VERSION    AR492169.1 GI:47260679
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 1041)
AUTHORS    Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B.
            and Sands,A.T.
TITLE      Human kinase proteins and polynucleotides encoding the same
JOURNAL    Patent: US 6716616-A 9 06-APR-2004;
FEATURES   Location/Qualifiers
            1..1041
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            /mol_type="genomic DNA"

ORIGIN
Query Match      88.8%; Score 839; DB 6; Length 1041;
Best Local Similarity 90.8%; Pred. No. 2.8e-181;
Matches 945; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

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Db      61  TCGAAGAACAAACCTCTGCAAGTAGTAGCTGTTTAAAGAAATTTGTGGAATCTGAAGAT 120
Qy      121  GATCCTCTGTTTGAAGAAATAGCACTAAGAAATAGTATGTTGAAGCAATTAAGCAAT 180
Db      121  GATCCTCTGTTTGAAGAAATAGCACTAAGAAATAGTATGTTGAAGCAATTAAGCAAT 180
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Db      181  CCAATCTTGTGAACCTCATCGAGGTGTTTCAGGAGAAAAGGAAATGCAATTAGTTTTT 240
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Db      301  GGAGTGATCAAAAGCGTATTATGCAAAACACTTCAAGCTCTTAATTTCTGTATATACAT 360
Qy      361  AACTGTATTCAAGAGATATAAAACCTGAAATATTTCTAATACTAAGCAAGGAATATC 420
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Db      421  AAGATTTGTGACTTCGGGTTTGCACAAATTTCTGATTCAGAGATGCTTACCGATTAT 480
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Db      961  TTTCAAGAGGCCCAATTAAGAAAAGCAAGTAAATGAAGGAAGAAAACAGAGAGCCCAA 1020
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Db      1021  CAGGTACTTTCGGCTCAAAAAGT 1041

RESULT 9
AXI07720
LOCUS      1041 bp
DEFINITION Sequence 9 from Patent WO0123579.
ACCESSION AXI07720
VERSION    AXI07720.1 GI:13923201
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1
AUTHORS    Donoho,G., Turner,C.A., Nehls,M., Friedrich,G., Zambrowicz,B. and
            Sands,A.T.
TITLE      Human kinase proteins and polynucleotides encoding the same
JOURNAL    Patent: WO 0123579-A 9 05-APR-2001;
            Lexicon Genetics Incorporated (US)

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Best Local Similarity 90.8%; Pred. No. 2.8e-181;
Matches 945; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

Qy 1 ATGGAAGATGATAAAATAGCTAAGACTGAGAGAGGCTTATGGGTTGTATTCAAA 60
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Db 841 GAGGAAAGTTCTCAGATGTTTCATCTGTGGCTCTGAACTTCTGAAGGGGTGTCTGAAG 900
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Db 1021 CAGGTACTTCCGCTCAAAAGT 1041

RESULT 10
AR492166
LOCUS AR492166 1068 bp DNA linear PAT 15-MAY-2004
DEFINITION Sequence 3 from patent US 6716616.
ACCESSION AR492166
VERSION AR492166.1 GI:47260676
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1068)
AUTHORS Donoho,G., Turner,C.A. Jr., Nehls,M.C., Friedrich,G., Zambrowicz,B.
and Sands,A.T.
TITLE Human kinase proteins and polynucleotides encoding the same
JOURNAL Patent: US 6716616-A 3 06-APR-2004;
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Best Local Similarity 90.6%; Pred. No. 1.3e-177;
Matches 929; Conservative 0; Mismatches 0; Indels 96; Gaps 1;

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Qy 805 ATGATCCAGATGACATTAACCTGTTCCAACTCTCTGGAGAGCTCTTACTTGTATCT 864

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REFERENCE 1
AUTHORS Kapeller-Libermann, R.
TITLE 14257, protein kinase molecules and uses therefor
JOURNAL Patent: WO 0179488-A 3 25-OCT-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
source 1..687
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ORIGIN
Query Match 68.5%; Score 647; DB 6; Length 687;
Best Local Similarity 99.2%; Pred. No. 2.3e-137;
Matches 650; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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RESULT 13
AX286067
LOCUS AX286067 882 bp DNA linear PAT 20-NOV-2001
DEFINITION Sequence 1 from Patent WO0179488.
ACCESSION AX286067
VERSION AX286067.1 GI:17045993
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1
AUTHORS Kapeller-Libermann, R.
TITLE 14257, protein kinase molecules and uses therefor
JOURNAL Patent: WO 0179488-A 1 25-OCT-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES Location/Qualifiers
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ORIGIN
Query Match 68.5%; Score 647; DB 6; Length 882;
Best Local Similarity 99.2%; Pred. No. 2.2e-137;
Matches 650; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 1 ATGGAAAGATGAAAAATTAGCTAAGACTGGAGAAGGCTTATGGGTTGTATTCAAA 60
Db 129 ATGGAAAGATGAAAAATTAGCTAAGACTGGAGAAGGCTTATGGGTTGTATTCAAA 188
Qy 61 TGCAGAAACAAAACCTCTGGACAAGTAGTAGCTGTAAAAAAATTTGCGAATCTGAAGAT 120
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Qy 121 GATCCTGTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTTAAACAT 180
Db 249 GATCCTATTTGTTAAGAAAAATAGCACTAAGAGAAATACGTATGTTGAAGCAATTTAAACAT 308
Qy 181 CCAATCTGTGAACCTCATCGAGTCTTCAGGAGAAAGGAAATGCAATTTAGTTTTT 240
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Db 369 GAATCTGTGATCATGCACTTTTAAATGAGCTGGAAGAAACCCAAATGAGTTGCTGAT 428
Qy 301 GGAGTGATCAAAAGCGTATTATGCAAACTTCAAGCTCTTAAATTTCTGTCAATACAT 360
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Qy 361 AACTGTATTCACAGAGATATAAACCCTGAAATATTTCTAATACTAAGCAAGGAATATC 420
Db 489 AACTGTATTCACAGAGATATAAACCCTGAAATATTTCTAATACTAAGCAAGGAATATC 548
Qy 421 AAGATTGTGACTTCGGGTTTGCAAAATCTGATTCAGGAGATGCTACACCGATTAT 480
Db 549 AAGATTGTGACTTCGGGTTTGCAAAATCTGATTCAGGAGATGCTACACCGATTAT 608
Qy 481 GTAGTACGAGATGGTACCGAGCTCCTGAACTTCTTGTGGAGATATCTCAGTATGGTTCT 540
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Qy 541 TCAGTCATATATGGGCTATTTGTTGTTTTCAGAGCTCCTGACAGGCGCCACTG 600
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Db	778	AAGGGCCCGCAGCAATCAACTGCT	801

Search completed: April 21, 2005, 23:37:14
Job time : 4113.75 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 01:23:15 ; Search time 87.5529 Seconds
(without alignments)
1391.497 Million cell updates/sec

Title: US-10-766-691-12
Perfect score: 1662
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
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2: Geneseqp1990s:*
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4: Geneseqp2001s:*
5: Geneseqp2002s:*
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7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1662	100.0	315	4 AAE00495	Aae00495 Human kin
2	1639	98.6	342	5 AAE19152	Aae19152 Human kin
3	1638	98.6	324	4 AAE00492	Aae00492 Human kin
4	1636	98.4	347	4 AAE00494	Aae00494 Human kin
5	1619	97.4	360	4 AAU03525	Aau03525 Human pro
6	1612	97.0	356	4 AAE00491	Aae00491 Human kin
7	1296.5	78.0	296	4 AAB65643	Abp62954 Human pro
8	1296.5	78.0	296	8 ADI29250	Adi29250 Mouse MAR
9	1188.5	71.5	358	5 ABP62954	Abp62954 Human pol
10	1183.5	71.2	358	8 ADO01538	Ado01538 Human cyc
11	1149	69.1	247	4 AAB65642	Abp62954 Human pro
12	1149	69.1	247	8 ADI29249	Adi29249 Human MAR
13	1140	68.6	228	5 AAG78547	Agg78547 Human kin
14	1027.5	61.8	392	4 ABB63118	Abb63118 Drosophil
15	967.5	58.2	566	3 AAY90724	Aay90724 Rabbit KK
16	948	57.0	197	6 ABU11689	Abu11689 Human MDD
17	941.5	56.6	493	7 ADC77659	Adc77659 Human 162
18	941.5	56.6	493	8 ADQ89156	Adq89156 Human uro
19	937.5	56.4	362	6 ABP96087	Abp96087 Human pro
20	791	47.6	183	8 ADI40875	Adi40875 Human kin
21	791	47.6	187	4 AAE00490	Aae00490 Human kin
22	791	47.6	198	4 AAE00493	Aae00493 Human kin
23	791	47.6	205	8 ADK71868	Adk71868 Human kin
24	784.5	47.2	455	3 AAY70126	Aay70126 Human los
25	784.5	47.2	455	8 ADI57233	Adi57233 NKIAMRE d

26	784.5	47.2	455	8 ADI57214	Adi57214 Human NKI
27	784.5	47.2	455	8 ADI57236	Adi57236 CDK3 domi
28	784.5	47.2	591	4 AAU03524	Aau03524 Human pro
29	763.5	45.9	457	3 AAY70125	Aay70125 Rat lost
30	763.5	45.9	505	3 AAY70124	Aay70124 Rat lost
31	725	43.6	562	8 ABM83922	Abm83922 Human dia
32	712.5	42.9	154	6 ABU05290	Abu05290 Human dia
33	656	39.5	534	4 AAB65645	Abp62954 Human pro
34	656	39.5	534	8 ADI29252	Adi29252 Human MAR
35	581	35.0	305	7 ADI29252	Adi29252 Human kin
36	581	35.0	305	7 ADJ68738	Adj68738 Human hea
37	581	35.0	305	8 ADI57200	Adi57200 Human CDK
38	581	35.0	305	8 ADI57237	Adi57237 CDK3 domi
39	581	35.0	333	4 AAM39276	Aam39276 Human pol
40	574	34.3	352	4 AAM41062	Aam41062 Human pol
41	570	34.3	298	2 AAW95689	Aaw95689 Homo sapi
42	570	34.3	544	2 AAW85028	Aaw85028 CDK2-gree
43	570	34.3	544	2 AAW85029	Aaw85029 Green flu
44	569	34.2	224	4 ABG06142	Abg06142 Novel hum
45	569	34.2	298	7 ADD21390	Add21390 Human cyc

ALIGNMENTS

RESULT 1
AAE00495
ID AAE00495 standard; protein; 315 AA.

XX AC AAE00495;
XX 19-JUN-2001 (first entry)
XX Human kinase #6.
XX Human, kinase; gene therapy; bioreactor; mental disorder;
XX Biological disorder.
XX Homo sapiens.
XX WO200123579-A1.
XX 05-APR-2001.
XX 27-SEP-2000; 2000WO-US026621.
XX 28-SEP-1999; 99US-0156511P.
XX (LEXI-) LEXICON GENETICS INC.
XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
XX Sands AT;
XX WPI; 2001-266166/27.
XX N-PSDB; AAD03817.

New isolated human kinase polynucleotide useful for generating antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases.
Claim 3; Page 33-34; 38pp; English.
The present sequence is novel human protein (NHP) known as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical

disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression

Sequence 315 AA;

Query Match 100.0%; Score 1662; DB 4; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.5e-168;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db |||||

QY 61 PNLVNLIEVFRKRKRWHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCCHI 120
Db |||||

QY 121 NCIHRIKPNILITKQGIKIICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDQYGS 180
Db |||||

QY 181 SVDIWAIGCVFAELLTGQPLWPKSGSDVDOLYLIIRTLGKLIIPRHOSIFKSNFGFHGISIP 240
Db |||||

QY 241 EPDMETLEEKFSVHPVVALNFMKGLKWNPDRLTCSQLLESSYFDSFQEAQIKRKARN 300
Db |||||

QY 301 EGRNRRRQVPLKS 315
Db |||||

RESULT 2

AAE19152

ID AAE19152 standard; protein; 342 AA.

XX AC AAE19152;

XX DT 21-MAY-2002 (first entry)

XX DE Human kinase polypeptide (PKIN-10).

XX KW Human; kinase polypeptide; PKIN-10; gene therapy; Addison's disease; leukaemia; immune disorder; lymphoma; melanoma; developmental disorder; acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension; asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis; cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer; cholestasis; cardiast; cardiovascular disorder; Niemann-Pick's disease; lipid disorder; fatty liver; Gaucher's disease; myocardial infarction; drug screening; transgenic animal; antiinflammatory; hepatotropic; hypotensive; anti-HIV; enzyme.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
XX Domain 4..286
XX FT /note= "Eukaryotic protein kinase domain"

XX PN WO200208399-A2.

XX PD 31-JAN-2002.

XX PF 20-JUL-2001; 2001WO-US023092.

XX

PR 21-JUL-2000; 2000US-0220038P.
PR 28-JUL-2000; 2000US-0222112P.
PR 04-AUG-2000; 2000US-0222831P.
PR 11-AUG-2000; 2000US-0224729P.
XX (INCY-) INCYTE GENOMICS INC.
PA (THOR/) THORNTON M.
XX Thornton M, Yue H, Khan FA, Gururajan R, Hafalia AJA, Wallia NK;
PI Patterson C, Ramkumar J, Gandhi AR, Policky JL, Baughn MR;
PI Tribouley CM, Bandman O, Nguyen DB, Lu Y, Burford N, Lal P, Ding L;
PI Yao MG, Elliott VS, Recipon SA, Kearney L, Lu DAM, Greenwald SR;
PI Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL;
XX WPI; 2002-206083/26.
DR N-PSDB; AAD30557.
XX New human kinase polypeptide, useful in diagnosis, prevention and treatment of cancer, immune disorder, growth and developmental disorder, cardiovascular disorder and lipid disorder.

Claim 1; Page 147-148; 196pp; English.

The present invention relates to an isolated human kinase polypeptide (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is useful for diagnosing, treating and preventing cancer (e.g., leukaemia, lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's disease, rheumatoid arthritis), a growth and developmental disorder (e.g. bursitis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial infarction), and a lipid disorder (e.g., fatty liver, cholestasis, Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of drug screening techniques and to analyse the proteome of a tissue or cell type. PKIN is useful for creating knockin humanised animals or transgenic animals to model human diseases, in somatic or germline gene therapy, to generate a transcript image of a tissue or cell type, for detecting differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier or affected individuals, and as hybridisation probes for mapping naturally occurring genomic sequences. PKIN is useful in southern or northern analysis, dot blot or other membrane-based technologies, in PCR technologies, in dipstick, pin, multiformat enzyme linked immunosorbent (ELISA)-like assays and in microarrays utilising fluids or tissues from patients to detect altered PKIN expression. The present sequence is human PKIN-10

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Query Match 98.6%; Score 1639; DB 5; Length 342;
Best Local Similarity 99.0%; Pred. No. 4.9e-166;
Matches 312; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

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QY 1 MEKYEKLATGEGSYGVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
Db |||||

QY 61 PNLVNLIEVFRKRKRWHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCCHI 120
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QY 121 NCIHRIKPNILITKQGIKIICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDQYGS 180
Db |||||

QY 181 SVDIWAIGCVFAELLTGQPLWPKSGSDVDOLYLIIRTLGKLIIPRHOSIFKSNFGFHGISIP 240
Db |||||

QY 241 EPDMETLEEKFSVHPVVALNFMKGLKWNPDRLTCSQLLESSYFDSFQEAQIKRKARN 300
Db |||||

QY 301 EGRNRRRQ--QVLP 313

Db 301 EGRNRQQQLLPL 315
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AAE00492 standard; protein; 324 AA.
XX AAE00492;
AC AAE00492;
XX 19-JUN-2001 (first entry)
DT Human kinase #3.
XX Human; kinase; gene therapy; bioreactor; mental disorder;
XX biological disorder.
KW Homo sapiens.
XX
XX WO200123579-A1.
XX
XX 05-APR-2001.
XX
XX 27-SEP-2000; 2000WO-US026621.
XX
XX 28-SEP-1999; 99US-0156511P.
XX
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
PI Sands AT;
PI
XX WPI; 2001-266166/27.
DR N-PSDB; AAD03814.
XX
XX New isolated human kinase polynucleotide useful for generating
PT antibodies, as reagents in diagnostic assays and for screening for
PT compounds useful for treating mental, biological or medical diseases.
XX
XX Disclosure; Page 30; 38pp; English.
XX
XX The present sequence is novel human protein (NHP) known as human kinase.
CC The human kinases share structural similarity with animal kinases, more
CC particularly serine or threonine protein kinases. Human kinase cDNA is
CC useful for the detection of mutant human kinase for the diagnosis of
CC disease, and also as a therapeutic. It is useful for screening drugs
CC effective in the treatment of symptomatic or phenotypic manifestations
CC perturbing the normal function of NHP in the body. The NHP nucleotide
CC sequences are useful for generation of antibodies, as reagents in
CC diagnostic assays, for the identification of other cellular gene products
CC related to human kinases, and as reagents in assays for screening
CC compounds that are useful for treating mental, biological or medical
CC disorders. NHP oligonucleotides are used as probes. The labelled NHP
CC probes are useful for screening human genomic library for identifying
CC polymorphisms and as primers in amplification assays to detect mutations
CC within the exons, introns and splice sites that can be used in
CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP
CC products are used to genetically engineer cells in vivo that functions as
CC bioreactors in the body delivering a continuous supply of NHP to the
CC body. Nucleotide constructs encoding functional NHPs are used in gene
CC therapy for the modulation of NHP expression
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SQ Sequence 324 AA;
Query Match 98.6%; Score 1638; DB 4; Length 324;
Best Local Similarity 100.0%; Pred. No. 5.8e-166; Mismatches 0; Gaps 0;
Matches 310; Conservative 0; Indels 0;
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Db 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKQLKH 60
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Db 61 PNLVNLIEVFRKRKMHLEVFYCDHTLLNELRPNPGVADGVIKSVLWQTLQALNFCIH 120
Qy 121 NCIHRIKPENILITKQGIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDQYGS 180
Db 121 NCIHRIKPENILITKQGIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDQYGS 180
Qy 181 SVDIWAIGCVFAELLTGOPLWPGKSDVDOLYLIIRTGLKLIPIHQSTPKSNGFFHGISIP 240
Db 181 SVDIWAIGCVFAELLTGOPLWPGKSDVDOLYLIIRTGLKLIPIHQSTPKSNGFFHGISIP 240
Qy 241 EPEDMETLEKFSVDHPVALNFMKGLKMPDDRLTCSQLLESYFDSFQEAQIKRKARN 300
Db 241 EPEDMETLEKFSVDHPVALNFMKGLKMPDDRLTCSQLLESYFDSFQEAQIKRKARN 300
Qy 301 EGRNRREQV 310
Db 301 EGRNRREQV 310
RESULT 4
AAE00494
ID AAE00494 standard; protein; 347 AA.
XX
XX AAE00494;
XX 19-JUN-2001 (first entry)
DT Human kinase #5.
XX Human; kinase; gene therapy; bioreactor; mental disorder;
KW biological disorder.
XX
XX Homo sapiens.
XX
XX WO200123579-A1.
XX
XX 05-APR-2001.
XX
XX 27-SEP-2000; 2000WO-US026621.
XX
XX 28-SEP-1999; 99US-0156511P.
XX (LEXI-) LEXICON GENETICS INC.
XX
XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
PI Sands AT;
PI
XX WPI; 2001-266166/27.
DR N-PSDB; AAD03816.
XX
XX New isolated human kinase polynucleotide useful for generating
PT antibodies, as reagents in diagnostic assays and for screening for
PT compounds useful for treating mental, biological or medical diseases.
XX
XX Claim 2; Page 32-33; 38pp; English.
XX
XX The present sequence is novel human protein (NHP) known as human kinase.
CC The human kinases share structural similarity with animal kinases, more
CC particularly serine or threonine protein kinases. Human kinase cDNA is
CC useful for the detection of mutant human kinase for the diagnosis of
CC disease, and also as a therapeutic. It is useful for screening drugs
CC effective in the treatment of symptomatic or phenotypic manifestations
CC perturbing the normal function of NHP in the body. The NHP nucleotide
CC sequences are useful for generation of antibodies, as reagents in
CC diagnostic assays, for the identification of other cellular gene products
CC related to human kinases, and as reagents in assays for screening
CC compounds that are useful for treating mental, biological or medical
CC disorders. NHP oligonucleotides are used as probes. The labelled NHP
CC probes are useful for screening human genomic library for identifying
CC polymorphisms and as primers in amplification assays to detect mutations
CC within the exons, introns and splice sites that can be used in
CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP

CC products are used to genetically engineer cells in vivo that functions as
 CC bio-reactors in the body delivering a continuous supply of NHP to the
 CC body. Nucleotide constructs encoding functional NHPs are used in gene
 CC therapy for the modulation of NHP expression
 XX
 SQ Sequence 347 AA;

Query Match 98.4%; Score 1636; DB 4; Length 347;
 Best Local Similarity 90.8%; Pred. No. 1e-165; Mismatches 0; Indels 32; Gaps 1;
 Matches 315; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
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 DB 1 MEKYELAKTGGSGYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKQLKH 60
 QY 61 PNLVNLIEVFRKRKQHLVFEYCDHTLLNELERNPNVADGVKSVLWQTLQALNFCCHI 120
 DB 61 PNLVNLIEVFRKRKQHLVFEYCDHTLLNELERNPNVADGVKSVLWQTLQALNFCCHI 120
 QY 121 NCIRDIKPNILITKQGIKICDFGFAQLIPGDAYTDYVATWYRAPELLVGDQVGS 180
 DB 121 NCIRDIKPNILITKQGIKICDFGFAQLIPGDAYTDYVATWYRAPELLVGDQVGS 180
 QY 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIINTL----- 217
 DB 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIINTLVEGFRHVDQAAGLELLTSSDPPA 240
 QY 218 -----GKLI PRHQSIKSNFGFHGISIPEPEMETLEKSDVHPVALNFMKGLK 268
 DB 241 VASQAGITGKLI PRHQSIKSNFGFHGISIPEPEMETLEKSDVHPVALNFMKGLK 300
 QY 269 MNPDDLTCSSQLLESSYFDSFQEAQIKRKARNEGRRRRQVPLKS 315
 DB 301 MNPDDLTCSSQLLESSYFDSFQEAQIKRKARNEGRRRRQVPLKS 347

RESULT 5
 ID AAU03525 standard; protein; 360 AA.
 XX
 AC AAU03525;
 DT 12-SEP-2001 (first entry)
 XX Human protein kinase #25.
 DE Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
 KW metabolic disorder; immune related disease; neurological disorder;
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;
 XX reproductve disorder.

XX Homo sapiens.
 OS
 XX WO200138503-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 22-NOV-2000; 2000WO-US032085.
 XX
 PR 24-NOV-1999; 99US-0167482P.
 XX
 PA (SUGEN-) SUGEN INC.
 XX
 PI Plowman CD, Whyte D, Manning G, Sudarsanam S, Martinez R;
 PI Flanagan P, Clary D;
 XX
 DR WPI; 2001-343950/36.
 DR N-PSDB; AAS06725.
 XX
 PT Nucleic acids encoding human kinase polypeptides, useful for preventing
 PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
 PT neuronal-associated diseases, and microbial infections.
 XX

PS Claim 7; Fig 2; 433pp; English.

XX AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel
 CC protein kinases have been identified as members of the tyrosine or
 CC serine/threonine kinase (PTK and STK) families. The polynucleotides
 CC encoding protein kinases and the polypeptides may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate kinase expression. For example, they may be used to treat
 CC cancers (especially cancers of haematopoietic origin), cardiovascular
 CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
 CC immune related diseases (e.g. rheumatoid arthritis), neurological
 CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
 CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
 CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
 CC Additionally, polynucleotides encoding protein kinases may be used for
 CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
 CC polypeptides may be used as antigens in the production of antibodies
 CC against the protein kinases and in assays to identify modulators of
 CC protein kinase expression and activity
 XX

SQ Sequence 360 AA;

Query Match 97.4%; Score 1619; DB 4; Length 360;
 Best Local Similarity 93.4%; Pred. No. 7.3e-164; Mismatches 0; Indels 20; Gaps 2;
 Matches 311; Conservative 2; Mismatches 0; Indels 20; Gaps 2;
 QY 1 MEKYELAKTGGSGYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKQLKH 60
 DB 1 MEKYELAKTGGSGYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKQLKH 60
 QY 61 PNLVNLIEVFRKRKQHLVFEYCDHTLLNELERNPNVADGVKSVLWQTLQALNFCCHI 120
 DB 61 PNLVNLIEVFRKRKQHLVFEYCDHTLLNELERNPNVADGVKSVLWQTLQALNFCCHI 120
 QY 121 NCIRDIKPNILITKQGIKICDFGFAQL-----IPGDAYTDYVA 162
 DB 121 NCIRDIKPNILITKQGIKICDFGFAQLNSHVRIDLPDIDAFVPGDAYTDYVA 180
 QY 163 TRWYRAPELLVGDQVGSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIINTLTKLIP 222
 DB 181 TRWYRAPELLVGDQVGSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIINTLTKLIP 240
 QY 223 RHQSIKSNFGFHGISIPEPEMETLEKFSVHPVALNFMKGLKMNPDRLTCSQLLE 282
 DB 241 RHQSIKSNFGFHGISIPEPEMETLEKFSVHPVALNFMKGLKMNPDRLTCSQLLE 300
 QY 283 SSYFDSFQEAQIKRKARNEGRRRRQ--QVPL 313
 DB 301 SSYFDSFQEAQIKRKARNEGRRRRQ--QVPL 333

RESULT 6
 ID AAU00491 standard; protein; 356 AA.
 XX
 AC AAU00491;
 DT 19-JUN-2001 (first entry)
 XX Human kinase #2.
 DE Human; kinase; gene therapy; bioreactor; mental disorder;
 KW biological disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200123579-A1.
 XX
 PD 05-APR-2001.
 XX
 PF 27-SEP-2000; 2000WO-US026621.
 XX
 PR 28-SEP-1999; 99US-0156511P.

XX PA (LEXI-) LEXICON GENETICS INC.
XX PI Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
XX PI Sands AT;
XX DR WPI: 2001-266166/27.
XX DR N-PSDB; AAD03813.
XX PT New isolated human kinase polynucleotide useful for generating
XX PT antibodies, as reagents in diagnostic assays and for screening for
XX PT compounds useful for treating mental, biological or medical diseases.
XX PS Disclosure; Page 28-29; 38pp; English.
XX CC The present sequence is novel human protein (NHP) known as human kinase.
XX CC The human kinases share structural similarity with animal kinases, more
XX CC particularly serine or threonine protein kinases. Human kinase cDNA is
XX CC useful for the detection of mutant human kinase for the diagnosis of
XX CC disease, and also as a therapeutic. It is useful for screening drugs
XX CC effective in the treatment of symptomatic or phenotypic manifestations
XX CC perturbing the normal function of NHP in the body. The NHP nucleotide
XX CC sequences are useful for generation of antibodies, as reagents in
XX CC diagnostic assays, for the identification of other cellular gene products
XX CC related to human kinases, and as reagents in assays for screening
XX CC compounds that are useful for treating mental, biological or medical
XX CC disorders. NHP oligonucleotides are used as probes. The labelled NHP
XX CC probes are useful for screening human genomic library for identifying
XX CC polymorphisms and as primers in amplification assays to detect mutations
XX CC within the exons, introns and splice sites that can be used in
XX CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP
XX CC products are used to genetically engineer cells in vivo that functions as
XX CC bioreactors in the body delivering a continuous supply of NHP to the
XX CC body. Nucleotide constructs encoding functional NHPs are used in gene
XX CC therapy for the modulation of NHP expression
XX SQ Sequence 356 AA;

Query Match 97.0%; Score 1612; DB 4; Length 356;
Best Local Similarity 90.6%; Pred. No. 4e-163;
Matches 310; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
Qy 1 MEKYEKLAKTGEISGVVFKCRNKTSGQVAVKVFVESEDDPVVKIALREIRMLKQKH 60
Db 1 MEKYEKLAKTGEISGVVFKCRNKTSGQVAVKVFVESEDDPVVKIALREIRMLKQKH 60
Qy 61 PNLVNLIEVFRKRKMLVPEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCFH 120
Db 61 PNLVNLIEVFRKRKMLVPEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCFH 120
Qy 121 NCIHRIKPNILITKQGIKICDFGFAQLIPGDAYTDVYVATRYRAPELLVGDYQGS 180
Db 121 NCIHRIKPNILITKQGIKICDFGFAQLIPGDAYTDVYVATRYRAPELLVGDYQGS 180
Qy 181 SVDIWAIGCVPAELLTGQPLWPKSDVDQLYLIIRTL----- 217
Db 181 SVDIWAIGCVPAELLTGQPLWPKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
Qy 218 -----GKLI PRHOSIFKSNGFHGISIPEDMETLEEKPSDVHPVVALNFMKGLK 268
Db 241 VASOSAGITGKLI PRHOSIFKSNGFHGISIPEDMETLEEKPSDVHPVVALNFMKGLK 300
Qy 269 MNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRRQV 310
Db 301 MNPDDRLTCSQLLESSYFDSFQEAQIKRKARNEGRNRRQV 342

RESULT 7
AAB65643
ID AAB65643 standard; protein; 296 AA.
XX AAB65643;
AC AAB65643;
XX

DT 27-MAR-2001 (first entry)
XX DE Novel protein kinase, SEQ ID NO: 170.
XX KW Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
XX KW immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic;
XX KW dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
XX KW immune disorder; cardiovascular disease; neurodegenerative disease;
XX KW cancer; autoimmune disorder; stroke; inflammatory bowel disease;
XX KW inflammatory pelvic disease; multiple sclerosis; psoriasis.
XX OS Mus musculus.
XX FN WO200073469-A2.
XX PD 07-DEC-2000.
XX PF 26-MAY-2000; 2000WO-US014842.
XX PR 28-MAY-1999; 99US-0136503P.
XX PA (SUGE-) SUGEN INC.
XX PI Plowman GD, Martinez R, Whyte D, Sudersanam S;
XX WI; 2001-032161/04.
XX DR N-PSDB; AAF44670.
XX PT Nucleic acids encoding kinase polypeptides, useful for diagnosing and
XX PT treating immune-related diseases and disorders, cardiovascular disease,
XX PT neurodegenerative diseases and/or cancers.
XX PS Claim 10; Fig 1; 310pp; English.
XX CC The present sequence is a novel protein kinase. The novel protein kinases
XX CC and the nucleic acids that encode them may be used in the treatment and
XX CC diagnosis of diseases associated with inappropriate kinase expression
XX CC such as immune-related diseases and disorders, cardiovascular disease,
XX CC neurodegenerative diseases and/or cancers. The nucleic acids and
XX CC complementary sequences may also be used as DNA probes in diagnostic
XX CC assays. The kinase polypeptides may be used as antigens in the production
XX CC of antibodies of kinase expression and activity. Anti-kinase antibodies
XX CC and kinase antagonists may also be used to down regulate kinase
XX CC expression and activity. Diseases related to kinase expression and
XX CC activity include rheumatoid arthritis, atherosclerosis, autoimmune
XX CC disorders, complications of organ transplantation, myocardial infarction,
XX CC immune disorders, cardiomyopathies, strokes, renal failure, oxidative-
XX CC stress related disorders, chronic inflammatory bowel disease, chronic
XX CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
XX CC psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive
XX CC disorders
XX SQ Sequence 296 AA;

Query Match 78.0%; Score 1296.5; DB 4; Length 296;
Best Local Similarity 50.0%; Pred. No. 1.7e-129;
Matches 243; Conservative 19; Mismatches 5; Indels 3; Gaps 2;
Qy 46 KIALREIRMLKQKHNLNLIIEVFRKRKMLVPEYCDHTLLNELRPNPGVADGVK 105
Db 1 KIALREIRMLK-LKHPNLVNLIEVFRKRKMLVPEYCDHTLLNELRPNPGVADGVK 59
Qy 106 VLWQTLQALNFCFHNCIHRIKPNILITKQGIKICDFGFAQLIPGDAYTDVATRW 165
Db 60 VLWQTLQALNFCFHNCIHRIKPNILITKQGIKICDFGFAQLIPGDAYTDVATRW 119
Qy 166 YRAPELLVGDYQGSVDIWAIGCVPAELLTGQPLWPKSDVDQLYLIIRTLKGLI PRHQ 225
Db 120 YRAPELLVGDYQGSVDVWAVGCVFAELLTGQPLWPKSDVDQLYLIIRTLKGLI PRHQ 179
Qy 226 SIPKSNGFHGISIPEDMETLEEKPSDVHPVVALNFMKGLKMPDRLTCSQLLESSY 285
Db 180 SIPRNOFFRGISIPEDMETLEEKPSVQVVALSFMKGLKMPDRLTCAQLLDAS 239

QY 286 FDSFQEAQIKRKARNEGRNRQ--QVLPL 313
 DB 240 FESFQEDQMKRKARSEGRSRQQLLPL 269

RESULT 8
 ID ADI29250
 XX ADI29250 standard; protein; 296 AA.
 AC ADI29250;
 DT 22-APR-2004 (first entry)
 DE Mouse MARK3-associated protein #12.
 KW Mouse; antisense gene therapy; MARK3;
 KW MAP/microtubule affinity-regulating kinase 3; cancer;
 KW Alzheimer's disease; neurodegenerative disorder;
 KW hyperproliferative disorder; cytostatic.
 OS Mus musculus.
 XX
 XX US2003232771-A1.
 PN 18-DEC-2003.
 PD 17-JUN-2002; 2002US-00174319.
 XX 17-JUN-2002; 2002US-00174319.
 PR 17-JUN-2002; 2002US-00174319.
 XX (ISIS-) ISIS PHARM INC.
 PA Ward DT, Freier SM, Dobie KW;
 PI WPI; 2004-052188/05.
 DR N-PSDB; ADI29368.
 XX
 XX New antisense compound targeted to a nucleic acid molecule encoding
 PT microtubule-affinity-regulating kinases (MARK3), useful for modulating
 PT expression of MARK3 or for treating cancer or Alzheimer's disease.
 XX
 PS Disclosure; SEQ ID NO 170; 233pp; English.

CC The invention relates to a compound comprising a sequence comprising 8-80
 CC base pairs (bp) targeted to a nucleic acid encoding MARK3
 CC (MAP/microtubule affinity-regulating kinase 3), that specifically
 CC hybridizes with the nucleic acid encoding MARK3 and inhibits expression
 CC of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a
 CC composition comprising the compound and a carrier or diluent, inhibiting
 CC the expression of MARK3 in cells or tissues, treating an animal having or
 CC suspected of having a disease or condition associated with MARK3 and
 CC screening for an antisense compound. The antisense oligonucleotide is
 CC useful for preparing a composition for treating hyperproliferative
 CC disorder, particularly cancer and neurodegenerative diseases e.g.
 CC Alzheimer's disease. The present sequence is a MARK3 associated protein
 CC included in the figures but not mentioned anywhere else in the
 CC specification.

XX Sequence 296 AA;

Query Match 78.0%; Score 1296.5; DB 8; Length 296;
 Best Local Similarity 90.0%; Pred. No. 1.7e-129;
 Matches 243; Conservative 19; Mismatches 5; Indels 3; Gaps 2;

QY 46 KIALREIRMLKQLKHPNLVNLIEVFRKRKRWHLVFEYCDHTLNELEPNNGVADGVKIS 105
 DB 1 KIALREIRMLK-LKHPNLVNLIEVFRKRKRWHLVFEYCDHTLNELEPNNGVADGVKIS 59

QY 106 VLWQTLQALNFCIHNCIHRDIPENILITKQGIKICDFGFAQIIPGDYDYVATRW 165
 DB 60 VLWQTLQALNFCIHNCIHRDIPENILITKQGIKICDFGFAQIIPGDYDYVATRW 119

QY 166 YRAPELLVGDYQYSSVDIWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTLGKLI PRHQ 225
 DB 120 YRAPELLVGDYQYSSVDVWAVGCVFAELLTGQPLWPKGSDVDQLYLIIRTLGKLI PRHQ 179

QY 226 SIFKSNGFHGISIPEPEDEMETLEEKSDVHPVALNFMKGLKKNPDRLTCSOLLESSY 285
 DB 180 SIFRSNQFFRGISIPEPEDEMETLEEKFSNVQFVALSMKGLKKNPDRLTCAQLDSAY 239

QY 286 FDSFQEAQIKRKARNEGRNRQ--QVLPL 313
 DB 240 FESFQEDQMKRKARSEGRSRQQLLPL 269

RESULT 9
 ABP62954
 ID ABP62954 standard; protein; 358 AA.
 XX
 AC ABP62954;
 XX 14-OCT-2002 (first entry)
 DT Human polypeptide SEQ ID NO 391.
 XX
 XX Human; vulnary; dermatological; neuroprotective; nootropic; cancer;
 KW antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;
 KW antidiabetic; anti-allergic; gene therapy; wound healing; tissue repair;
 KW burn; central nervous system disorder; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; immune disorder;
 KW autoimmune disorder; multiple sclerosis; diabetes; allergy.
 XX
 OS Homo sapiens.
 XX
 XX WO200218424-A2.
 PN 07-MAR-2002.
 PD 31-AUG-2001; 2001WO-US027093.
 XX 01-SEP-2000; 2000US-00654935.
 PR (HYSE-) HYSEQ INC.
 XX
 XX Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
 PI Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;
 DR WPI; 2002-583321/62.
 DR N-PSDB; AB093433.

XX New polynucleotide and polypeptides, useful for treatment and diagnosis
 PT of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral
 PT sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple
 PT sclerosis, diabetes and allergies.
 XX
 PS Claim 20; SEQ ID NO 391; 284pp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide (I) comprising one of
 CC 245 sequences (AB093288-AB093532). Treating a condition comprising
 CC administering to a mammalian subject a composition comprising the protein
 CC (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).
 CC (I), (II) and (III) are useful for diagnosis and (II) can be used for
 CC therapeutic treatment. Diseases that may be treated include wound healing
 CC and tissue repair, burns, central nervous system disorders (e.g.
 CC Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral
 CC sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple
 CC sclerosis, diabetes and allergies. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 358 AA;

Query Match 71.5%; Score 1188.5; DB 5; Length 358;

Best Local Similarity 70.5%; Pred. No. 8e-118;
Matches 213; Conservative 42; Mismatches 46; Indels 1; Gaps 1;
Qy 1 MEKYEKLAKTGEYSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQKH 60
Db 2 MEKYEKIGKIGESYGVVFKCRNRTGQIVAIKKFLESEDDPVKKIALREIRMLKQKH 61
Qy 61 PNLVNLLEVFRRKRRLHLVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCIH 120
Db 62 PNLVNLLEVFRRKRRLHLVFEYCDHTVLHLDYQGVPEHLVKSITWQTLQAVNFCCHK 121
Qy 121 NCIRHDIKPENILITKQGIKICDPGFAQILI-PGDAYTDYVATRWYRAPPELLVGDQY 179
Db 122 NCIRHDVKNENILITKHSVVKLCDFGARLLTGSDYITDVAWYRSPPELLVGDQY 181
Qy 180 SSVDIWAIGCVFABLLTGQPLWPKGSDVDQYLIIRTLGKLI PRHQSIFKSNFGFHGSI 239
Db 182 PPVDVWAIGCVFABLLSGVPLWPKGSDVDQYLIIRTKLTDGLI PRHQVFTSNQYFSGVKI 241
Qy 240 PEPDMETLEKFSVDVHPVAFNFMKGLKMPDRLTCSQLLESSYFDSFQEAQIKRKAR 299
Db 242 PDPEDMEPLEKFPNISYPALGKLGCLHMDPTERTLTCEQLLHHPYFENIREIEDLAKEH 301
Qy 300 NE 301
Db 302 NK 303

RESULT 10
AD001538
ID AD001538 standard; protein; 358 AA.
AC AD001538;
XX
XX
XX
XX 29-JUL-2004 (first entry)
XX
XX Human cyclin-dependent kinase like 1 (CDKL1) protein SEQ ID NO:4.

human; cyclin-dependent kinase like 1; CDKL1; branching morphogenesis;
branching morphogenesis modulator; angiogenic disorder;
apoptotic disorder; proliferation disorder; chromosome 14.
XX Homo sapiens.
XX WO2004038372-A2.
XX
XX 06-MAY-2004.
XX
XX 22-OCT-2003; 2003WO-US033483.
XX
XX 23-OCT-2002; 2002US-0420554P.
XX
XX (EXEL-) EXELIXIS INC.
XX
XX Plowman GD, Karim PD, Swimmer C, Habeck HA, Koblizek TI;
PI Schulte-Werker S, Langheinrich U, Stott GM, Trowe T, Vogel AM;
PI Odenthal JH, Scheel JK, Will TT, Jin Y, Hai B;
XX
XX WPI; 2004-365563/34.
XX N-PSDB; ADO01535.
XX
XX Use of cyclin-dependent kinase like 1 polypeptides or nucleic acids for
modulating branching morphogenesis in a mammalian cell or for diagnosing
a disease e.g. angiogenic, apoptotic or proliferation disorder in a
patient.
XX
XX Example; SEQ ID NO 4; 52pp; English.

The present invention describes the use of a cyclin-dependent kinase like
1 (CDKL1) polypeptide or nucleic acid for modulating branching
morphogenesis in a mammalian cell or for diagnosing a disease in a
patient. Also described: (1) identifying a candidate branching
morphogenesis modulating agent; (2) modulating branching morphogenesis in

a mammalian cell comprising contacting the cell with an agent that
specifically binds a CDKL1 polypeptide or nucleic acid; and (3) a method
for diagnosing a disease in a patient. The CDKL1 polypeptide or nucleic
acid is useful for modulating branching morphogenesis in a mammalian
cell. It is also useful for diagnosing a disease, e.g. angiogenic,
apoptotic or proliferation disorder in a patient. The present sequence
represents human CDKL1, which is used in the exemplification of the
present invention. The human CDKL1 gene is located on chromosome 14, more
specifically to 14q22.1.

XX Sequence 358 AA;

Query Match 71.2%; Score 1183.5; DB 8; Length 358;
Best Local Similarity 71.8%; Pred. No. 2.8e-117;
Matches 211; Conservative 41; Mismatches 41; Indels 1; Gaps 1;
Qy 1 MEKYEKLAKTGEYSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQKH 60
Db 2 MEKYEKIGKIGESYGVVFKCRNRTGQIVAIKKFLESEDDPVKKIALREIRMLKQKH 61
Qy 61 PNLVNLLEVFRRKRRLHLVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCIH 120
Db 62 PNLVNLLEVFRRKRRLHLVFEYCDHTVLHLDYQGVPEHLVKSITWQTLQAVNFCCHK 121
Qy 121 NCIRHDIKPENILITKQGIKICDPGFAQILI-PGDAYTDYVATRWYRAPPELLVGDQY 179
Db 122 NCIRHDVKNENILITKHSVVKLCDFGARLLTGSDYITDVAWYRSPPELLVGDQY 181
Qy 180 SSVDIWAIGCVFABLLTGQPLWPKGSDVDQYLIIRTLGKLI PRHQSIFKSNFGFHGSI 239
Db 182 PPVDVWAIGCVFABLLSGVPLWPKGSDVDQYLIIRTKLTDGLI PRHQVFTSNQYFSGVKI 241
Qy 240 PEPDMETLEKFSVDVHPVAFNFMKGLKMPDRLTCSQLLESSYFDSFQEAQ 293
Db 242 PDPEDMEPLEKFPNISYPALGKLGCLHMDPTERTLTCEQLLHHPYFENIREIE 295

RESULT 11

AAB65642
ID AAB65642 standard; protein; 247 AA.
XX
XX AAB65642;
XX
XX 27-MAR-2001 (first entry)
XX
XX Novel protein kinase, SEQ ID NO: 169.
XX
XX Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic;
XX immunosuppressive; cardiac; renal; antiinflammatory; antiasthmatic;
XX dermatological; antidiabetic; antiinfertility; gene therapy; vaccine;
XX immune disorder; cardiovascular disease; neurodegenerative disease;
XX cancer; autoimmune disorder; stroke; inflammatory bowel disease;
XX inflammatory pelvic disease; multiple sclerosis; psoriasis.
XX
XX Homo sapiens.
XX
XX WO2000073469-A2.
XX
XX 07-DEC-2000.
XX
XX 26-MAY-2000; 2000WO-US014842.
XX
XX 28-MAY-1999; 99US-0136503P.
XX
XX (SUGE-) SUGEN INC.
XX
XX Plowman GD, Martinez R, Whyte D, Sudersanam S;
XX
XX WPI; 2001-032161/04.
XX N-PSDB; AAF44669.
XX
XX Nucleic acids encoding kinase polypeptides, useful for diagnosing and
PT treating immune-related diseases and disorders, cardiovascular disease,

neurodegenerative diseases and/or cancers.

Claim 10; Fig 1; 310pp; English.

The present sequence is a novel protein kinase. The novel protein kinases and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase antagonists may also be used to down regulate kinase expression and activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative stress related disorders, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive disorders

Sequence 247 AA;

Query Match 69.1%; Score 1149; DB 4; Length 247;
Best Local Similarity 98.6%; Pred. No. 7.7e-114;
Matches 217; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
QY 96 NGVADGVKSVLWQTLQALNFCCHHNCIHRDIPENILITKQGIKICDFGFAQILIPGD 155
DB 1 NGVADGVKSVLWQTLQALNFCCHHNCIHRDIPENILITKQGIKICDFGFAQILIPGD 60
QY 156 AYTDVATRWYRAPELLVGDQYGVSSVDIWAIGCVFAELLTGQPLWPKSDVDQYLIIR 215
DB 61 AYTDVATRWYRAPELLVGDQYGVSSVDIWAIGCVFAELLTGQPLWPKSDVDQYLIIR 120
QY 216 TLGKLIHQSIKSNFGPHGISIPEPEMETLEEKFSVHPVAFNFMKGLKKNPDRL 275
DB 121 TLGKLIHQSIKSNFGPHGISIPEPEMETLEEKFSVHPVAFNFMKGLKKNPDRL 180
QY 276 TCSQLLESSYFDSFOEAQIKRKARNEGRRRQ--QVLEPL 313
DB 181 TCSQLLESSYFDSFOEAQIKRKARNEGRRRQ--QVLEPL 220

RESULT 12
ADI29249

ID ADI29249 standard; protein; 247 AA.

AC ADI29249;

DT 22-APR-2004 (first entry)

DE Human MARK3-associated protein #37.

KW Human; antisense gene therapy; MARK3;
KW MAP/microtubule affinity-regulating kinase 3; cancer;
KW Alzheimer's disease; neurodegenerative disorder;
KW hyperproliferative disorder; cytostatic.

OS Homo sapiens.

PN US2003232771-A1.

PD 18-DEC-2003.

XX 17-JUN-2002; 2002US-00174319.

XX 17-JUN-2002; 2002US-00174319.

XX (ISIS-) ISIS PHARM INC.

PI Ward DT, Freier SM, Dobie KW;

XX

DR WPI; 2004-052188/05.
DR N-PSDB; ADI29367.

XX New antisense compound targeted to a nucleic acid molecule encoding microtubule-affinity-regulating kinases (MARK3); useful for modulating expression of MARK3 or for treating cancer or Alzheimer's disease.

PS Disclosure; SEQ ID NO 169; 233pp; English.

XX The invention relates to a compound comprising a sequence comprising 8-80 base pairs (bp) targeted to a nucleic acid encoding MARK3 (MAP/microtubule affinity-regulating kinase 3), that specifically hybridizes with the nucleic acid encoding MARK3 and inhibits expression of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a composition comprising the compound and a carrier or diluent, inhibiting the expression of MARK3 in cells or tissues, treating an animal having or suspected of having a disease or condition associated with MARK3 and screening for an antisense compound. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder, particularly cancer and neurodegenerative diseases e.g. Alzheimer's disease. The present sequence is a MARK3 associated protein included in the figures but not mentioned anywhere else in the specification.

XX Sequence 247 AA;

Query Match 69.1%; Score 1149; DB 8; Length 247;
Best Local Similarity 98.6%; Pred. No. 7.7e-114;
Matches 217; Conservative 1; Mismatches 0; Indels 2; Gaps 1;
QY 96 NGVADGVKSVLWQTLQALNFCCHHNCIHRDIPENILITKQGIKICDFGFAQILIPGD 155
DB 1 NGVADGVKSVLWQTLQALNFCCHHNCIHRDIPENILITKQGIKICDFGFAQILIPGD 60
QY 156 AYTDVATRWYRAPELLVGDQYGVSSVDIWAIGCVFAELLTGQPLWPKSDVDQYLIIR 215
DB 61 AYTDVATRWYRAPELLVGDQYGVSSVDIWAIGCVFAELLTGQPLWPKSDVDQYLIIR 120
QY 216 TLGKLIHQSIKSNFGPHGISIPEPEMETLEEKFSVHPVAFNFMKGLKKNPDRL 275
DB 121 TLGKLIHQSIKSNFGPHGISIPEPEMETLEEKFSVHPVAFNFMKGLKKNPDRL 180
QY 276 TCSQLLESSYFDSFOEAQIKRKARNEGRRRQ--QVLEPL 313
DB 181 TCSQLLESSYFDSFOEAQIKRKARNEGRRRQ--QVLEPL 220

RESULT 13
AAG78547

ID AAG78547 standard; protein; 228 AA.

XX AAG78547;

XX 08-MAR-2002 (first entry)

DT Human kinase 14257 amino acid sequence.

XX Protein kinase; enzyme; cytostatic; osteopathic; hepatotropic;
KW antiadipetic; neuroprotective; antiarthritic; dermatological;
KW immunosuppressive; antiinflammatory; antithyroid; antipsoriatic;
KW ophthalmological; antiallergic; antiasthmatic; antiatherosclerotic;
KW hypotensive; vasotropic; antiarrhythmic; virucide; anorectic; metabolic;
KW immunomodulator; analgesic; cellular proliferative disorder; cancer;
KW acute lymphoblastic leukaemia; Hodgkin's disease;
KW bone metabolism disorder; osteoporosis; immune system disorder;
KW inflammatory; diabetes mellitus; osteoarthritis; asthma;
KW cardiovascular disorder; hypertension; coronary artery disease;
KW endothelial cell disorder; psoriasis.

OS Homo sapiens.

XX Key Location/Qualifiers

PH

FT Domain 4. .218
FT /note= "eukaryotic protein kinase domain"
FT Modified-site 9. .15
FT /note= "tyrosine kinase phosphorylation site"
FT Modified-site 23. .26
FT /note= "N-glycosylation site"
FT Modified-site 27. .32
FT /note= "N-myristoylation site"
FT Modified-site 38. .41
FT /note= "casein kinase II phosphorylation site"
FT Modified-site 97. .102
FT /note= "N-myristoylation site"
FT Modified-site 132. .134
FT /note= "serine/threonine protein kinase active-site
FT signal site"
FT 161. .218
FT /note= "kinase transferase protein serine/threonine-
FT protein ATP-binding II phosphorylation casein alpha chain
FT domain"
FT Modified-site 180. .183
FT /note= "casein kinase II phosphorylation site"
FT Modified-site 188. .193
FT /note= "N-myristoylation site"
FT Modified-site 204. .211
FT /note= "tyrosine kinase phosphorylation site"
FT Modified-site 205. .208
FT /note= "casein kinase II phosphorylation site"
FT XX
FT W0200179488-A2.
PN
XX
XX 25-OCT-2001.
XX
XX 13-APR-2001; 2001WO-US012188.
XX
XX 13-APR-2000; 2000US-0196910P.
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Kapeller-Libermann R.
XX
XX WPI; 2002-034355/04.
XX N-PSDB; AAI64248.
XX
XX New 14257 polypeptides (protein kinases), useful as diagnostic targets
XX and therapeutic agents for controlling cellular proliferative and/or
XX differentiative disorder, bone disorders, immune disorders and
XX cardiovascular disorders.
XX
XX Claim 1c; Fig 1A; 98pp; English.
XX
XX The invention relates to an isolated 14257 polypeptide and nucleic acid
XX encoding it. The 14257 protein is a protein kinase that acts as a
XX modulating agent in regulating a variety of cellular processes, including
XX cell proliferation, differentiation, growth and division. The activity of
XX the protein of the invention may be described as: cytostatic; osteopathic
XX ; hepatotropic; antidiabetic; neuroprotective; antiarthritic;
XX dermatological; immunosuppressive; antiinflammatory; antithyroid;
XX antipsoriatic; ophthalmological; antiallergic; antiaesthmic;
XX antiatherosclerotic; hypotensive; vasotropic; antiarrhythmic; virucide;
XX anorectic; metabolic; immunomodulator and analgesic. The protein of the
XX invention may act as a novel diagnostic target or therapeutic agent
XX controlling certain disorders, for example kinase-associated or other
XX 14257-associated disorders. These may include cellular proliferative
XX disorders such as cancers e.g. acute lymphoblastic leukemia or Hodgkin's
XX disease. Other disorders include bone metabolism disorders such as
XX osteoporosis, disorders of the immune system, e.g. inflammatory,
XX diabetes mellitus, osteoarthritis and asthma. Proteins of the invention
XX may also be of use as therapeutic agents in cardiovascular disorders such
XX as hypertension and coronary artery disease, and some endothelial cell
XX disorders, including psoriasis. The current sequence represents a human
XX kinase 14257 amino acid sequence

XX Sequence 228 AA;

Query Match 68.6%; Score 1140; DB 5; Length 228;
Best Local Similarity 98.2%; Pred. No. 6.3e-113;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MEYKEKLAKTGEYSYGVVFKCRNKTSGOVAVKVFVESEDDPVVKKTALREIRMLKQKH 60
Db 1 MGKYEKLAKTGEYSYGVVFKCRNKTSGOVAVKVFVESEDDPIVKKTALREIRMLKQKH 60
Qy 61 PNLVNLIEVFRRRKRMHLVFEYCDHTLLNELERNPNPVGADGVIKSVLWQTLQALNFCHIH 120
Db 61 PNLVNLIEVFRRRKRMHLVFEYCDHALLNELERNPNPVGADGVIKSVLWQTLQALNFCHIH 120
Qy 121 NCIHRDKPENILITKQGIKICDFGPAQILIPGDATYDVVATRWYRAPELLVGDTOYGS 180
Db 121 NCIHRDVKPNILITKQGIKICDFGPAQILIPGDATYDVVATRWYRAPELLVGDTOYGS 180
Qy 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTIG 218
Db 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTIG 218
RESULT 14
ABB63118
ID ABB63118 standard; protein; 392 AA.
XX AC ABB63118;
XX AC
XX 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 16146.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX OS Drosophila melanogaster.
XX PN W0200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US009231.
XX PR 23-MAR-2000; 2000US-0191637P.
XX PR 11-JUL-2000; 2000US-00614150.
XX PA (PEKE) PE CORP NY.
XX PF Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX N-PSDB; ABL07221.
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX PS Disclosure; SEQ ID NO 16146; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 392 AA;

Query Match 61.8%; Score 1027.5; DB 4; Length 392;

Best Local Similarity 58.4%; Pred. No. 1.5e-100;
 Matches 184; Conservative 65; Mismatches 61; Indels 5; Gaps 2;

QY 1 MEKYEKLAKTGEISGVVFKCRNKTSGOVAVKVFESDDPVVKIALREIRMLKOLKH 60
 DB 1 MDREKLSRLGSGVGVVYKCRDRETDGALVAVKRFESDDPAIRKIALREIRMLKOLKH 60

QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPGVADGVKSVLWQTLQALNFCIH 120
 DB 61 PNLVNLIEVFRKRRLHLVFEFCETLVLELHHPGQPEHLTKQICQTLGVAICHKQ 120

QY 121 NCIHRIKIPENILITKQIIKICDFGPAQLIPDAYTDYVATRWYRAPELLVGDQYGS 180
 DB 121 GCLHRDIKIPENILLTAQGVKLCDFGFARMLSPGENYTDYVATRWYRAPELLVGDQYGT 180

QY 181 SVDIWAIGCVFAELLTGQPLWPKSDVDOLYLIIRTLGLKIPRHOSIFKSNFGFHGISIP 240
 DB 181 PVDWAIIGLFAELVRGALWPGRSVDOLYLIIRTLGLDLPRHIQIFGQNEYFKGITLP 240

QY 241 EPEDMETLEEF--SDVHPVALNFMKGLKMNPPDRLTCSQLLESSYFDSF--QEAQIK 295
 DB 241 VPPTLEPLEDKWPAKSQQNLTIDFLKCKLDKDPTRKWSCEKLTGHSYFDDYIAKQRELE 300

QY 296 RKARNEGRNRROQV 310
 DB 301 HVNSLEAANLRQQOL 315

RESULT 15
 AA90724
 ID AA90724 standard; protein; 566 AA.
 XX
 AC AA90724;
 DT 15-AUG-2000 (first entry)
 XX
 DE Rabbit KKIAMRE kinase SEQ ID NO:4.
 XX
 KW Rabbit; KKIAMRE kinase; learning-induced kinase; learning; memory;
 KW cdc2-related kinase; brain; gene therapy; genetic disorder; detection;
 KW identification.
 XX
 OS Oryctolagus cuniculus.
 XX
 PN WO200020567-A2.
 XX
 PD 13-APR-2000.
 XX
 PF 01-OCT-1999; 99WO-US023010.
 XX
 PR 02-OCT-1998; 98US-0102906P.
 XX
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
 XX
 PI Thompson RF, Gomi H, Sun W;
 XX
 DR WPI; 2000-328932/28.
 DR N-FSDE; AAA29745.
 XX
 PT Novel learning induced kinase polynucleotides and polypeptides, useful
 PT for the analysis of learning and memory, and for gene therapy.
 XX
 PS Claim 1; Fig 4; 64pp; English.
 XX

The present sequence represents a learning-induced kinase, designated KKIAMRE kinase, which is isolated from rabbit brain tissue. KKIAMRE kinase is a cdc2-related kinase. The KKIAMRE kinase polynucleotides can be used to express recombinant protein for analysis, characterisation or therapeutic use, as markers for tissues in which the protein is preferentially expressed, as molecular weight markers on Southern gels, as chromosome markers or tags, to compare endogenous DNA sequences in patients to identify potential genetic disorders, as probes to hybridise and discover novel related sequences, as a source of PCR primers, and as

an antigen to induce anti-DNA antibodies. The polypeptides can be used in assay to discover biological activity, to raise antibodies, as tissue markers, and to isolate correlative receptors or ligands. The polynucleotides may also be used for gene therapy for the treatment of disorders which are mediated by KKIAMRE kinase

Sequence 566 AA;
 Query Match 58.2%; Score 967.5; DB 3; Length 566;
 Best Local Similarity 54.6%; Pred. No. 6.9e-94;
 Matches 177; Conservative 67; Mismatches 65; Indels 15; Gaps 5;

QY 1 MEKYEKLAKTGEISGVVFKCRNKTSGOVAVKVFESDDPVVKIALREIRMLKOLKH 60
 DB 1 MEKYENIGLVGEGSGVMVCKRNKDSGRIVAIFLESDDDKMVKTIAMREIKLLKOLRH 60

QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPGVADGVKSVLWQTLQALNFCIH 120
 DB 61 ENLVNLIEVCKKRWLVFEFVDHTLIDLELFPNGLDQVQVKYLFQIINGIGFCHSH 120

QY 121 NCIHRIKIPENILITKQIIKICDFGPAQLIPDAYTDYVATRWYRAPELLVGDQYGS 179
 DB 121 NIHRDIKIPENILVSOSGVVVKLCDFGFARTLAAPGEVYTDYVATRWYRAPELLVGDVKYG 180

QY 180 SVDIWAIGCVFAELLTGQPLWPKSDVDOLYLIIRTLGLKIPRHOSIFKSNFGFHGISI 239
 DB 181 KAVDVAIGLCLVTEMLMGEPLFDSDIDOLYLIMRCLGNLIPRHOELFYKNPVFAGVRL 240

QY 240 PEPEMETLEEFSDVHPVALNFMKGLKMNPPDRLTCSQLLESSYF--DSF-----QEA 292
 DB 241 PEIKSEPLERRYPKLSVVVIDLAKKCLHVDKPRPFCAELLHHDFFQMDGFAERFSQEL 300

QY 293 QIK--RKARN-----EGRNRROQ 309
 DB 301 QMKVQKDARNISLSKKSQNRKKEK 324

Search completed: April 22, 2005, 06:47:32
 Job time : 88.5529 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 04:37:19 ; Search time 30.929 Seconds
(without alignments)
760.272 Million cell updates/sec

Title: US-10-766-691-12

Perfect score: 1662

Sequence: 1 MEKYEKLAKTGEISYGVFK.....RKARNEGRNRROQVLPLKS 315

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCITUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1662	100.0	315	4	US-09-671-050-12
2	1638	98.6	324	4	US-09-671-050-6
3	1636	98.4	347	4	US-09-671-050-10
4	1612	97.0	356	4	US-09-671-050-4
5	1188.5	71.5	367	4	US-09-949-016-7552
6	1183.5	71.2	358	4	US-09-411-628-11
7	1183.5	71.2	358	4	US-10-174-794-11
8	967.5	58.2	566	4	US-09-411-628-4
9	967.5	58.2	566	4	US-10-174-794-4
10	941.5	56.6	475	4	US-09-949-016-7954
11	941.5	56.6	493	4	US-09-411-628-10
12	941.5	56.6	493	4	US-10-174-794-10
13	791	47.6	187	4	US-09-671-050-2
14	791	47.6	198	4	US-09-671-050-8
15	581	35.0	305	4	US-09-538-092-1236
16	581	35.0	305	4	US-09-949-016-6052
17	581	35.0	334	4	US-09-949-016-10777
18	570	34.3	298	2	US-08-874-347-25
19	570	34.3	298	2	US-08-969-106-2
20	570	34.3	298	3	US-09-093-522-25
21	570	34.3	298	4	US-09-338-125-2
22	570	34.3	298	4	US-09-266-225D-14
23	570	34.3	544	4	US-09-417-197-113
24	570	34.3	544	4	US-09-417-197-115
25	569	34.2	298	4	US-09-411-628-13
26	569	34.2	298	4	US-10-174-794-13
27	568.5	34.2	294	2	US-08-874-347-26

28	568.5	34.2	294	3	US-09-093-522-26	Sequence 26, Appl
29	567	34.1	298	3	US-09-457-040B-29	Sequence 29, Appl
30	567	34.1	298	4	US-09-538-092-1006	Sequence 1006, Ap
31	567	34.1	354	4	US-09-949-016-8025	Sequence 8025, Ap
32	565	34.0	297	1	US-08-176-620A-16	Sequence 16, Appl
33	565	34.0	297	2	US-08-461-985-16	Sequence 16, Appl
34	557	33.5	297	2	US-08-874-347-23	Sequence 23, Appl
35	557	33.5	297	3	US-09-093-522-23	Sequence 23, Appl
36	556	33.5	297	2	US-08-874-347-24	Sequence 24, Appl
37	556	33.5	297	3	US-09-093-522-24	Sequence 24, Appl
38	556	33.5	297	4	US-09-411-628-12	Sequence 12, Appl
39	556	33.5	297	4	US-10-174-794-12	Sequence 12, Appl
40	555.5	33.4	300	2	US-08-874-347-10	Sequence 10, Appl
41	555.5	33.4	300	3	US-09-093-522-10	Sequence 10, Appl
42	555	33.4	270	2	US-07-857-224B-31	Sequence 31, Appl
43	551	33.2	274	1	US-08-318-947A-20	Sequence 20, Appl
44	551	33.2	274	2	US-08-795-303-20	Sequence 20, Appl
45	551	33.2	299	4	US-09-949-016-10673	Sequence 10673, A

ALIGNMENTS

RESULT 1:

US-09-671-050-12

; Sequence 12, Application US/09671050

; Patent No. 6716616

; GENERAL INFORMATION:

; APPLICANT: Donoho, Gregory

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Nehls, Michael

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and

; FILE REFERENCE: Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0046-USA

; CURRENT APPLICATION NUMBER: US/09/671.050

; CURRENT FILING DATE: 2001-06-11

; PRIOR APPLICATION NUMBER: US 60/156,511

; PRIOR FILING DATE: 1999-09-28

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 315

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-671-050-12

Query Match 100.0%; Score 1662; DB 4; Length 315;
Best Local Similarity 100.0%; Pred. No. 1.1e-166;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEKYEKLAKTGEISYGVFKCRNTSGQVAVKVFVSEDDPVVKKTALRIRMLKQLKH	60
Db	1	MEKYEKLAKTGEISYGVFKCRNTSGQVAVKVFVSEDDPVVKKTALRIRMLKQLKH	60
Qy	61	PNLVNLIEVPRRKKMHLVREYCDHTLLNELRPNGVADGVIKSLVWQLQALNFCIH	120
Db	61	PNLVNLIEVPRRKKMHLVREYCDHTLLNELRPNGVADGVIKSLVWQLQALNFCIH	120
Qy	121	NCIHRDIKPNILITKQIICIDFGFAQLIPGDAYTIVVATRYRAPELLVGDTOYGS	180
Db	121	NCIHRDIKPNILITKQIICIDFGFAQLIPGDAYTIVVATRYRAPELLVGDTOYGS	180
Qy	181	SVDIWAIGCVFAELLTQGPLWPKGSDVDQYLIIRITGLKLIPIRHSQIFKSNGFHGISIP	240
Db	181	SVDIWAIGCVFAELLTQGPLWPKGSDVDQYLIIRITGLKLIPIRHSQIFKSNGFHGISIP	240
Qy	241	EPDMETLEKFSFSDVHPVALNFMKGCIMKMPDRLTCSQLLESSYFDSFQEAQIKRKARN	300
Db	241	EPDMETLEKFSFSDVHPVALNFMKGCIMKMPDRLTCSQLLESSYFDSFQEAQIKRKARN	300

Qy 301 EGRNRRQQVPLPKS 315
 Db 301 EGRNRRQQVPLPKS 315

RESULT 2

US-09-671-050-6
 ; Sequence 6, Application US/09671050
 ; Patent No. 6716616
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
 ; FILE REFERENCE: LEX-0046-USA
 ; CURRENT APPLICATION NUMBER: US/09/671,050
 ; CURRENT FILING DATE: 2001-06-11
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6
 ; LENGTH: 324
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 ; US-09-671-050-6

Query Match 98.6%; Score 1638; DB 4; Length 324;
 Best Local Similarity 100.0%; Pred. No. 3.8e-164;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
 Db 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
 Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNVGVADGVKSVLWOTLOALNFCIH 120
 Db 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNVGVADGVKSVLWOTLOALNFCIH 120
 Qy 121 NCIRHDIKPENILITKQGIKICDFGFAQILIPGDAYTDVATWYRAPPELLVGDTOYGS 180
 Db 121 NCIRHDIKPENILITKQGIKICDFGFAQILIPGDAYTDVATWYRAPPELLVGDTOYGS 180
 Qy 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 Db 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 Qy 241 EPDMETLEEFSDVHPVAFNFMKGCLKMPNDDRLTCSQLLESSYFDSFQEAQIKRKARN 300
 Db 241 EPDMETLEEFSDVHPVAFNFMKGCLKMPNDDRLTCSQLLESSYFDSFQEAQIKRKARN 300
 Qy 301 EGRNRRQQV 310
 Db 301 EGRNRRQQV 310

RESULT 3

US-09-671-050-10
 ; Sequence 10, Application US/09671050
 ; Patent No. 6716616
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
 ; FILE REFERENCE: LEX-0046-USA

FILE REFERENCE: LEX-0046-USA
 ; CURRENT APPLICATION NUMBER: US/09/671,050
 ; CURRENT FILING DATE: 2001-06-11
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10
 ; LENGTH: 347
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 ; US-09-671-050-10

Query Match 98.4%; Score 1636; DB 4; Length 347;
 Best Local Similarity 90.8%; Pred. No. 6.9e-164;
 Matches 315; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
 Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
 Db 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
 Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNVGVADGVKSVLWOTLOALNFCIH 120
 Db 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNVGVADGVKSVLWOTLOALNFCIH 120
 Qy 121 NCIRHDIKPENILITKQGIKICDFGFAQILIPGDAYTDVATWYRAPPELLVGDTOYGS 180
 Db 121 NCIRHDIKPENILITKQGIKICDFGFAQILIPGDAYTDVATWYRAPPELLVGDTOYGS 180
 Qy 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 Db 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 Qy 218 -----GKLPRHQSIFKSNFGFFHGISIPEDMETLEEFSDVHPVAFNFMKGCLK 268
 Db 241 VASQSAGITGKLPRHQSIFKSNFGFFHGISIPEDMETLEEFSDVHPVAFNFMKGCLK 300
 Qy 269 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNRNRQQVPLPKS 315
 Db 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNRNRQQVPLPKS 347

RESULT 4

US-09-671-050-4
 ; Sequence 4, Application US/09671050
 ; Patent No. 6716616
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
 ; FILE REFERENCE: LEX-0046-USA
 ; CURRENT APPLICATION NUMBER: US/09/671,050
 ; CURRENT FILING DATE: 2001-06-11
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 356
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 ; US-09-671-050-4

Query Match 97.0%; Score 1612; DB 4; Length 356;
 Best Local Similarity 90.8%; Pred. No. 2.4e-161;
 Matches 310; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
 Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60

Db 1 MEKYEKLAKTCEGSGYGVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
Qy 61 PNLVNLIEVFRKRKRLHVLVEYCDHTLLNELERNPNVGADVGVKSVLWQTLQALNFCCHI 120
Db 61 PNLVNLIEVFRKRKRLHVLVEYCDHTLLNELERNPNVGADVGVKSVLWQTLQALNFCCHI 120
Qy 121 NCIRDIKPENILITKQIHKICDPGFAQILI-PGDATDYVATRWYRAPELLVGDTOYG 180
Db 121 NCIRDIKPENILITKQIHKICDPGFAQILI-PGDATDYVATRWYRAPELLVGDTOYG 180
Qy 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTL----- 217
Db 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTLVETGFRVDAQLELLTSSPPA 240
Qy 218 -----GKLI PRHQSIFKSNFGFFHGISIPEDMETLEEKFSVDHPVAFNMFKGLK 268
Db 241 VASQAGITGKLI PRHQSIFKSNFGFFHGISIPEDMETLEEKFSVDHPVAFNMFKGLK 300
Qy 269 MNPDDLTCSSQLLESSYFDSFOEAQIKRKARNEGRRRQOV 310
Db 301 MNPDDLTCSSQLLESSYFDSFOEAQIKRKARNEGRRRQOV 342

RESULT 5
US-09-949-016-7552
; Sequence 7552, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7552
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7552

Query Match 71.5%; Score 1188.5; DB 4; Length 367;
Best Local Similarity 70.5%; Pred. No. 1.1e-116;
Matches 213; Conservative 42; Mismatches 46; Indels 1; Gaps 1;

Qy 1 MEKYEKLAKTCEGSGYGVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
Db 11 MEKYEKGKIGEGSYGVFKCRNRDTCQIVAIKKFLESEDDPVVKKIALREIRMLKQLKH 70
Qy 61 PNLVNLIEVFRKRKRLHVLVEYCDHTLLNELERNPNVGADVGVKSVLWQTLQALNFCCHI 120
Db 71 PNLVNLIEVFRKRKRLHVLVEYCDHTVHLEDRVQGVPEHLVKSITWQTLQANFCHKH 130
Qy 121 NCIRDIKPENILITKQIHKICDPGFAQILI-PGDATDYVATRWYRAPELLVGDTOYG 179
Db 131 NCIRDIKPENILITKHSVIKLCDFGARLLTGPSDYVTDYVATRWYRSPPELLVGDTOYG 190
Qy 180 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTLGKLI PRHQSIFKSNFGFHGISI 239
Db 191 PPVDVWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTKLTGLDIPRHQQVFNSTNQYFSGVKI 250
Qy 240 PEPEDMETLEEKFSVDHPVAFNMFKGLKNPDDLTCSSQLLESSYFDSFOEAQIKRKAR 299
Db 251 PEPEDMEPLKFPNISYPALGLLKGCLHMDPTERLTCEQLLHHHPYPENIREIEDLAKH 310

Qy 300 NE 301
Db 311 NK 312

RESULT 6
US-09-411-628-11
; Sequence 11, Application US/09411628
; Patent No. 6428994
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/09/411,628
; CURRENT FILING DATE: 1999-10-01
; EARLIER FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-411-628-11

Query Match 71.2%; Score 1183.5; DB 4; Length 358;
Best Local Similarity 71.8%; Pred. No. 3.6e-116;
Matches 211; Conservative 41; Mismatches 41; Indels 1; Gaps 1;

Qy 1 MEKYEKLAKTCEGSGYGVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
Db 2 MEKYEKGKIGEGSYGVFKCRNRDTCQIVAIKKFLESEDDPVVKKIALREIRMLKQLKH 61
Qy 61 PNLVNLIEVFRKRKRLHVLVEYCDHTLLNELERNPNVGADVGVKSVLWQTLQALNFCCHI 120
Db 62 PNLVNLIEVFRKRKRLHVLVEYCDHTVHLEDRVQGVPEHLVKSITWQTLQANFCHKH 121
Qy 121 NCIRDIKPENILITKQIHKICDPGFAQILI-PGDATDYVATRWYRAPELLVGDTOYG 179
Db 122 NCIRDIKPENILITKHSVIKLCDFGARLLTGPSDYVTDYVATRWYRSPPELLVGDTOYG 181
Qy 180 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTLGKLI PRHQSIFKSNFGFHGISI 239
Db 182 PPVDVWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTKLTGLDIPRHQQVFNSTNQYFSGVKI 241
Qy 240 PEPEDMETLEEKFSVDHPVAFNMFKGLKNPDDLTCSSQLLESSYFDSFOEAQ 293
Db 242 PEPEDMEPLKFPNISYPALGLLKGCLHMDPTERLTCEQLLHHHPYPENIREIE 295

RESULT 7
US-10-174-794-11
; Sequence 11, Application US/10174794
; Patent No. 6664086
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-794-11

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7954
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7954

Query Match 56.6%; Score 941.5; DB 4; Length 475;
Best Local Similarity 53.1%; Pred. No. 1.9e-90;
Matches 172; Conservative 68; Mismatches 69; Indels 15; Gaps 5;

Qy 1 MEKYEKLAKTGEYSYGVVFKCRNKTSGOVAVKVFVESEDDPVVKIALREIMLKQLKH 60
Db 3 MEKYNLGLVGEYSYGVVFKCRNKTSGOVAVKVFVESEDDPVVKIALREIMLKQLKH 62
Qy 61 PNLVNLIEVFRKRKMLVFEYCDHTLLNELRNPNVGVADGVKSVLWQTLQALNFCIH 120
Db 63 ENLVNLLEVCCKRWYLVFEVDHTLLDELFPNGLDYQVQKYLFIINGIGFCHSH 122
Qy 121 NCIRDIKPNILITKOGIIKICDFGPAQIL-IPGDAYTDVATRWYRAPELLVGDTOYG 179
Db 123 NIHRDIKPNILVQSQGVKLCDFGPAQIL-IPGDAYTDVATRWYRAPELLVGDVKYG 182
Qy 180 SSVDIWAIGCVFAELLTGOPLWPKSDVDQYLIIRTLGKLI PRHQSIFKSNPFHGLSI 239
Db 183 KAVDVWAIGCLVTEMFMGEPLFGDSDIDQYHIMMCLGNLIPRHQELFNKNPVFAGVRL 242
Qy 240 PEPEDMETLEKFSVHPVAFNFMKGLKMPDRLTCSOLLESSYF--DSF-----QEA 292
Db 243 PEIKEREPLERRYPKLSEVVIDLAKCLHIDDPKRPFCALLHHDDFFQMDGFAERFSQEL 302
Qy 293 QIK--RKARN-----EGRNRRRQ 309
Db 303 QLVKQKDARNVSLSKSKSQRKKEK 326

RESULT 11
US-09-411-628-10
; Sequence 10, Application US/09411628
; Patent No. 6428994
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/09/411.628
; EARLIER FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-411-628-10

Query Match 56.6%; Score 941.5; DB 4; Length 493;
Best Local Similarity 53.1%; Pred. No. 1.9e-90;
Matches 172; Conservative 68; Mismatches 69; Indels 15; Gaps 5;

Qy 1 MEKYEKLAKTGEYSYGVVFKCRNKTSGOVAVKVFVESEDDPVVKIALREIMLKQLKH 60
Db 1 MEKYNLGLVGEYSYGVVFKCRNKTSGOVAVKVFVESEDDPVVKIALREIMLKQLKH 62
Qy 61 PNLVNLIEVFRKRKMLVFEYCDHTLLNELRNPNVGVADGVKSVLWQTLQALNFCIH 120
Db 63 ENLVNLLEVCCKRWYLVFEVDHTLLDELFPNGLDYQVQKYLFIINGIGFCHSH 122
Qy 121 NCIRDIKPNILITKOGIIKICDFGPAQIL-IPGDAYTDVATRWYRAPELLVGDTOYG 179
Db 123 NIHRDIKPNILVQSQGVKLCDFGPAQIL-IPGDAYTDVATRWYRAPELLVGDVKYG 180

Qy 180 SSVDIWAIGCVFAELLTGOPLWPKSDVDQYLIIRTLGKLI PRHQSIFKSNPFHGLSI 239
Db 181 KAVDVWAIGCLVTEMFMGEPLFGDSDIDQYHIMMCLGNLIPRHQELFNKNPVFAGVRL 240
Qy 240 PEPEDMETLEKFSVHPVAFNFMKGLKMPDRLTCSOLLESSYF--DSF-----QEA 292
Db 241 PEIKEREPLERRYPKLSEVVIDLAKCLHIDDPKRPFCALLHHDDFFQMDGFAERFSQEL 300
Qy 293 QIK--RKARN-----EGRNRRRQ 309
Db 301 QLVKQKDARNVSLSKSKSQRKKEK 324

RESULT 12
US-10-174-794-10
; Sequence 10, Application US/10174794
; Patent No. 6664086
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174.794
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411.628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-794-10

Query Match 56.6%; Score 941.5; DB 4; Length 493;
Best Local Similarity 53.1%; Pred. No. 1.9e-90;
Matches 172; Conservative 68; Mismatches 69; Indels 15; Gaps 5;

Qy 1 MEKYEKLAKTGEYSYGVVFKCRNKTSGOVAVKVFVESEDDPVVKIALREIMLKQLKH 60
Db 1 MEKYNLGLVGEYSYGVVFKCRNKTSGOVAVKVFVESEDDPVVKIALREIMLKQLKH 62
Qy 61 PNLVNLIEVFRKRKMLVFEYCDHTLLNELRNPNVGVADGVKSVLWQTLQALNFCIH 120
Db 63 ENLVNLLEVCCKRWYLVFEVDHTLLDELFPNGLDYQVQKYLFIINGIGFCHSH 122
Qy 121 NCIRDIKPNILITKOGIIKICDFGPAQIL-IPGDAYTDVATRWYRAPELLVGDTOYG 179
Db 123 NIHRDIKPNILVQSQGVKLCDFGPAQIL-IPGDAYTDVATRWYRAPELLVGDVKYG 180
Qy 180 SSVDIWAIGCVFAELLTGOPLWPKSDVDQYLIIRTLGKLI PRHQSIFKSNPFHGLSI 239
Db 181 KAVDVWAIGCLVTEMFMGEPLFGDSDIDQYHIMMCLGNLIPRHQELFNKNPVFAGVRL 240
Qy 240 PEPEDMETLEKFSVHPVAFNFMKGLKMPDRLTCSOLLESSYF--DSF-----QEA 292
Db 241 PEIKEREPLERRYPKLSEVVIDLAKCLHIDDPKRPFCALLHHDDFFQMDGFAERFSQEL 300
Qy 293 QIK--RKARN-----EGRNRRRQ 309
Db 301 QLVKQKDARNVSLSKSKSQRKKEK 324

RESULT 13
US-09-671-050-2
; Sequence 2, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael

APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
FILE REFERENCE: Lex-0046-USA
CURRENT APPLICATION NUMBER: US/09/671,050
PRIOR FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: US 60/156,511
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 187
TYPE: PRT
ORGANISM: homo sapiens
US-09-671-050-2

Query Match 47.6%; Score 791; DB 4; Length 187;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MEKYEKLAKTGGSGVGVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKQLKH 60
QY 61 PNLVNLIEVFRKRKRWHLVFEYCDHTLLNELERNPVGADGVKSVLWQTLQALNFCIH 120
DB 61 PNLVNLIEVFRKRKRWHLVFEYCDHTLLNELERNPVGADGVKSVLWQTLQALNFCIH 120
QY 121 NCIIHRDIKPENLITKQGIKICDPGFAQIL 151
DB 121 NCIIHRDIKPENLITKQGIKICDPGFAQIL 151

RESULT 14
US-09-671-050-8
Sequence 8, Application US/09671050
Patent No. 6716616
GENERAL INFORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Nehls, Michael
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
FILE REFERENCE: Lex-0046-USA
CURRENT APPLICATION NUMBER: US/09/671,050
PRIOR FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: US 60/156,511
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 198
TYPE: PRT
ORGANISM: homo sapiens
US-09-671-050-8

Query Match 47.6%; Score 791; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 3.3e-75;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEKYEKLAKTGGSGVGVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKQLKH 60
DB 1 MEKYEKLAKTGGSGVGVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKQLKH 60
QY 61 PNLVNLIEVFRKRKRWHLVFEYCDHTLLNELERNPVGADGVKSVLWQTLQALNFCIH 120
DB 61 PNLVNLIEVFRKRKRWHLVFEYCDHTLLNELERNPVGADGVKSVLWQTLQALNFCIH 120

QY 121 NCIIHRDIKPENLITKQGIKICDPGFAQIL 151
DB 121 NCIIHRDIKPENLITKQGIKICDPGFAQIL 151
RESULT 15
US-09-538-092-1236
Sequence 1236, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Giot, Loic
APPLICANT: Mansfield, Traci A.
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurapatSeqFormatter Version 0.9
SEQ ID NO 1236
LENGTH: 305
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: misc feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number Q00526
US-09-538-092-1236

Query Match 35.0%; Score 581; DB 4; Length 305;
Best Local Similarity 39.8%; Pred. No. 9.4e-53;
Matches 123; Conservative 66; Mismatches 96; Indels 24; Gaps 8;
QY 1 MEKYEKLAKTGGSGVGVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKQ 57
DB 1 MDMFQVKEIGEGTYGVVYKAKNREGQLVAKKIRLDEMEGVPESTAREISLLKE 57
QY 58 LKHPNVLNLIIEVFRKRKRWHLVFEYCDHTLLNELERNPVGADGVKSVLWQTLQALNF 116
DB 58 LKHPNVLNLIIEVFRKRKRWHLVFEYCDHTLLNELERNPVGADGVKSVLWQTLQALNF 117
QY 117 CHHNCIHRDIKPENLITKQGIKICDPGFAQIL-IPGDAYTDVAVFWYAPPELLVGD 175
DB 118 CHSHRVHRLDLPQNLINELGAIKLADFLARAFGVPLRTYTHEVTVLWYAPPELLGS 177
QY 176 TOYGSVDIWAIGCVFAELLTQOPLMPGKSDVDQLYLIIRTLGKLIPIRHSIFKSNPFH 235
DB 178 KEYTTAVDIWSIGCIFAEMVTRKALFPGDSEIDQLFRIFRMLGT-----PSEDTPW 228
QY 236 GIS-IPE-----PE-DMETLEKFSVDVHPVALFMKGCIMNPPDRRLTCSQLLESSYFDS 288
DB 229 GVTQLPDYKGSFPKWRKGLEIEIVNLEPEGRDLMLQLLOYDPSQRIITAKTALAHYPFSS 288
QY 289 FOEAQIKRK 297
DB 289 PEPSPAARQ 297

Search completed: April 22, 2005, 06:52:57
Job time : 31.929 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 06:50:50 ; Search time 780.363 Seconds
(without alignments)
134.334 Million cell updates/sec

Title: US-10-766-691-12

Perfect score: 1662

Sequence: 1 MEKYEKLATGEGSYGVVFK.....RKARNEGRRRQOVLPKLS 315

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:*
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 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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 - 15: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/1/pubpaa/US10F_PUBCOMB.pep.*
 - 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1662	100.0	315	17	US-10-766-691-12
2	1639	98.6	324	15	US-10-333-314-10
3	1638	98.6	324	17	US-10-766-691-6
4	1636	98.4	347	17	US-10-766-691-10
5	1612	97.0	356	17	US-10-766-691-4
6	1188.5	71.5	358	15	US-10-363-616-391
7	1186.5	71.4	338	16	US-10-664-421-97
8	1183.5	71.2	358	14	US-10-174-794-11
9	1140	68.6	228	9	US-09-834-496A-2
10	967.5	58.2	566	14	US-10-174-794-4
11	941.5	56.6	493	14	US-10-174-794-10
12	941.5	56.6	493	15	US-10-369-022-22
13	941.5	56.6	493	16	US-10-757-262-108

14	791	47.6	187	17	US-10-766-691-2	Sequence 2, Appli
15	791	47.6	198	17	US-10-766-691-8	Sequence 8, Appli
16	784.5	47.2	455	16	US-10-620-052A-34	Sequence 34, Appli
17	712.5	42.9	154	16	US-10-250-889-62	Sequence 62, Appli
18	581	35.0	305	15	US-10-394-322A-8	Sequence 8, Appli
19	581	35.0	305	16	US-10-408-765A-544	Sequence 544, App
20	581	35.0	305	16	US-10-620-052A-20	Sequence 20, Appli
21	570	34.3	298	9	US-09-771-161A-187	Sequence 187, App
22	570	34.3	544	14	US-10-072-036-113	Sequence 113, App
23	570	34.3	544	14	US-10-072-036-115	Sequence 115, App
24	569	34.2	298	14	US-10-174-794-13	Sequence 13, Appli
25	569	34.2	298	14	US-10-295-681-27	Sequence 27, Appli
26	567	34.1	298	11	US-09-969-034-4493	Sequence 4493, Ap
27	567	34.1	298	15	US-10-394-322A-7	Sequence 7, Appli
28	567	34.1	298	16	US-10-620-052A-55	Sequence 55, Appli
29	567	34.1	298	16	US-10-664-421-14	Sequence 14, Appli
30	567	34.1	298	16	US-10-664-421-51	Sequence 51, Appli
31	565.5	34.0	297	14	US-10-295-681-51	Sequence 51, Appli
32	564	33.9	294	15	US-10-334-143-181	Sequence 181, Appli
33	563	33.9	298	14	US-10-295-681-31	Sequence 31, Appli
34	563	33.9	298	14	US-10-295-681-39	Sequence 39, Appli
35	561.5	33.8	294	15	US-10-389-566-1333	Sequence 1333, Ap
36	561	33.8	298	14	US-10-295-681-29	Sequence 29, Appli
37	561	33.8	298	14	US-10-295-681-43	Sequence 43, Appli
38	559	33.6	298	14	US-10-295-681-35	Sequence 35, Appli
39	556.5	33.5	294	15	US-10-389-566-1030	Sequence 1030, Ap
40	556	33.5	297	14	US-10-060-065-11	Sequence 11, Appli
41	556	33.5	297	14	US-10-059-585-32	Sequence 32, Appli
42	556	33.5	297	14	US-10-177-293-41	Sequence 41, Appli
43	556	33.5	297	14	US-10-174-794-12	Sequence 12, Appli
44	556	33.5	297	14	US-10-204-041-8	Sequence 8, Appli
45	556	33.5	297	15	US-10-394-322A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-766-691-12
; Sequence 12, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/10/766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 315
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-766-691-12

Query Match 100.0%; Score 1662; DB 17; Length 315;
Best Local Similarity 100.0%; Pred. No. 2e-132;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEKYEKLATGEGSYGVVFKCRNKTSGQVAVKKFVESEDDPVVKKIALREIMLKQKH 60
Db 1 MEKYEKLATGEGSYGVVFKCRNKTSGQVAVKKFVESEDDPVVKKIALREIMLKQKH 60

QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVADVGVKSVLWQTLQALNFCIH 120
DB 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVADVGVKSVLWQTLQALNFCIH 120
QY 121 NCIRHDIKPENILITKQGIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
DB 121 NCIRHDIKPENILITKQGIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
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DB 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTGLKLIIPRHOSIFKSNFGFHGISIP 240
QY 241 EPEDMETLEEFSDVHPVAFNFMKGLKMNPPDRITCSQLLESSYFDSFOEAQIKRKARN 300
DB 241 EPEDMETLEEFSDVHPVAFNFMKGLKMNPPDRITCSQLLESSYFDSFOEAQIKRKARN 300
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DB 301 EGRNRRQOVLPLKS 315

RESULT 2

US-10-333-314-10

; Sequence 10, Application US/10333314

; Publication No. US20030211093A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry

; APPLICANT: KHAN, Farrah A.; GURURATAN, Rajagopal

; APPLICANT: HAPALIA, April J.A.; CHAWLA, Narinder K.

; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi

; APPLICANT: BAUGHN, Ameena R.; POLICKY, Jennifer L.

; APPLICANT: THORNTON, Michael B.; TRIBOULEY, Catherine M.

; APPLICANT: NGUYEN, Daniel B.; BANDMAN, Olga

; APPLICANT: BURFORD, Neil; LAL, Preeti G.

; APPLICANT: DING, Li; YAO, Monique G.

; APPLICANT: ELLIOTT, Vicki S.; RECIPON, Shirley A.

; APPLICANT: KEARNEY, Liam; LU, Dying Aina M.

; APPLICANT: GREENWALD, Sara R.; TANG, Y. Tom

; APPLICANT: XU, Yuming; WALSH, Roderick T.

; APPLICANT: GIETZEN, Kimberly J.; YANG, Junming

; APPLICANT: JACKSON, Jennifer L.

; TITLE OF INVENTION: HUMAN KINASES

; FILE REFERENCE: PI-0162 USN

; CURRENT APPLICATION NUMBER: US/10/333,314

; PRIOR FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: PCT/US01/23092

; PRIOR FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 60/220,038

; PRIOR FILING DATE: 2000-07-21

; PRIOR APPLICATION NUMBER: US 60/222,112

; PRIOR FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: US 60/222,831

; PRIOR FILING DATE: 2000-08-04

; PRIOR APPLICATION NUMBER: US 60/224,729

; PRIOR FILING DATE: 2000-08-11

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: PERL Program

; SEQ ID NO 10

; LENGTH: 342

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No: 1698381CD1

US-10-333-314-10

Query Match 98.6%; Score 1639; DB 15; Length 342;
Best Local Similarity 99.0%; Pred. No. 1.9e-130;
Matches 312; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 1 MEKYEKLAKTGSGYGVVFKCRNKTSGQVAVKVFSEDDPVVKIALREIRMLKOLKH 60
|||||

DB 1 MEKYEKLAKTGSGYGVVFKCRNKTSGQVAVKVFSEDDPVVKIALREIRMLKOLKH 60
QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVADVGVKSVLWQTLQALNFCIH 120
DB 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVADVGVKSVLWQTLQALNFCIH 120
QY 121 NCIRHDIKPENILITKQGIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
DB 121 NCIRHDIKPENILITKQGIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
QY 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTGLKLIIPRHOSIFKSNFGFHGISIP 240
DB 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTGLKLIIPRHOSIFKSNFGFHGISIP 240
QY 241 EPEDMETLEEFSDVHPVAFNFMKGLKMNPPDRITCSQLLESSYFDSFOEAQIKRKARN 300
DB 241 EPEDMETLEEFSDVHPVAFNFMKGLKMNPPDRITCSQLLESSYFDSFOEAQIKRKARN 300
QY 301 EGRNRRQOVLPL 313
DB 301 EGRNRRQOVLPL 315

RESULT 3

US-10-766-691-6

; Sequence 6, Application US/10766691

; Publication No. US20050042626A1

; GENERAL INFORMATION:

; APPLICANT: Donoho, Gregory

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Nehls, Michael

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: Novel Human Kinase Proteins and

; FILE REFERENCE: Polynucleotides Encoding the Same

; CURRENT APPLICATION NUMBER: US/10/766,691

; PRIOR FILING DATE: 2004-01-28

; PRIOR APPLICATION NUMBER: US 60/156,511

; PRIOR FILING DATE: 1999-09-28

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 324

; TYPE: PRT

; ORGANISM: homo sapiens

US-10-766-691-6

Query Match 98.6%; Score 1638; DB 17; Length 324;
Best Local Similarity 100.0%; Pred. No. 2.2e-130;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKYEKLAKTGSGYGVVFKCRNKTSGQVAVKVFSEDDPVVKIALREIRMLKOLKH 60
DB 1 MEKYEKLAKTGSGYGVVFKCRNKTSGQVAVKVFSEDDPVVKIALREIRMLKOLKH 60
QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVADVGVKSVLWQTLQALNFCIH 120
DB 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVADVGVKSVLWQTLQALNFCIH 120
QY 121 NCIRHDIKPENILITKQGIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
DB 121 NCIRHDIKPENILITKQGIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
QY 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTGLKLIIPRHOSIFKSNFGFHGISIP 240
DB 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQYLIIRTGLKLIIPRHOSIFKSNFGFHGISIP 240
QY 241 EPEDMETLEEFSDVHPVAFNFMKGLKMNPPDRITCSQLLESSYFDSFOEAQIKRKARN 300
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Db 241 EPDMETLEEFSDVHPVAFNFMKGLKQNPDDRLTCSQLLESSYFDSFQEAQIKRKARN 300
Qy 301 EGRNRRRQOV 310
Db 301 EGRNRRRQOV 310

RESULT 4
US-10-766-691-10
; Sequence 10, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10/766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 2000-09-27
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 347
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-766-691-10

Query Match 98.4%; Score 1636; DB 17; Length 347;
Best Local Similarity 90.8%; Pred. No. 3.5e-130;
Matches 315; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Qy 1 MEKYEKLAKTGEYSYGVVFKCRNKTSGQVAVKVFSEDDPVVVKIALRIRMLKQLKH 60
Db 1 MEKYEKLAKTGEYSYGVVFKCRNKTSGQVAVKVFSEDDPVVVKIALRIRMLKQLKH 60

Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCIH 120
Db 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCIH 120

Qy 121 NCIRDIKPENILITKQIIKICDFGFAQLIPGDATDYVATRYRAPELLVGDYQGS 180
Db 121 NCIRDIKPENILITKQIIKICDFGFAQLIPGDATDYVATRYRAPELLVGDYQGS 180

Qy 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDOLYLIIRTL----- 217
Db 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDOLYLIIRTLVETGFRHVDQAGLELLTSSDDPA 240

Qy 218 -----GKLI PRHOSIFKSNFGFHGISIPEPEMETLEEFSDVHPVAFNFMKGLK 268
Db 241 VASQAGITGKLI PRHOSIFKSNFGFHGISIPEPEMETLEEFSDVHPVAFNFMKGLK 300

Qy 269 MNPDDLRTCSQLLESSYFDSFQEAQIKRKARNEGRNRQOVLPKS 315
Db 301 MNPDDLRTCSQLLESSYFDSFQEAQIKRKARNEGRNRQOVLPKS 347

RESULT 5
US-10-766-691-4
; Sequence 4, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn

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; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10/766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 356
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-766-691-4

Query Match 97.0%; Score 1612; DB 17; Length 356;
Best Local Similarity 90.6%; Pred. No. 3.9e-128;
Matches 310; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Qy 1 MEKYEKLAKTGEYSYGVVFKCRNKTSGQVAVKVFSEDDPVVVKIALRIRMLKQLKH 60
Db 1 MEKYEKLAKTGEYSYGVVFKCRNKTSGQVAVKVFSEDDPVVVKIALRIRMLKQLKH 60

Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCIH 120
Db 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCIH 120

Qy 121 NCIRDIKPENILITKQIIKICDFGFAQLIPGDATDYVATRYRAPELLVGDYQGS 180
Db 121 NCIRDIKPENILITKQIIKICDFGFAQLIPGDATDYVATRYRAPELLVGDYQGS 180

Qy 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDOLYLIIRTL----- 217
Db 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDOLYLIIRTLVETGFRHVDQAGLELLTSSDDPA 240

Qy 218 -----GKLI PRHOSIFKSNFGFHGISIPEPEMETLEEFSDVHPVAFNFMKGLK 268
Db 241 VASQAGITGKLI PRHOSIFKSNFGFHGISIPEPEMETLEEFSDVHPVAFNFMKGLK 300

Qy 269 MNPDDLRTCSQLLESSYFDSFQEAQIKRKARNEGRNRQOV 310
Db 301 MNPDDLRTCSQLLESSYFDSFQEAQIKRKARNEGRNRQOV 342

RESULT 6
US-10-363-616-391
; Sequence 391, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hysq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 391
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-391

Query Match 71.5%; Score 1188.5; DB 15; Length 358;
Best Local Similarity 70.5%; Pred. No. 2.7e-92;
Matches 213; Conservative 42; Mismatches 46; Indels 1; Gaps 1;

Qy 1 MEKYEKLAKTGEYSYGVVFKCRNKTSGQVAVKVFSEDDPVVVKIALRIRMLKQLKH 60

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Db 2 MEKYEKIGKIGEGSYGVVFKCRNRDTQGIKVAIKKFFLESDDPVKKIALREIRMLKQLKH 61
Qy 61 PNLVNLIEVFRKRRKMHVFEYCDHTLLNELERNPNGVADVGVKSVLWOTLOALNFCHIH 120
Db 62 PNLVNLIEVFRKRRKMHVFEYCDHTVHLHEDRYQGVPEHLVKSITWOTLOAVNFCCHKH 121
Qy 121 NCIRDIPKPNILITKGGIIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTOYG 179
Db 122 NCIRDIPKPNILITKHSVIKLCDFGARLLTGPSDYTDYVATRWYRAPELLVGDTOYG 181
Qy 180 SSVDIWAIGCVFAELLTGQPLWPKGSDVDOLYLIIRTLGKLIPRHQSIFKSNFGPHGISI 239
Db 182 PPVDVWAIGCVFAELLSGVPLWPKGSDVDOLYLIIRTLGKLIPRHQSIFKSNFGPHGISI 241
Qy 240 PEPEDMETLEKFSVDHPVAFNMKGLKMNPDRLTCSQLLESSYFDSFQEAQIKRKAR 299
Db 242 PEPEDMEPLKFPNISYPALGKLLKGLHMDPTRLTCEQLLHHPYFENIREIEDLAKHEH 301
Qy 300 NE 301
Db 302 NK 303

RESULT 7

US-10-664-421-97
; Sequence 97, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KUMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 97
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-97

Query Match 71.4%; Score 1186.5; DB 16; Length 338;
Best Local Similarity 70.5%; Pred. No. 3.8e-92;
Matches 213; Conservative 41; Mismatches 47; Indels 1; Gaps 1;
Qy 1 MEKYEKIAKTGEGSYGVVFKCRNKTSGQVAVKFFVESEDDPVKKIALREIRMLKQLKH 60
Db 2 MEKYEKIGKIGEGSYGVVFKCRNRDTQGIKVAIKKFFLESDDPVKKIALREIRMLKQLKH 61
Qy 61 PNLVNLIEVFRKRRKMHVFEYCDHTLLNELERNPNGVADVGVKSVLWOTLOALNFCHIH 120
Db 62 PNLVNLIEVFRKRRKMHVFEYCDHTVHLHEDRYQGVPEHLVKSITWOTLOAVNFCCHKH 121
Qy 121 NCIRDIPKPNILITKGGIIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTOYG 179
Db 122 NCIRDIPKPNILITKHSVIKLCDFGARLLTGPSDYTDYVATRWYRAPELLVGDTOYG 181
Qy 180 SSVDIWAIGCVFAELLTGQPLWPKGSDVDOLYLIIRTLGKLIPRHQSIFKSNFGPHGISI 239
Db 182 PPVDVWAIGCVFAELLSGVPLWPKGSDVDOLYLIIRTLGKLIPRHQSIFKSNFGPHGISI 241
Qy 240 PEPEDMETLEKFSVDHPVAFNMKGLKMNPDRLTCSQLLESSYFDSFQEAQIKRKAR 299
Db 242 PEPEDMEPLKFPNISYPALGKLLKGLHMDPTRLTCEQLLHHPYFENIREIEDLAKHEH 301

Qy 300 NE 301
Db 302 NK 303

RESULT 8

US-10-174-794-11
; Sequence 11, Application US/10174794
; Publication No. US20030166220A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-794-11

Query Match 71.2%; Score 1183.5; DB 14; Length 358;
Best Local Similarity 71.8%; Pred. No. 7.2e-92;
Matches 211; Conservative 41; Mismatches 41; Indels 1; Gaps 1;
Qy 1 MEKYEKIAKTGEGSYGVVFKCRNKTSGQVAVKFFVESEDDPVKKIALREIRMLKQLKH 60
Db 2 MEKYEKIGKIGEGSYGVVFKCRNRDTQGIKVAIKKFFLESDDPVKKIALREIRMLKQLKH 61
Qy 61 PNLVNLIEVFRKRRKMHVFEYCDHTLLNELERNPNGVADVGVKSVLWOTLOALNFCHIH 120
Db 62 PNLVNLIEVFRKRRKMHVFEYCDHTVHLHEDRYQGVPEHLVKSITWOTLOAVNFCCHKH 121
Qy 121 NCIRDIPKPNILITKGGIIKICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGDTOYG 179
Db 122 NCIRDIPKPNILITKHSVIKLCDFGARLLTGPSDYTDYVATRWYRAPELLVGDTOYG 181
Qy 180 SSVDIWAIGCVFAELLTGQPLWPKGSDVDOLYLIIRTLGKLIPRHQSIFKSNFGPHGISI 239
Db 182 PPVDVWAIGCVFAELLSGVPLWPKGSDVDOLYLIIRTLGKLIPRHQSIFKSNFGPHGISI 241
Qy 240 PEPEDMETLEKFSVDHPVAFNMKGLKMNPDRLTCSQLLESSYFDSFQEAQ 293
Db 242 PEPEDMEPLKFPNISYPALGKLLKGLHMDPTRLTCEQLLHHPYFENIREIE 295

RESULT 9

US-09-834-496A-2
; Sequence 2, Application US/09834496A
; Patent No. US20020090701A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann
; TITLE OF INVENTION: 14257 NOVEL PROTEIN KINASE MOLECULES AND
; FILE REFERENCE: 38155200900
; CURRENT APPLICATION NUMBER: US/09/834,496A
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/196,910
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-496A-2

Query Match 68.6%; Score 1140; DB 9; Length 228;
Best Local Similarity 98.2%; Pred. No. 2e-88;
Matches 214; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 MEKYEKLAKTGEBSYGVVFKCRNKTSGOVAVKVFSEDDPVVKIATLREIRMLKQLKH 60
DB 1 MGKYEKLAKTGEBSYGVVFKCRNKTSGOVAVKVFSEDDPVVKIATLREIRMLKQLKH 60
QY 61 PNLVNLIEVFRKRKMHLEVFYCDHTLLNELERNPNVGVADGVKSVLWQTLQALNFCIH 120
DB 61 PNLVNLIEVFRKRKMHLEVFYCDHTLLNELERNPNVGVADGVKSVLWQTLQALNFCIH 120
QY 121 NCIRDIKPENILITKOGIHKICDFGAQILIPGDATDYVATRWYRAPELLVGDTOYGS 180
DB 121 NCIRDIKPENILITKOGIHKICDFGAQILIPGDATDYVATRWYRAPELLVGDTOYGS 180
QY 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQVLIIRTLG 218
DB 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQVLIIRTLG 218

RESULT 10
US-10-174-794-4
; Sequence 4, Application US/10174794
; Publication No. US20030166220A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Oryctolagus cuniculus
US-10-174-794-4

Query Match 58.2%; Score 967.5; DB 14; Length 566;
Best Local Similarity 54.6%; Pred. No. 2.3e-73;
Matches 177; Conservative 67; Mismatches 65; Indels 15; Gaps 5;
QY 1 MEKYEKLAKTGEBSYGVVFKCRNKTSGOVAVKVFSEDDPVVKIATLREIRMLKQLKH 60
DB 1 MEKYEKLAKTGEBSYGVVFKCRNKTSGOVAVKVFSEDDPVVKIATLREIRMLKQLKH 60
QY 61 PNLVNLIEVFRKRKMHLEVFYCDHTLLNELERNPNVGVADGVKSVLWQTLQALNFCIH 120
DB 61 ENLVNLLEVCKKRWYLVFEFVDHTLDDLELFPNGLDQVQVQYLFQIINGIGFCHSH 120
QY 121 NCIRDIKPENILITKOGIHKICDFGAQILIPGDATDYVATRWYRAPELLVGDTOYGS 179
DB 121 NCIRDIKPENILITKOGIHKICDFGAQILIPGDATDYVATRWYRAPELLVGDTOYGS 179
QY 180 SVDIWAIGCVFAELLTGQPLWPGKSDVDQVLIIRTLGIPRHQSIKSNPFHGISI 239
DB 181 KAVDVWAIGCLVTEMLNGEPLFCGSDIDQLYLMRCGLNLIPIHQELFNKNPVFAGVRL 240
QY 240 PEPEDMETLEKFSVDHPVALNFMKGLKNPDDRLTCSQLLESYF--DSF-----QEA 292
DB 241 PEIKESPLERRYPKLSSEVIDLAKCLHDPDKRPFCAELLHDDFFQMDGFAERFSOEL 300
QY 293 QIK--RKARN-----EGNRNRQ 309
DB 301 QMKVQKDARNISLSKSKQNRKKEK 324

RESULT 11
US-10-174-794-10
; Sequence 10, Application US/10174794
; Publication No. US20030166220A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-794-10

Query Match 56.6%; Score 941.5; DB 14; Length 493;
Best Local Similarity 53.1%; Pred. No. 3.2e-71;
Matches 172; Conservative 68; Mismatches 69; Indels 15; Gaps 5;
QY 1 MEKYEKLAKTGEBSYGVVFKCRNKTSGOVAVKVFSEDDPVVKIATLREIRMLKQLKH 60
DB 1 MEKYEKLAKTGEBSYGVVFKCRNKTSGOVAVKVFSEDDPVVKIATLREIRMLKQLKH 60
QY 61 PNLVNLIEVFRKRKMHLEVFYCDHTLLNELERNPNVGVADGVKSVLWQTLQALNFCIH 120
DB 61 ENLVNLLEVCKKRWYLVFEFVDHTLDDLELFPNGLDQVQVQYLFQIINGIGFCHSH 120
QY 121 NCIRDIKPENILITKOGIHKICDFGAQILIPGDATDYVATRWYRAPELLVGDTOYGS 179
DB 121 NCIRDIKPENILITKOGIHKICDFGAQILIPGDATDYVATRWYRAPELLVGDTOYGS 179
QY 180 SVDIWAIGCVFAELLTGQPLWPGKSDVDQVLIIRTLGIPRHQSIKSNPFHGISI 239
DB 181 KAVDVWAIGCLVTEMLNGEPLFCGSDIDQLYLMRCGLNLIPIHQELFNKNPVFAGVRL 240
QY 240 PEPEDMETLEKFSVDHPVALNFMKGLKNPDDRLTCSQLLESYF--DSF-----QEA 292
DB 241 PEIKESPLERRYPKLSSEVIDLAKCLHDPDKRPFCAELLHDDFFQMDGFAERFSOEL 300
QY 293 QIK--RKARN-----EGNRNRQ 309
DB 301 QMKVQKDARNISLSKSKQNRKKEK 324

RESULT 12
US-10-369-022-22
; Sequence 22, Application US/10369022
; Publication No. US20030203847A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Beth
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS USING 9949, 14230, 760, 62553,
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44373,
; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
; FILE REFERENCE: MEI02-027PIRNONMIM
; CURRENT APPLICATION NUMBER: US/10/369,022
; PRIOR FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US 60/360,495
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/370,121

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/ PRIOR FILING DATE: 2002-04-04
/ PRIOR APPLICATION NUMBER: US 60/373,010
/ PRIOR FILING DATE: 2002-04-16
/ PRIOR APPLICATION NUMBER: US 60/373,908
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: US 60/377,717
/ PRIOR FILING DATE: 2002-05-03
/ PRIOR APPLICATION NUMBER: US 60/379,949
/ PRIOR FILING DATE: 2002-05-13
/ PRIOR APPLICATION NUMBER: US 60/382,409
/ PRIOR FILING DATE: 2002-05-21
/ PRIOR APPLICATION NUMBER: US 60/385,280
/ PRIOR FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: US 60/386,879
/ PRIOR FILING DATE: 2002-06-06
/ PRIOR APPLICATION NUMBER: US 60/387,536
/ PRIOR FILING DATE: 2002-06-10
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 22
/ LENGTH: 493
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-369-022-22

Query Match          56.6%; Score 941.5; DB 15; Length 493;
Best Local Similarity 53.1%; Pred. No. 3.2e-71;
Matches 172; Conservative 68; Mismatches 69; Indels 15; Gaps 5;

QY 1 MEKYEKLTGSGYGVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
Db 1 MEKYEKLTGSGYGVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
QY 61 PNLVNLIEVFRKRKQHLVFEYCDHTLLNELERNPNGVADGVKISVLWQTLQALNFCIH 120
Db 61 ENLVNLLEVCCKKRWLVFEVDHTILDDLEFNGLDYQVVKYLFQIINGIFGCHSH 120
QY 121 NCIHRIKIPENILITKQGIKICDFGPAQIL-IPGDATDYVATRWYRAPELLVGDYQY 179
Db 121 NCIHRIKIPENILVSGGVKLCDFGFARTLAAPGEVTDYVATRWYRAPELLVGDYQY 180
QY 180 SSVDTWAIGCVFAELLTQPLWPGKSDVDQLYLIIRTLGKLI PRHOSIFKSNPFHGISI 239
Db 181 KAVDVWALGCLVTEMFGEPLFGDSIDQLYHIMMCLGNLIPRHQELFNKNPVPFAGVRL 240
QY 240 PEPEDMETLEKFSVHPVAFNMFKGCLKMPDRLTCSQLLESSYF--DSF-----QEA 292
Db 241 PEIKEREPLRRYPKLSVWIDLAKKCLHIDPKRPFCAELLHHDFQMDGFAERFSQEL 300
QY 293 QIK--RKARN-----EGNRRRQ 309
Db 301 QLKVKQDARNVSLSKSKSNRKKKEK 324

RESULT 13
US-10-757-262-108
/ Sequence 108, Application US/10757262
/ Publication No. US20040197825A1
/ GENERAL INFORMATION:
/ APPLICANT: Karicheti, Venkateswarlu
/ APPLICANT: Silos-Santiago, Inmaculada
/ APPLICANT: Eliasof, Scott D.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
/ TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
/ TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
/ TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
/ TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22245, 2387, 52908, 69112, 14990,
/ TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,
/ TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
/ TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
/ TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 32678 OR
/ TITLE OF INVENTION: 55053
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/ FILE REFERENCE: MPI03-007P1RNMNMIM
/ CURRENT APPLICATION NUMBER: US/10/757,262
/ CURRENT FILING DATE: 2004-01-14
/ PRIOR APPLICATION NUMBER: US 60/440,318
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/444,783
/ PRIOR FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: US 60/457,901
/ PRIOR FILING DATE: 2003-03-27
/ PRIOR APPLICATION NUMBER: US 60/468,775
/ PRIOR FILING DATE: 2003-05-08
/ PRIOR APPLICATION NUMBER: US 60/471,614
/ PRIOR FILING DATE: 2003-05-19
/ PRIOR APPLICATION NUMBER: US 60/478,742
/ PRIOR FILING DATE: 2003-06-16
/ PRIOR APPLICATION NUMBER: US 60/488,529
/ PRIOR FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: US 60/491,156
/ PRIOR FILING DATE: 2003-07-30
/ PRIOR APPLICATION NUMBER: US 60/499,594
/ PRIOR FILING DATE: 2003-09-02
/ PRIOR APPLICATION NUMBER: US 60/506,332
/ PRIOR FILING DATE: 2003-09-26
/ NUMBER OF SEQ ID NOS: 136
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 108
/ LENGTH: 493
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-757-262-108

Query Match          56.6%; Score 941.5; DB 16; Length 493;
Best Local Similarity 53.1%; Pred. No. 3.2e-71;
Matches 172; Conservative 68; Mismatches 69; Indels 15; Gaps 5;

QY 1 MEKYEKLTGSGYGVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
Db 1 MEKYEKLTGSGYGVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
QY 61 PNLVNLIEVFRKRKQHLVFEYCDHTLLNELERNPNGVADGVKISVLWQTLQALNFCIH 120
Db 61 ENLVNLLEVCCKKRWLVFEVDHTILDDLEFNGLDYQVVKYLFQIINGIFGCHSH 120
QY 121 NCIHRIKIPENILITKQGIKICDFGPAQIL-IPGDATDYVATRWYRAPELLVGDYQY 179
Db 121 NCIHRIKIPENILVSGGVKLCDFGFARTLAAPGEVTDYVATRWYRAPELLVGDYQY 180
QY 180 SSVDTWAIGCVFAELLTQPLWPGKSDVDQLYLIIRTLGKLI PRHOSIFKSNPFHGISI 239
Db 181 KAVDVWALGCLVTEMFGEPLFGDSIDQLYHIMMCLGNLIPRHQELFNKNPVPFAGVRL 240
QY 240 PEPEDMETLEKFSVHPVAFNMFKGCLKMPDRLTCSQLLESSYF--DSF-----QEA 292
Db 241 PEIKEREPLRRYPKLSVWIDLAKKCLHIDPKRPFCAELLHHDFQMDGFAERFSQEL 300
QY 293 QIK--RKARN-----EGNRRRQ 309
Db 301 QLKVKQDARNVSLSKSKSNRKKKEK 324

RESULT 14
US-10-766-691-2
/ Sequence 2, Application US/10766691
/ Publication No. US20050042626A1
/ GENERAL INFORMATION:
/ APPLICANT: Donoho, Gregory
/ APPLICANT: Turner, C. Alexander Jr.
/ APPLICANT: Nehls, Michael
/ APPLICANT: Friedrich, Glenn
/ APPLICANT: Zambrowicz, Brian
/ APPLICANT: Sands, Arthur T.
/ TITLE OF INVENTION: Novel Human Kinase Proteins and
/ TITLE OF INVENTION: Polynucleotides Encoding the Same
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; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10/766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 187
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-766-691-2

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Query Match      47.6%; Score 791; DB 17; Length 187;
Best Local Similarity 100.0%; Pred. No. 5.6e-59;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKYEKLAKTGEQSYGVVFKCRNKTSGQVAVKVFVESEDDPVVVKIALREIRMLKOLKH 60
Db 1 MEKYEKLAKTGEQSYGVVFKCRNKTSGQVAVKVFVESEDDPVVVKIALREIRMLKOLKH 60

Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVGADGVKSVLWQTLQALNFCFHH 120
Db 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVGADGVKSVLWQTLQALNFCFHH 120

Qy 121 NCIHRIKIPENILITKQGIKICDFGFAQIL 151
Db 121 NCIHRIKIPENILITKQGIKICDFGFAQIL 151

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RESULT 15

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US-10-766-691-8
; Sequence 8, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10/766,691
; PRIOR FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 198
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-766-691-8

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Query Match      47.6%; Score 791; DB 17; Length 198;
Best Local Similarity 100.0%; Pred. No. 6e-59;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEKYEKLAKTGEQSYGVVFKCRNKTSGQVAVKVFVESEDDPVVVKIALREIRMLKOLKH 60
Db 1 MEKYEKLAKTGEQSYGVVFKCRNKTSGQVAVKVFVESEDDPVVVKIALREIRMLKOLKH 60

Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVGADGVKSVLWQTLQALNFCFHH 120
Db 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVGADGVKSVLWQTLQALNFCFHH 120

Qy 121 NCIHRIKIPENILITKQGIKICDFGFAQIL 151

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Db 121 NCIHRIKIPENILITKQGIKICDFGFAQIL 151

Search completed: April 22, 2005, 07:36:43
Job time : 781.363 secs

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OM protein - protein search, using sw model

Run on: April 22, 2005, 06:47:40 ; Search time 14.2749 Seconds
(without alignments)
1576.747 Million cell updates/sec

Title: US-10-766-691-12

Perfect score: 1562

Sequence: 1 MEKYEKLAKTGEYSYGVVFK.....RKARNEGRNRROQVLPKLS 315

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 314081 seqs, 71453778 residues

Total number of hits satisfying chosen parameters: 314081

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:*

- 1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*
- 2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
- 3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
- 4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
- 5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
- 6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
- 7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*
- 8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1504	90.5	485	1	PCT-US05-03526-7
2	1183.5	71.2	338	1	PCT-US04-30360-97
3	1183.5	71.2	338	6	US-10-941-635-97
4	941.5	56.6	493	1	PCT-US05-03526-5
5	909	54.7	350	8	US-60-655-875-129900
6	784.5	47.2	455	1	PCT-US05-03526-6
7	720.5	43.4	1030	1	PCT-US05-03526-8
8	569	34.2	224	6	US-10-450-763-36501
9	567	34.1	298	1	PCT-US04-30360-14
10	567	34.1	298	1	PCT-US04-30360-51
11	567	34.1	298	6	US-10-941-635-14
12	567	34.1	298	6	US-10-941-635-51
13	567	34.1	298	7	US-11-021-951-168
14	561.5	33.8	294	8	US-60-643-717-18889
15	555.5	33.4	300	8	US-60-643-717-7327
16	555.5	33.4	300	8	US-60-643-717-7328
17	554.5	33.4	294	8	US-60-643-717-9856
18	551.5	33.2	294	8	US-60-643-717-9196
19	550.5	33.1	294	8	US-60-643-717-1362
20	549.5	33.1	294	8	US-60-643-717-11788
21	549.5	33.1	294	8	US-60-643-717-12472
22	549.5	33.1	294	8	US-60-643-717-17436
23	547.5	32.9	294	8	US-60-643-717-3546
24	544.5	32.8	290	8	US-60-643-717-10996
25	544.5	32.8	294	8	US-60-643-717-10239

26	542.5	32.6	294	8	US-60-643-717-14313	Sequence 14313, A
27	542.5	32.6	294	8	US-60-643-717-14791	Sequence 14791, A
28	541.5	32.6	294	8	US-60-643-717-11662	Sequence 11662, A
29	540.5	32.5	294	8	US-60-643-717-13623	Sequence 13623, A
30	539.5	32.5	294	8	US-60-643-717-15844	Sequence 15844, A
31	536.5	32.3	298	8	US-60-643-717-16355	Sequence 16355, A
32	530.5	31.9	345	1	PCT-US04-30360-71	Sequence 71, Appl
33	530.5	31.9	345	6	US-10-941-635-71	Sequence 71, Appl
34	525.5	31.6	341	8	US-60-643-717-16441	Sequence 16441, A
35	522	31.4	293	8	US-60-643-717-14335	Sequence 14335, A
36	522	31.4	326	8	US-60-643-717-8068	Sequence 8068, Ap
37	520.5	31.3	303	8	US-60-643-717-16553	Sequence 16553, A
38	517	31.1	304	8	US-60-643-717-14840	Sequence 14840, A
39	516.5	31.1	291	8	US-60-643-717-18659	Sequence 18659, A
40	515	31.0	303	8	US-60-643-717-3781	Sequence 3781, Ap
41	514.5	31.0	280	8	US-60-643-717-15222	Sequence 15222, A
42	511.5	30.8	307	8	US-60-643-717-3350	Sequence 3350, Ap
43	509.5	30.7	379	8	US-60-643-717-11541	Sequence 11541, A
44	505.5	30.4	317	8	US-60-643-717-17906	Sequence 17906, A
45	505.5	30.4	527	7	US-11-033-515-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
PCT-US05-03526-7
; Sequence 7, Application PC/TUS0503526
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; FILE OF INVENTION: MEMS AS MODIFIERS OF BRANCHING MORPHOGENESIS AND METHODS OF USE
; CURRENT APPLICATION NUMBER: PCT/US05/03526
; CURRENT FILING DATE: 2005-01-27
; PRIOR APPLICATION NUMBER: US60/539,835
; PRIOR FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-03526-7

Query Match 90.5%; Score 1504; DB 1; Length 485;
Best Local Similarity 91.9%; Pred. No. 9.8e-89;
Matches 294; Conservative 6; Mismatches 14; Indels 6; Gaps 2;

Qy	2	EKYEKLAKTGEYSYGVVFKCRNKTSGQVAVKKEVEDDDPVVKKIALREIMLKQLKHP	61
Db	166	DPYEKLAKTGEYSYGVVFKCRNKTSGQVAVKKEVEDDDPVVKKIALREIMLKQLKHP	225
Qy	62	NLVNLIIEVFRKRKMHVFEYCDHTLNELEARNPNGVAD----	115
Db	226	NLVNLIIEVFRKRKMHVFEYCDHTLNELEARNPNGVAD----	285
Qy	116	FCIHNCIHRDKIPENILITKQGIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGD	175
Db	286	QIMLQCIHRDKIPENILITKQGIKICDFGFAQILIPGDAYTDYVATRWYRAPELLVGD	345
Qy	176	TOYSSVDIWAIGCVFAELLTQGPLWFGKSDVDLYLIIRTLGKLIIRHQIFKNSGFFH	235
Db	346	TOYSSVDIWAIGCVFAELLTQGPLWFGKSDVDLYLIIRTLGKLIIRHQIFKNSGFFH	405
Qy	236	GISTPEPEDMETLEKEFSVHPVAFNMKGLKKNPDRLTCSQLLESSYFDSFOEAQIK	295
Db	406	GISTPEPEDMETLEKEFSVHPVAFNMKGLKKNPDRLTCSQLLESSYFDSFOEAQIK	465
Qy	296	RKARNEGRNRROQVLPKLS	315
Db	466	RKARNEGRNRROQVLPKLS	485

RESULT 2
PCT-US04-30360-97
; Sequence 97, Application PC/TUS0430360
; GENERAL INFORMATION:
; APPLICANT: PLEXIKON, INC.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1703
; CURRENT APPLICATION NUMBER: PCT/US04/30360
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 97
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
PCT-US04-30360-97

Query Match 71.2%; Score 1183.5; DB 1; Length 338;
Best Local Similarity 71.8%; Pred. No. 1.8e-68;
Matches 211; Conservative 41; Mismatches 41; Indels 1; Gaps 1;
QY 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGOVAVKVFSEDDPVVKKIALREIRMLKOLKH 60
DB 2 MEKYEKIGKIGEGSYGVVFKCRNRTGQIVAKKFLSEDDPVVKKIALREIRMLKOLKH 61
QY 61 PNLVNLIEVFRKRKRLHVLVEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCCHI 120
DB 62 PNLVNLLEVFRKRRLHVLVEYCDHTVHLEDYQGVPEHLVKSITWQTLQAVNFCCHK 121
QY 121 NCIHRIKPENILITKOGIIKICDFGPAQILI-PCDAYTDYVATRWYRAPELLVGDTOYG 179
DB 122 NCIHRIKPENILITKOGIIKICDFGPAQILI-PCDAYTDYVATRWYRAPELLVGDTOYG 181
QY 180 SSVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLGLKLI PRHQSIFKSNPFHGISI 239
DB 182 PPVDVWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLGLKLI PRHQSIFKSNPFHGISI 241
QY 240 PEPEDMETLEKFSVHPVAFNFMKGLKMPDRRLTCSOLLESSYFDSFOEAQ 293
DB 242 PDPEDMEPLKFPNISYPALGKLLKGLHMDPTERLTCEQLLHHPYFENIREIE 295

RESULT 3
US-10-941-635-97
; Sequence 97, Application US/10941635
; GENERAL INFORMATION:
; APPLICANT: ARTIS, DEAN R.
; APPLICANT: BREMER, RYAN E.
; APPLICANT: GILLETTE, SAMUEL J.
; APPLICANT: HURT, CLARENCE R.
; APPLICANT: IBRAHIM, PRABHA L.
; APPLICANT: ZUCKERMAN, REBECCA L.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1702
; CURRENT APPLICATION NUMBER: US/10/941,635
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 97
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
US-10-941-635-97

Query Match 71.2%; Score 1183.5; DB 6; Length 338;
Best Local Similarity 71.8%; Pred. No. 1.8e-68;
Matches 211; Conservative 41; Mismatches 41; Indels 1; Gaps 1;
QY 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGOVAVKVFSEDDPVVKKIALREIRMLKOLKH 60
DB 2 MEKYEKIGKIGEGSYGVVFKCRNRTGQIVAKKFLSEDDPVVKKIALREIRMLKOLKH 61
QY 61 PNLVNLIEVFRKRKRLHVLVEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCCHI 120
DB 62 PNLVNLLEVFRKRRLHVLVEYCDHTVHLEDYQGVPEHLVKSITWQTLQAVNFCCHK 121
QY 121 NCIHRIKPENILITKOGIIKICDFGPAQILI-PCDAYTDYVATRWYRAPELLVGDTOYG 179
DB 122 NCIHRIKPENILITKOGIIKICDFGPAQILI-PCDAYTDYVATRWYRAPELLVGDTOYG 181
QY 180 SSVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLGLKLI PRHQSIFKSNPFHGISI 239
DB 182 PPVDVWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLGLKLI PRHQSIFKSNPFHGISI 241
QY 240 PEPEDMETLEKFSVHPVAFNFMKGLKMPDRRLTCSOLLESSYFDSFOEAQ 293
DB 242 PDPEDMEPLKFPNISYPALGKLLKGLHMDPTERLTCEQLLHHPYFENIREIE 295

RESULT 4
PCT-US05-03526-5
; Sequence 5, Application PC/TUS0503526
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: MEMS AS MODIFIERS OF BRANCHING MORPHOGENESIS AND METHODS OF USE
; FILE REFERENCE: EX05-003C-PC
; CURRENT APPLICATION NUMBER: PCT/US05/03526
; CURRENT FILING DATE: 2005-01-27
; PRIOR APPLICATION NUMBER: US60/539,835
; PRIOR FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US05-03526-5

Query Match 56.6%; Score 941.5; DB 1; Length 493;
Best Local Similarity 53.1%; Pred. No. 6.4e-53;
Matches 172; Conservative 68; Mismatches 69; Indels 15; Gaps 5;
QY 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGOVAVKVFSEDDPVVKKIALREIRMLKOLKH 60
DB 1 MEKYEKIGKIGEGSYGVVFKCRNKTGRIVAKKFLSEDDPVVKKIALREIRMLKOLKH 60
QY 61 PNLVNLIEVFRKRKRLHVLVEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCCHI 120
DB 61 ENLVNLLEVCCKKRWLVVFEVDHTILDDLEFPNGLDYQVVQYVLFQINGIGFCHSH 120
QY 121 NCIHRIKPENILITKOGIIKICDFGPAQILI-PCDAYTDYVATRWYRAPELLVGDTOYG 179
DB 121 NCIHRIKPENILITKOGIIKICDFGPAQILI-PCDAYTDYVATRWYRAPELLVGDTOYG 180
QY 180 SSVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLGLKLI PRHQSIFKSNPFHGISI 239
DB 181 KAVDVWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLGLKLI PRHQSIFKSNPFHGISI 240
QY 240 PEPEDMETLEKFSVHPVAFNFMKGLKMPDRRLTCSOLLESSYFDSFOEAQ 292
DB 241 PEIKEREPLERRYPKLVSEVWIDLAKKCLHIDPKFPFCAELLHHDFFQWMDGFAERFSOEL 300
QY 293 QIK--RKARN-----EGRNRRRQ 309
DB 301 QLKVKQKDARNVSLSKSKSNRKK 324

70 ENIVELKEAFRRGRKYLIVFEYVEKNMLLEEMPNGVPEKVKSYIQLIKAIHCHKN 129
121 NCIHRIKIPENIIITQGIITKICDFGFAQIILPGD--AYTDYATWRYRABELLIGDYOY 178
130 DIVHRDIKIPENIIISHNDVILKDFGFPARNUSEGNANYTEYVATRWYRSEPELLG-APY 188
179 GSSVDIWAIGCVFABELLTQGLPWPKGSVDQVLYIIRTLGKLIPRHQSIFKSNQFPFGHS 238
189 GKSVDMSVSGCITGLSLSQGLFPFGSEIDQLFTIQKVLGFLPSEQMKLYFSNPREHGLR 248
239 IPEPEDMETLEBKFSDV-HPVALNFMKGCUKMPPDRLTCSOLLESSYFDSFOEAIKKN 297
249 FAVNHQPQLERRYLGIILNSVLLDMKNLLKLPADRYLTEQCIN--HPTFTQRLDLDR 305
298 ARNEGRNRRROOV 310
306 SPSRSACEKPYHV 318

RESULT 8

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US-10-450-763-36501
; Sequence 36501, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 36501
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (115)..(146)
; OTHER INFORMATION: Protein kinases ATP-binding region proteins domain identified
; OTHER INFORMATION: by eMATRIX, accession number BL00107A, p-value=8.500e-27, raw
; OTHER INFORMATION: score of 18.39
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (4)..(190)
; OTHER INFORMATION: Eukaryotic protein kinase domain identified by Pfam,
; OTHER INFORMATION: accession name pkinase, E-value=3.5e-65, Pfam score of 230.0
US-10-450-763-36501

```

```

; GENERAL INFORMATION:
; APPLICANT: PLEXIKON, INC.
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1703
; CURRENT APPLICATION NUMBER: PCT/US04/30360
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 14
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
PCT-US04-30360-14

```

RESULT 10

```

RESULT 10
PCT-US04-30360-51
; Sequence 51, Application PC/TUS0430360
; GENERAL INFORMATION:
; APPLICANT: PLEXIKON, INC..
; TITLE OF INVENTION: MOLECULAR SCAFFOLDS FOR KINASE LIGAND DEVELOPMENT
; FILE REFERENCE: 039363-1703
; CURRENT APPLICATION NUMBER: PCT/US04/30360
; CURRENT FILING DATE: 2004-09-15
; PRIOR APPLICATION NUMBER: 60/503,277
; PRIOR FILING DATE: 2003-09-15
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 51
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Mammalian
; OTHER INFORMATION: protein sequence
PCT-US04-30360-51

Query Match          34.1%; Score 567; DB 1; Length 298;
Best Local Similarity 40.0%; Pred. No. 2.8e-29;
Matches 118; Conservative 60; Mismatches 99; Indels 18; Gaps 6;

QY      1 MEKYEKLAKTGEGSYGVFKCRNKTSGQVAVKFESEDDFVVKVIALREIRMLKQLKH 60
DB      1 MENQFQKEIGEGTYGVVYKARNKLTGEVVALKKIRLDITETGVPSTAIRKISLSKELNH 60

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; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-021-951-168

```

```

Query Match      34.1%; Score 567; DB 7; Length 298;
Best Local Similarity 40.0%; Pred. No. 2.8e-23;
Matches 118; Conservative 60; Mismatches 99; Indels 18; Gaps 6

QY      1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKKFVESEDDPVVKIALRETRMLKQLKH 60
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      1 MENFQKEKIGEGTVGVVYKARNKLTGEVVALKIRLDTEGVPSTAREISLUKELNH 60

QY      61 PNLVNLIEVFRKRNHLYFPYCKDHTLLNLELRNP-NGVADGVKSVLMQTLQALNFCHI 119
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      61 PNIVKLLDVINTENKLYLVFEFLQDLKCFMDASALTGPLPLIKSYLPQLLQGLAFCHS 120

QY      120 HNCIHRDIKPNILITKQGIKIICDFGFAQIL-IPGDVATDVYATRWYRAPELLVGDTCY 178
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      121 HRVLHRDLKPNQLINTEGAIKLADFLARAFGVPVRTYTHEVVTLYWRAPELLGCKKY 180

QY      179 GSSVDVIAWGCVFAELTGGPLWPGKSDVDOLYLIIRTGLKLIPIHQSTFKNGSFGHGI- 237
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      181 STAVDINSLGCIPIAWTRRALFPDGEISDQLPRIFRTLTG-----PDEVVMPGT 231

QY      238 SIPE--PDMETLSEKSDVHPV-----ALNFMKGCLOKMPDRLTCSQLLESSYF 286
      |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db      232 SMPDYKSFPPKWAQSDKCVKVPPLDEDGRSLLSOMLHYDNPKNRIKAKALAHPPF 286

```

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RESULT 14
US-60-643-717-18889
; Sequence 18889, Application US/60643717
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)A
; CURRENT APPLICATION NUMBER: US/60/643,717
; CURRENT FILING DATE: 2005-01-12
; NUMBER OF SEQ ID NOS: 19247
; SEQ ID NO 18889
; LENGTH: 294
; TYPE: PRT
; ORGANISM: Saccharum officinarum
US-60-643-717-18889

```

Query Match	33.8%	Score 561.5;	DB 8;	Length 294;
Best Local Similarity	37.0%;	Mismatches 69;	Indels 35;	Gaps 9;
Matches 115;	Conservative 92;	Mismatches 69;	Indels 35;	Gaps 9;
1	MEKYEKLAKTGECSYGVFKCRNKTSQGVAVKFKVESEDDPVVKKTALRRLMKOLKH	60		
1	MEQYKEVKEIGEGYGVYTKGDKATNETIALUKIRLQEDEGVSPFAIRSTLSLKKMMNH	60		
61	PNLVNLIIEVRRKRKMHLYEYCDHTLLN-----ELERNPNNGVADGVKISVLWQTLQAL	114		
61	DNIVRLHDVTHSEKRIYLVFEFLDLDLKKFMDSCPEFAKNPT-----LKSILYQLIRGV	115		
115	NFCHIHNCIHRDITKPNILITKQ-GIIKICDEGFAQL-IPGDAYTYVATRWVRAPELL	172		
116	AYCHSHRFLRDLKPNLLIDRTWTLLADFGUSAFGIPVTRITHEVVTLMYRAPEIL	175		
173	VGDTQYGVSSVDWAICGVFAELLTGOPLPWCKSDVDQLYLIIRTLGKLIIRHQSIFKSNQ	232		
176	LGAKQYSTVDVMSVGCIPFAEMVNGKLPFGDSEIDLFKIFVLG--TNEQS-----	227		

```

Qy 233 FFGIS-IP-----EPDMETLEKFSDFVHPVALNFMKGLQVNPDR LTCQSOLLE 282
Db 228 -WGVSLDFDKTAPFRWQAO LATI---:VNLEPAGLDLISKMLRYEPSKRITARQALE 283
Qy 283 SSYDFSQBEAQ 293
Db 284 HEYFKOLEMVQ 294

```

```

RESULT 15
US-60-643-717-7327
; Sequence 7327, Application US/60643717
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; TITLE OF INVENTION: Genes and Uses for Plant Improvement
; FILE REFERENCE: 38-21(53629)A
; CURRENT APPLICATION NUMBER: US/60/643,717
; CURRENT FILING DATE: 2005-01-12
; NUMBER OF SEQ ID NOS: 19247
; SEQ ID NO 7327
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Pneumocystis carinii
US-60-643-717-7327

```

Query Match	33.4%	Score	555.5	DB	8	Length	300		
Best Local Similarity	37.3%	Pred.	No. 1.5e-28						
Matches	113	Conservative	72	Mismatches	91	Indels	27	Gaps	8
QY	1	MEKYELAKTGGSGVGVFKCRNKTSGOVAVKFKFVESEDDPVVKIALREITMLKQJHK	60						
Db	1	MEQVORLEKIGEGYGVVYKAKLESGTIVALKKIRLEAEDEGVPSTAREITSLKKEHN	60						
QY	61	PNLVNLIEVFRKRKMKHLPEYCDHTLLNELERNPNGVADG--VTKSVLWOTLQALNFCH	118						
Db	61	DNVRLNLIHQESRLYLVEFLDLDLKKYMSIPKDMVLMGAEMIKKQMSQVSGVKYCH	120						
QY	119	IHNCHRDIPENILITPKOGIKICDFGFAQIL-IPGDAYDTVATWYRAPELVAGDTQ	177						
Db	121	SHRILHRDLKPQNLLIDREGNLKLDGLARAFGVLPRGYTHEVVTWYRAPEVLGGQ	180						
QY	178	YGSSVDIWAICGCPFAELLTCQPLWPKGSDVDQYLIIRTLGKLI PRHOSIFKSGFFHGI	237						
Db	181	YATALDIWSIGCFIAENATKPLPFGDSIDEIFRITLG--TPDENS-----WPGI	231						
QY	238	-SIPE-----PEDM-ETLEEKTSDVHPVALNFMKGLKQNDRLTSCQLLESYVF	286						
Db	232	TSYDFKATFKPKSPNUGELITELDS-----GIDLLQKCLRYPAERISAKALDHPYF	287						
QY	287	DSF	289						
Db	288	DDF	290						

Search completed: April 22, 2005, 07:09:11
Job time : 15.2749 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2005, 03:32:53 ; Search time 25.6949 Seconds
(without alignments)
1179.546 Million cell updates/sec

Title: US-10-766-691-12
Perfect score: 1662
Sequence: 1 MEKYEKLAKTGECSYGVVFK.....RKARNEGRRRQQLPLKS 315

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR.79:*

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1183.5	71.2	358	2 S23383	protein kinase (EC
2	1175.5	70.7	376	2 S22745	serine/threonine p
3	581	35.0	305	2 S23382	protein kinase (EC
4	574.5	34.6	292	2 S40021	protein kinase (EC
5	571.5	34.4	294	1 A40444	protein kinase (EC
6	571.5	34.4	294	2 B40444	protein kinase (EC
7	570.5	34.3	302	1 S50474	protein kinase (EC
8	568.5	34.2	294	2 S22440	protein kinase (EC
9	567	34.1	298	2 A41227	protein kinase (EC
10	565.5	34.0	297	2 A37871	protein kinase (EC
11	561.5	33.8	294	2 S23095	protein kinase (EC
12	559	33.6	302	1 A4349	protein kinase (EC
13	557	33.5	297	1 S24913	protein kinase (EC
14	556.5	33.5	294	2 T49271	CELL DIVISION CONT
15	556	33.5	297	2 A29539	protein kinase (EC
16	556	33.5	297	2 I45977	cyclin-dependent k
17	556	33.5	302	2 B44349	protein kinase (EC
18	554	33.3	301	1 S19209	protein kinase (EC
19	553	33.3	298	1 A44878	protein kinase (EC
20	551.5	33.2	311	2 S36619	protein kinase (EC
21	551	33.2	288	1 S42566	protein kinase (EC
22	550.5	33.1	294	1 S57928	protein kinase (EC
23	550.5	33.1	294	1 J02243	protein kinase (EC
24	550.5	33.1	294	1 S42049	protein kinase (EC
25	547.5	32.9	303	1 S06011	protein kinase (EC
26	547.5	32.9	308	1 S53538	protein kinase (EC
27	546.5	32.9	297	1 S12009	protein kinase cdc
28	545	32.8	297	1 A46355	protein kinase (EC
29	544.5	32.8	291	2 S23386	protein kinase (EC

30 544 32.7 293 2 JE0374 cyclin-dependent k
31 543 32.7 292 1 A45091 protein kinase (EC
32 543 32.7 292 1 I49592 protein kinase (EC
33 543 32.7 297 1 A36074 protein kinase (EC
34 543 32.7 301 1 S42101 protein kinase (EC
35 541.5 32.6 294 1 S31332 protein kinase (EC
36 540 32.5 296 2 S24386 protein kinase (EC
37 539 32.4 302 1 OKB185 protein kinase PHO
38 535.5 32.2 302 2 T17115 protein kinase cdc
39 530.5 31.9 346 2 A54820 CDK-activating pro
40 530 31.9 294 2 S51008 protein kinase (EC
41 528 31.8 292 2 S22441 protein kinase (EC
42 527.5 31.7 346 2 A56231 MO15/CDK-activatin
43 527 31.7 346 1 I78840 protein kinase (EC
44 525 31.6 332 1 S41003 protein kinase (EC
45 525 31.6 346 1 I48157 protein kinase (EC

ALIGNMENTS

protein kinase (EC 2.7.1.37) cdc2-related KKIALRE - human
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C:Accession: S23383; S22744
R:Meyerson, M.; Enders, G.H.; Wu, C.L.; Su, L.K.; Gorka, C.; Nelson, C.; Harlow, E.; Tsai;
EMBO J. 11, 2909-2917, 1992
A:Title: A family of human cdc2-related protein kinases.
A:Reference number: S23382; MUID:92347325; PMID:1639063
A:Accession: S23383
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-358 <MEY>
A:Cross-references: UNIPROT:Q00532; EMBL:X66358; NID:G36614; PIDN:CAA7002.1; PID:G36615
C:Superfamily: kinase-related transforming protein; protein kinase homology
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F:3-278/Domain: protein kinase homology <KIN>
F:11-19/Region: protein kinase ATP-binding motif
F:34,52,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 71.2%; Score 1183.5; DB 2; Length 358;
Best Local Similarity 71.8%; Pred. No. 5.1e-48;
Matches 211; Conservative 41; Mismatches 41; Indels 1; Gaps 1;
Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFESDDPVVKIALREIRMLKQLKH 60
Db 2 MEKYEKIGKIGESYGVVFKCRNRTGQIVAKKFLSEDDPVVKIALREIRMLKQLKH 61
Qy 61 PNLVNLEIEVFRKRKRLHVFYCDHTLLNLELRNPNGVADGVKSVLWQTLQALNFCIH 120
Db 62 PNLVNLEIEVFRKRKRLHVFYCDHTLVHLDYRQGVPEHLVKSITWQTLQAVNFCIKH 121
Qy 121 NCHTRDKPENILITKQGIKICDFGFAQILI-PGDAYTDYVATRWYRAPPELLVGDYQYG 179
Db 122 NCHTRDKPENILITKHSVIKLCDFGFAQLTGESDYITDYVATRWYRSPELLVGDYQYG 181
Qy 180 SSVDIWAIGCVFAELLTGQPLWPKGSVDVQLYIIRTLGKLIPIRHOQIFKSNFFHGISI 239
Db 182 PPVDVWAIGCVFAELLSGVLPWPKGSVDVQLYIRKTLGDLIPRHOQVFSNQYFSGVKI 241
Qy 240 PEPEDMETLEKFSVDHPVAFNFMKGLKNPDDRLTCSQLLESSYFDSFQEAQ 293
Db 242 PDPEDMEPLKFPNISYPALGLLKGLHMDPTERTLTCQQLLHHHPYENIREIE 295

RESULT 2
S22745
serine/threonine protein kinase KKIALRE (EC 2.7.1.1-) - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 19-Dec-1997
C:Accession: S22745

R;Meyerson, M.L.
submitted to the EMBL Data Library, May 1992

submitted to the EMBL Data Library, May 1992

A;Reference number: S22743

A;Accession: S22745

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-376 <MEY>

A;Cross-references: EMBL:X66359

C;Genetics:

A; Introns: 152/3; 170/3

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F;3-296/Domain: protein kinase homology <KIN>

F;11-19/Region: protein kinase ATP-binding motif

Query Match	70.7%;	Score 1175.5;	DB 2;	Length 376;
Best Local Similarity	67.6%;	Pred. No. 1.2e-47;		
Matches 211;	Conservative .41;	Mismatches 41;	Indels 19;	Gaps 1;

	Qy	db
1	MEKYEKLAKTGE	MEKYEKIGEGSY
2	GGVGFKCRNKT	GGVGFKCRNRT
3	SGQVAVKFFVE	SGQVAVKFFVE
4	SEDDPVVKIAL	SEDDPVVKIAL
5	REIRMLKOLKH	REIRMLKOLKH
6	60	61

Qy	61	P N L V N L I E V F R R K M H L V F E Y C D H T L L N E L R N P N G A D G V I K S V L W Q T I Q A I N F C H I H	120
		: : : : : : : : : :	
Db	62	P N L V N L I E V F R R K R L H L V F E Y C D H T V L H E L D R Y O R G V P H E L V K S T W T I Q A V N F C H K H	121

Qy	121	NCIHRDIKPENILITKQGIKICDFGFAQILI-----PGDAYTDYV	161
		: : :	
		: : :	
Db	122	NCIHRDVKPENILITKHSVIKLCDFGFARLLFXEQPSAAVFCPSITGXTGSPDYTDYV	181

Qy	162	182	221
Qy	ATRWYRAPELLVGD	ATRWYRAPELLVGD	ATRWYRAPELLVGD
	QYSSVD	QYSSVD	QYSSVD
	IAIGCVFAELLTGQ	IAIGCVFAELLTGQ	IAIGCVFAELLTGQ
	PLWPGKSDVDQL	PLWPGKSDVDQL	PLWPGKSDVDQL
	YLIIRTKGLI	YLIIRTKGLI	YLIIRTKGLI
	221	221	221
Db	ATRWYRSPPELLVGD	ATRWYRSPPELLVGD	ATRWYRSPPELLVGD
	QYPPVDVMAIGCVFAELL	QYPPVDVMAIGCVFAELL	QYPPVDVMAIGCVFAELL
	SGVLWPGKSDVDQL	SGVLWPGKSDVDQL	SGVLWPGKSDVDQL
	YLIIRTKGLI	YLIIRTKGLI	YLIIRTKGLI
	241	241	241

QY	222	PRHQSTFKSNGFFHGHSISPEPEDEMETLEEKFSVDHPVALNFMKGCKMNPDDRLLTCSQLL	281
		: : : : : :	
Ddb	242	PRHQVFSTNQVFGSVKIPDPEDMEPLEKFPNISYPALGLLKGCILHMDTERLTCEQLL	301

QY	282	ESSYFDSFQEAQ	293
		::: :	
Db	302	HHPYFNIREIE	313

RESULT 3
S23382
protein kinase (EC 2.7.1.37) cdk3 - human

C:Species: Homo sapiens (man)
 F:Date: 18-Jun-1993 #sequence
 F:Accession: S23382; S27243
 F:Meveverson, M.; Enders, G.H.; Wh. C.L.; Su L.K.; Gorka C.; Nelson C.; Harl

PMO J. 11, 2909-2917, 1992
Title: A family of human cdc2-related protein kinases.
Reference number: S23382; MUID:92347325; PMID:1639063
Accession: S23382

;Molecule type: mRNA
 ;Status: nucleic acid sequence not shown
 ;Cross-references: UNIPROT:Q00526; EMBL:X66357; NID:α36612; PTDN-CAA47001 1.

Genetics: 12q13-12q13
Gene: GDB:CDK3
Cross-references: GDB:283456
Map position: 12q13-12q13

;superfamily: kinase-related transforming protein; protein kinase homology
 ;;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific
 ;2-235/Domain: protein kinase homology <KIN>
 ;10-18/Region: protein kinase ATP-binding motif

Query Match	35.0%;	Score 581;	DB 2;	Length 305;
Best Local Similarity	39.8%;	Pred. No. 1.9e-20;		

Mismatches	125;	Conservative	66;	Mismatches	96;	Indels	24;	Gaps	8;
------------	------	--------------	-----	------------	-----	--------	-----	------	----

Qy	1	MEKEK	LAKTGGSGVVPFKCRNKTSGQVAVKKP----	VESEDDPVVVKIALREIRMLKQ	57	
Db	1	MMFQK	VEKIGSTGVVYKAKNRETQOLVALKIRLDLEMEGVP---	STAIREISLLKE	57	
Qy	58	LKHPNL	VNLIIIEVFRKRKXOMHIVFEYCDHTLLNELERNPNG-	VADGVTKSVLWQTQALNP	116	
Db	58	LKHPNI	VRLLDVVHNERKLYLVFFELSSODLKKYMDSTPGSEL	PLHLIKSVLFQOLGVSF	117	
Qy	117	CHHNCH	IRHDIKPENILITKOGIKICDFGPAQL-IPGDAYT	YVATRYRAPPELLVGD	175	
Db	118	CHSHRV	IHRLDPQNLINELGAIKLADFLGARAFGVPELT	YTHEVVVWLYRAPPELLGS	177	
Qy	176	TOYGS	SVIWAIGCVFAELLTQPLWPKSGSDVDQLYLI	IRTLGKLPRHQSIKSNPFH	235	
Db	178	KEYTAV	DVWSIGCFIAEWMVRKALPFGDSEIDOLF	FRFMLET-----PSEDTP	228	
Qy	236	GIS-LPE	-----PE-DMETLEEKESDVHPV	ALNFMKGLKONPDDRLTCS	LLSESYFOS	288
Db	229	GVTPQ	PDYKSGFPKWRKGLSEIIVPNLEPEGRD	LLMQLLQYDPSQRITAKTALA	HPFYSS	288
Qy	289	FOEAQ	IKRK	297		
Db	289	PEPSA	ARO	297		

RESULT 4

protein kinase (EC 2.7.1.37) cdc2 homolog - slime mold (Dictyostelium discoideum)
S40021
C:Species: Dictyostelium discoideum
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S40021; S39071
R:Michaelis, C.E.; Weeks, G.
submitted to the EMBL Data Library, August 1992
A:Description: The unicellular organism Dictyostelium discoideum possesses a highly related
A:Reference number: S40021
A:Accession: S40021
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-292 <MIC>
A:Cross-references: UNIPROT:P34117; EMBL:L00652; NID:G167695; PID:G167695
R:Michaelis, C.; Weeks, G.
Biochim. Biophys. Acta 1179, 117-124, 1993
A:Title: The isolation from a unicellular organism, Dictyostelium discoideum, of a highly
A:Reference number: S39071; MUID:94032415; PMID:8218353
A:Accession: S39071

A;Molecule type: mRNA

A,Residues: 1-18,'Y',20-188,'G',190-232 <MI2>
A,Cross-references: ENBL:100652
C,Complex: In various organisms, cdc2 has been identified as a component of the M-phase
C,Superfamily: kinase-related transforming protein; protein kinase homology
C,Keywords: ATP; cell cycle control; phosphoprotein; phosphotransferase; serine/threonine
F,2-254/Domain: protein kinase homology <KIN>
F,10-18/Region: protein kinase ATP-binding motif
F,33-51,126,128/Active site: Lys, Glu, Asp, Lys <status predicted>

Query Match 34.6%; Score 574.5; DB 2; Length 292;
Best Local Similarity 37.5%; Pred. No. 3.7e-20;
Matches 115; Conservative 64; Mismatches 93; Indels 35; Gaps 5;

	Qy
1 MEKYELAKTGESGVVFKCRNKTSGQVVAVKFFVESEDDPVVKIALREIRMLKOLKH	60
: : : :	:
: : : :	: : :
1 MEYSKIEKLGEYGYIVNAKANRETGEI VALKRILRDSDEGVPCTAIRISLLKELKH	60

61 PNVLNLIIEVRRKRKMHLLVFECYDHTLLNELERNPNGVADGVIKSVLWOTIQAALNFCHH 120
||'| : ||| : |||| | - : ||| : ||| : ||| :
61 PNIVRLHDVITHTRKLTLVFAYLDQDLKKYLDECCEISPTIKSPMYQLLKGVAFCHDH 120

[illegible]

180 SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLG-----KLIPRHQSIF- 228

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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-294 <COL>
C;Cross-references: GB:M60526
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase
F;2-256/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 34.4%; Score 571.5; DB 2; Length 294;
Best Local Similarity 37.6%; Pred. No. 5.1e-20;
Matches 117; Conservative 67; Mismatches 92; Indels 35; Gaps 9;

Qy 1 MEKYEKLAKTGEQGVVFKCNKTSQGVAVVKFVESEDDPVVKIALREIRMLKQLKH 60
Db 1 MEQYKEVKEIGETGVVYKALDKTANETIALKIRLEQDEGVSPSTAIREISLLKEMNH 60
Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLN-----ELERNPNGVADGVIKSLVMTQLQAL 114
Db 61 GNVRLHDVHSEKRIYLVFEYLDLKKFMDSCPEFAKNPT-----LIKSYLQILRGV 115
Qy 115 NFCHHNCIHRDIKPNILITKQ-GIIKCDFGFAQIL-IPGDAYTDYVATRWYRAPELL 172
Db 116 AYCHSHRVLHDLKQPNLILDRNNALKADFGARAFGIPVTFTHVVTWLYRAPEIL 175
Qy 173 VGDQYQSSVDIWAIGCVFAELLTQPLWPGKSDVDOLYLIIRTLGKLIIPRHQIFKSNG 232
Db 176 LGARQYSTPVDVWSVGCIFAEWVNGKLPFGDSEIDELFKIPVLG--TPNEQG----- 227
Qy 233 PFHGIS-IP-----EPEDMETLEKFSVDHPVALNFMKGLKKNPPDRLTCSOLLE 282
Db 228 -WPGVSLCPDPEKTAAPRWQAQDLATY--VPNLEPAGLDLLSKMLRYEPSKRITARQALE 283
Qy 283 SSYFDSFQEAQ 293
Db 284 HEYFADLEMVQ 294

RESULT 7
I50474
protein kinase (EC 2.7.1.37) cdc2 [similarity] - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 05-May-2000 #sequence_validation 05-May-2000 #text_change 09-Jul-2004
C;Accession: I50474
R;Kajiura, H.; Yamashita, M.; Katsu, Y.; Nagahama, Y.
Dev Growth Differ. 35, 647-654, 1993
A;Title: Isolation and characterization of goldfish cdc2, a catalytic component of mature
A;Reference number: I50474
A;Accession: I50474
A;Status: translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-302 <KAL>
A;Cross-references: UNIPROT:P51958; GB:D17758; NID:9471097; PIDN:BA04605.1; PID:9471098
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase
F;2-256/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,128,130/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 34.3%; Score 570.5; DB 1; Length 302;
Best Local Similarity 38.6%; Pred. No. 5.8e-20;
Matches 120; Conservative 68; Mismatches 90; Indels 33; Gaps 7;

Qy 1 MEKYEKLAKTGEQGVVFKCNKTSQGVAVVKF-VESEDDPVVKIALREIRMLKOLK 59
Db 1 MDDYLKIEKIGETGVVYKGNKNTGTGVAVWKKIRLSEEEG-VPSTAVREISLLKELQ 59
Qy 60 HPNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNG--VADGVIKSLVMTQLQALNFC 117
Db 60 HPNVVRLDLVLMQESKLYLVFEFLSMDLKKYLDLSIPSGQFMDPMLVKSLYQLILEGILFC 119
Qy 118 HHNCIHRDIKPNILITKQGIKIKCDFGFAQIL-IPGDAYTDYVATRWYRAPELLVQDT 176

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Db 120 HCRVLRHDLKPNLLIDNKGVIKLAADFGARAFGVPRVYTHEVVTLMYRAPEVLIGAS 179
Qy 177 QYGSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLG-----KLIPRHOS 226
Db 180 RYTPVDVMSIGTIFAEALATKPLFHDGSEIDQLFRIFRTLGTNPNEVPDVESLPDYKN 239
Qy 227 IF---KSNGFPHGISPEPEDMETLEKFSVDHPVAFNFMKGLKKNPDDRLTCSQLLES 283
Db 240 TFPKWKSG-----NLASTVKNLDKNGIDLTTRMLIYDPPKRSARQAMTH 284
Qy 284 SYFDSFOEAQI 294
Db 285 PYFDDLDKSTL 295

RESULT 8
S22440
Protein kinase (EC 2.7.1.37) cdc2 homolog 1 - rice
C/Species: Oryza sativa (rice)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S22440
R/Hashimoto, J.; Hirabayashi, T.; Hayano, Y.; Hata, S.; Ohashi, Y.; Suzuki, I.; Utsugi,
Mol. Gen. Genet. 233, 10-16, 1992
A/Title: Isolation and characterization of cDNA clones encoding cdc2 homologues from Ory
A/Reference number: S22440; MUID:92293101; PMID:1376401
A/Accession: S22440
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-294 <HAS>
A/Cross-references: UNIPROT:P29618; EMBL:X60374; NID:G20342; PIDN:CAA42922.1; PID:G20343
C/Superfamily: kinase-related transforming protein; protein kinase homology
C/Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
F;2-256/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
Query Match 34.2%; Score 568.5; DB 2; Length 294;
Best Local Similarity 37.6%; Pred. No. 7e-20;
Matches 117; Conservative 67; Mismatches 92; Indels 35; Gaps 9;
Qy 1 MEKYEKLAKTGSGYGVVFKCRNKTSGOVAVKFESEDDPVVKIALREIRMLKQLKH 60
Db 1 MEQYEKEKIGEGYGVVYRARDKVTNETIALKIRLEQDEGVPTAIRISLLKEMH 60
Qy 61 PNLVNLIEVFRKRMHLVFEYCDHTLLN-----ELERNPVGADGVKSVLWQTLQAL 114
Db 61 GNIVRLHDVHSEKRIYLVFEYLDLKKFMDSCPEPAKNPT-----LIKSYLYQLRGV 115
Qy 115 NFCHINCHIRDIKPENILITKQ-GIIKICDFGPAQIL-IPGDAYTDYVATRYRAPELL 172
Db 116 AYCHSHRVLRHDLKPNLLIDRRNALKLDADFGARAFGIPVTFTHVVTLMYRAPEIL 175
Qy 173 VGDYQSGSDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLGKLIPRHOSIFKSN 232
Db 176 LGSRYQYTPVDVMSVGCIFAEVNWQKPLFGDSEIDELFKIFVLG--TFNEQS----- 227
Qy 233 FFHGI-SIP-----EPEDMETLEKFSVDHPVAFNFMKGLKKNPDDRLTCSQLLE 282
Db 228 -WPGVSLPYKSAFPKQQAQDLATI---VPTLDPAGLDLSKMLRYEPNKRITARQALE 283
Qy 283 SSYFDSFOEAQ 293
Db 284 HEYFKOLEMVQ 294

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RESULT 9
A41227
Protein kinase (EC 2.7.1.37) cdk2 - human
N/Alternate names: Egi homolog; protein kinase p34
C/Species: Homo sapiens (man)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C/Accession: A41227; S17873; S16520

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R/Ninomiya-Tsujii, J.; Nomoto, S.; Yasuda, H.; Reed, S.I.; Matsumoto, K.
Proc. Natl. Acad. Sci. U.S.A. 88, 9006-9010, 1991
A/Title: Cloning of a human cDNA encoding a CDC2-related kinase by complementation of a t
A/Reference number: A41227; MUID:92020980; PMID:1717994
A/Accession: A41227
A/Molecule type: mRNA
A/Residues: 1-298 <NIN>
A/Cross-references: UNIPROT:P24941; GB:M68520; NID:G180177; PIDN:AAA35667.1; PID:G180178
R/Tsai, L.H.; Harlow, E.; Meyerson, M.
Nature 353, 174-177, 1991
A/Title: Isolation of the human cdk2 gene that encodes the cyclin A- and adenovirus E1A-
A/Reference number: S17873; MUID:91367262; PMID:1653904
A/Accession: S17873
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-298 <TSA>
A/Cross-references: GB:X62071; NID:G312802; PIDN:CAA43985.1; PID:G312803
R/Elledge, S.J.; Spottswood, M.R.
EMBO J. 10, 2653-2659, 1991
A/Title: A new human p34 protein kinase, CDK2, identified by complementation of a cdc28 n
A/Reference number: S16520; MUID:91330891; PMID:1714386
A/Accession: S16520
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-176, 'S', 178-298 <ELL>
A/Cross-references: EMBL:X61622; NID:G29848; PIDN:CAA43807.1; PID:G29849
C/Genetics:
A/Gene: GDB:CDK2
A/Cross-references: GDB:128984; OMIM:116953
A/Map position: 12q13-12q13
C/Superfamily: kinase-related transforming protein; protein kinase homology
C/Keywords: ATP; cell cycle control; mitosis; phosphoprotein; phosphotransferase; serine,
F;2-255/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;14,160/Binding site: phosphate (Thr) (covalent) #status predicted
F;15/Binding site: phosphate (Tyr) (covalent) #status predicted
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
Query Match 34.1%; Score 567; DB 2; Length 298;
Best Local Similarity 40.0%; Pred. No. 8.3e-20;
Matches 118; Conservative 60; Mismatches 99; Indels 18; Gaps 6;
Qy 1 MEKYEKLAKTGSGYGVVFKCRNKTSGOVAVKFESEDDPVVKIALREIRMLKQLKH 60
Db 1 MENFQVKEKIGEGYGVVYKARKLTGVAVKIRLDTETEGVPSTAIRISLLKELNH 60
Qy 61 PNLVNLIEVFRKRMHLVFEYCDHTLLNELRN-NGVADGVKSVLWQTLQALNFCHE 119
Db 61 PNIVKLLDVHTEKNKLYLVFEFLHQDLKKFMDAGALTGIPLPKSYLFQLLOGLAFCHS 120
Qy 120 HNCIHRDIKPENILITKQIIGIICDFGPAQIL-IPGDAYTDYVATRYRAPELLVGDYQ 178
Db 121 HVLVLRHDLKPNLLIDRRNALKLDADFGARAFGIPVTFTHVVTLMYRAPEILLGCKY 180
Qy 179 GSSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLGKLIPRHOSIFKSNFFHGI- 237
Db 181 STAVDINSLGICFAEMVTRALFGDSEIDQLFRIFTLGT-----PDEVVWFQVT 231
Qy 238 SIPE--PEDMETLEKFSVDHPV-----ALNFMKGLKKNPDDRLTCSQLLESYF 286
Db 232 SMPDYKSFPKWARQDFSKVVPPLDEDRSLLSQMLHYDENKRIKSAKAAHAHPFF 286

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RESULT 10
A37871
Protein kinase (EC 2.7.1.37) cdk2 - African clawed frog
N/Alternate names: cell division control protein CDC2 homolog Egi
C/Species: Xenopus laevis (African clawed frog)
C/Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
C/Accession: A37871; S15866; I51662; S14410
R/Paris, J.; Le Guellec, R.; Couturier, A.; Le Guellec, K.; Omilli, F.; Camonis, J.; Macn
Proc. Natl. Acad. Sci. U.S.A. 88, 1039-1043, 1991
A/Title: Cloning by differential screening of a Xenopus cDNA coding for a protein highly

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A;Reference number: A37871; MUID:91126051; PMID:1704128

A;Accession: A37871

A;Molecule type: mRNA

A;Residues: 1-297 <PAR>

A;Cross-references: UNIPROT:P23437; UNIPROT:Q9PSU0; GB:X14227

R;le Guellac, R.

submitted to the EMBL Data Library, January 1989

A;Reference number: S15866

A;Accession: S15866

A;Molecule type: mRNA

A;Residues: 1-92,'R',94-297 <LEA>

A;Cross-references: EMBL:X14227; NID:964665; PIDN:CAA32443.1; PID:964666

R;Olive, M.; Theze, N.; Philippe, M.; Le Pennec, J.P.; Leirivay, H.

Gene 151, 81-88, 1994

A;Title: Cloning of the Xenopus laevis cdk2 promoter and functional analysis in oocytes

A;Reference number: S151662; MUID:95129896; PMID:7828909

A;Accession: S151662

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-39 <OLI>

A;Cross-references: EMBL:U07979; NID:9473584; PIDN:AAA82123.1; PID:9473585

C;Genetics:

A;Gene: cdk2

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase

F;2-255/Domain: protein kinase homology <KIN>

F;10-18/Region: protein kinase ATP-binding motif

F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 34.0%; Score 565.5; DB 2; Length 297;

Best Local Similarity 37.8%; Pred. No. 9.7e-20;

Matches 116; Conservative 65; Mismatches 85; Indels 41; Gaps 6;

Qy 1 MEKYEKLAKTGESEYGVVFKCRNKTSGQVAVKVFSEDDPVVKVKTALREIRMLKQLKH 60

Db 1 MENFQKEKIGEGYGVVYKARNETGEIVALKRLDTEGVPSVTAIREISLLKELNH 60

Qy 61 PNLVNLIEVFRKRRKMHVFEYCDHTLLNELE-RNPNGVADGVTKSVLWOTLQALNFCI 119

Db 61 PNLVNLIEVFRKRRKMHVFEYCDHTLLNELE-RNPNGVADGVTKSVLWOTLQALNFCI 120

Qy 120 HNCIHRDIKPEINILITKQIKICDFGAQIL-IPGDAYTDYVATRYRAPELLVGDQY 178

Db 121 HRVLRDLKPNLLIDRTNSLKLADFLARAFGIPVRTFTHVVTLYRAPELLVGSHT 180

Qy 179 GSSVDIWAIGCVFAELLTQGPLWPKGSDVDQYLIIRTLG-----KLIPRHQSI 228

Db 181 STAVDIWLSGCIFAEMITRRAFLFGDSEIDQLFRIFTLGTPDEVSNPGVTTMPDYKSTP 240

Qy 229 KSNQFFHGISIPEPEMETLEEFSDVHPVAFNFMKGLKMPDRLTCSQLLESSYFDS 288

Db 241 P-----KWIRQDFSKVVP-----PLDEGRDLAQLQ---YDS 271

Qy 289 FQEAQIK 295

Db 272 NKRTSAK 278

RESULT 11

S23095

protein kinase (EC 2.7.1.37) cdc2 - Arabidopsis thaliana

N;Alternate names: cdc2 protein homolog; CDC2a protein; cell division control protein 2

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 22-Nov-1993 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004

C;Accession: S23095; A49884; J01337; JQ0967; S18202

R;Imajuku, Y.; Hirayama, T.; Endoh, H.; Oka, A.

FEBS Lett. 304, 73-77, 1992

A;Title: Exon-intron organization of the Arabidopsis thaliana protein kinase genes CDC2a

A;Reference number: S23095; MUID:92316202; PMID:1618302

A;Accession: S23095

A;Molecule type: DNA

A;Residues: 1-294 <INA>

A;Cross-references: UNIPROT:P24100; EMBL:D10850; NID:9217848; PIDN:BAA01623.1; PID:92178

R;Inze, D.; Ferreira, P.; Hemerly, A.; Van Montagu, M.

Biochem. Soc. Trans. 20, 80-84, 1992

A;Title: Control of cell division in plants.

A;Reference number: A48984; MUID:92339744; PMID:1634002

A;Accession: A48984

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-294 <INZ>

A;Experimental source: flower

A;Note: sequence extracted from NCBI backbone (NCBIP:109461)

R;Hirayama, T.; Imajuku, Y.; Anai, T.; Matsui, M.; Oka, A.

Gene 105, 159-165, 1991

A;Title: Identification of two cell-cycle-controlling cdc2 gene homologs in Arabidopsis

A;Reference number: JQ1337; MUID:92039027; PMID:1937013

A;Accession: JQ1337

A;Molecule type: mRNA

A;Residues: 1-294 <HIF>

A;Cross-references: EMBL:X57839; NID:916218; PIDN:CAA40971.1; PID:916219

R;Ferreira, P.C.G.; Hemerly, A.S.; Villarroel, R.; Van Montagu, M.; Inze, D.

Plant Cell 3, 531-540, 1991

A;Title: The Arabidopsis functional homolog of the p34cdc2 protein kinase.

A;Reference number: JQ0967; MUID:93005715; PMID:1840925

A;Accession: JQ0967

A;Molecule type: mRNA

A;Residues: 1-294 <FER>

A;Cross-references: GB:S45387; NID:9257373; PIDN:AAB23643.1; PID:9257374

A;Experimental source: flower

C;Comment: The protein is a key component of the eukaryotic cell cycle.

C;Genetics:

A;Gene: cdc2

A;Introns: 3/3; 65/2; 105/3; 163/3; 218/2; 247/3; 265/3

C;Function:

A;Description: phosphotransferase; protein kinase; required for G1 to S-phase transition;

C;Superfamily: kinase-related transforming protein; protein kinase homology

C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase

F;2-256/Domain: protein kinase homology <KIN>

F;10-18/Region: protein kinase ATP-binding motif

F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 33.8%; Score 561.5; DB 2; Length 294;

Best Local Similarity 37.1%; Pred. No. 1.5e-19;

Matches 111; Conservative 70; Mismatches 93; Indels 25; Gaps 6;

Qy 1 MEKYEKLAKTGESEYGVVFKCRNKTSGQVAVKVFSEDDPVVKVKTALREIRMLKQLKH 60

Db 1 MDQYKEKIGEGYGVVYKARNETGEIVALKRLDTEGVPSVTAIREISLLKELNH 60

Qy 61 PNLVNLIEVFRKRRKMHVFEYCDHTLLNELE-RNPNGVAD-GVTKSVLWOTLQALNFCI 119

Db 61 SNIVKQDVVHSEKRLVLFYDLDDUKHMDSTPDFSKDLHMKTLYQLRGIAYCHS 120

Qy 120 HNCIHRDIKPEINILITKQ-GIHKICDFGAQIL-IPGDAYTDYVATRYRAPELLVGDQY 177

Db 121 HRVLRDLKPNLLIDRTNSLKLADFLARAFGIPVRTFTHVVTLYRAPELLVGSHT 180

Qy 178 YGSSVDIWAIGCVFAELLTQGPLWPKGSDVDQYLIIRTLG-----KLIPRHQSI 227

Db 181 YSTPVDIWSVGCIFAEMISQKPLFGDSEIDQLFRIFRIMGTPEYDTRWGVTSLPDYKSA 240

Qy 228 FKSNGFFHGISIPEPEMETLEEFSDVHPVAFNFMKGLKMPDRLTCSQLLESSYF 286

Db 241 FPX-----WKPTDLETF---VPLNDPGVDLLSKMLMDPTKKNARAALAEHYF 287

RESULT 12

A44349

protein kinase (EC 2.7.1.37) cdc2-A [similarity] - African clawed frog

N;Alternate names: maturation-promoting factor p34cdc2 chain A

C;Species: Xenopus laevis (African clawed frog)

C;Date: 05-May-2000 #sequence revision 05-May-2000 #text_change 09-Jul-2004

C;Accession: A44349

R;Pickham, K.M.; Meyer, A.N.; Li, J.; Donoghue, D.J.

Mol. Cell. Biol. 12, 3192-3203, 1992

A:Title: Requirement of mos(Xe) protein kinase for meiotic maturation of Xenopus oocytes
 A:Reference number: A44349; MUID:92318937; PMID:137775

A:Accession: A44349
 A:Molecule type: mRNA
 A:Residues: 1-302 <PIC>
 A:Cross-references: UNIPROT:P35567; GB:M60680; NID:g214022; PIDN:AAA63561.1; PID:g214023
 A:Experimental source: oocytes
 A:Note: sequence extracted from NCBI backbone (NCBI:107682, NCBI:P107683)
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
 F:2-256/Domain: protein kinase homology <KIN>
 F:10-18/Region: protein kinase ATP-binding motif
 F:33,51,128,130/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 33.5%; Score 559; DB 1; Length 302;
 Best Local Similarity 36.7%; Pred. No. 2e-19;
 Matches 117; Conservative 68; Mismatches 102; Indels 32; Gaps 6;

QY 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKQLKH 60
 DB 1 MDEYTKIEKIGEGTYGVVYKGRHKATQGVVAMKIRLENERGVSPSTAIRISLKELOH 60
 QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLNELEPNNG--VADGVKSVLMOTLQALNFC 118
 DB 61 PNLVNLIEVFRKRKMHVFEYCDHTLNELEPNNG--VADGVKSVLMOTLQALNFC 118
 QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLNELEPNNG--VADGVKSVLMOTLQALNFC 120
 DB 61 PNLVNLIEVFRKRKMHVFEYCDHTLNELEPNNG--VADGVKSVLMOTLQALNFC 120
 QY 119 INNCIHRDKPENILITKQGIKIICDFGFAQIL-IPGDAYTDYVATRYRAPELLVGDQ 177
 DB 121 SRRLVRLDLKPQNLIDDKRTNSKLADFGARAFGIPVRTTFHEVVTLYWYRAPELLVGDQ 177
 QY 178 YGSSVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLGLKLIPIRHOSIFKSNQFFHG 237
 DB 181 YSTPVDIWSIGTIFAEIATKPLFHGSDSEIDQLFRIFALG--TPNNE----- 226
 QY 238 SIPEPEMETLEEKFSFSDVHPVA-----SDVHPVAFNFMKGLKMPDDRLTCSQLLESSY 285
 DB 227 VNPVESLQDYKNTFPKPKGSLASHVKNLDLGLSKMLVYDPAKRIQSGKMALEHYP 286
 QY 286 FDSFQBAQIKR 304
 DB 287 FDDLKSSL---PDNQIRN 302

RESULT 13
 S24913

protein kinase (EC 2.7.1.37) cdc2 [similarity] - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C:Accession: S24913
 R:Kanaoka, Y.; Nojima, H.; Okayama, H.
 A:Description: Nucleotide sequences of cDNAs encoding rat cdc2 + and cyclin 2.
 A:Reference number: S20658

A:Accession: S24913
 A:Molecule type: mRNA
 A:Residues: 1-297 <KAN>
 A:Cross-references: UNIPROT:P39951; EMBL:X60767; NID:g57533; PIDN:CAA43177.1; PID:g57534
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
 F:2-256/Domain: protein kinase homology <KIN>
 F:10-18/Region: protein kinase ATP-binding motif
 F:33,51,128,130/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 33.5%; Score 557; DB 1; Length 297;
 Best Local Similarity 39.1%; Pred. No. 2.4e-19;
 Matches 122; Conservative 63; Mismatches 95; Indels 32; Gaps 8;

QY 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKQLKH 59
 DB 1 MEDYTKIEKIGEGTYGVVYKGRHRTTQGVVAMKIRLENERGVSPSTAIRISLKELOH 59
 QY 60 HPLVNLIEVFRKRKMHVFEYCDHTLNELEPNNG--VADGVKSVLMOTLQALNFC 117

DB 60 HENIVSLQDVLWQDSRLYLIFEFLSMDLKYKLDLSDIPPGQFMDSSIVKSYLYQILQGVFC 119
 QY 118 HHCNCIHRDKPENILITKQGIKIICDFGFAQIL-IPGDAYTDYVATRYRAPELLVGD 176
 DB 120 HSRVLRLDLKPQNLIDDKRTNSKLADFGARAFGIPVRTTFHEVVTLYWYRAPELLVGD 179
 QY 177 YGSSVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLGLKLIPIRHOSIFKSNQFFHG 236
 DB 180 RYSTPVDIWSIGTIFAEIATKPLFHGSDSEIDQLFRIFALG--TPNNE----- 226
 QY 237 SIPEPEMETLEEKFSFSDVHPVA-----LNMFKGCLKMPDDRLTCSQLLESS 284
 DB 227 VNPVESLQDYKNTFPKPKGSLASHVKNLDLGLSKMLVYDPAKRIQSGKMALEHYP 285
 QY 285 YFDSFQBAQIKR 296
 DB 286 YFDDL-DNQIKK 296

RESULT 14
 T49271

CELL DIVISION CONTROL PROTEIN 2 HOMOLOG A - Arabidopsis thaliana
 N:Alternate names: protein T2J18.20
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
 C:Accession: T49271
 R:Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Rudd, S.;
 A:Submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z25021

A:Accession: T49271
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-294 <RIE>
 A:Cross-references: EMBL:AL132963; GSPDB:GN00061; ATSP:T2J18.20
 A:Experimental source: cultivar Columbia; BAC clone T2J18
 C:Genetics:
 A:Gene: ATSP:T2J18.20
 A:Map position: 3
 A:Introns: 3/3; 67/3; 105/3; 163/3; 218/2; 247/3; 265/3
 C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 33.5%; Score 556.5; DB 2; Length 294;
 Best Local Similarity 36.8%; Pred. No. 2.5e-19;
 Matches 110; Conservative 70; Mismatches 94; Indels 25; Gaps 6;

QY 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKQLKH 60
 DB 1 MDOYEKVEKIGEGTYGVVYKARDKVTNETIALKKIRLEQDEGVSPSTAIRISLKELOH 60
 QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLNELEPNNGVAD-GVIKSVLMOTLQALNFC 119
 DB 61 SNIVKYDDVHSEKRLVYFVYLDLKKHMDSPDFSKLHMLTKYLYQLRGAYCHS 120
 QY 120 HNCIHRDKPENILITKQ-GIIKICDFGFAQIL-IPGDAYTDYVATRYRAPELLVGD 177
 DB 121 HRLVRLDLKPQNLIDDKRTNSKLADFGARAFGIPVRTTFHEVVTLYWYRAPELLVGD 180
 QY 178 YGSSVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLG-----KLIPRHOSI 227
 DB 191 YSTPVDIWSIGTIFAEIATKPLFHGSDSEIDQLFRIFALG--TPNNE----- 240
 QY 228 FKSNGFFHGSIPEPEMETLEEKFSFSDVHPVAFNFMKGLKMPDDRLTCSQLLESSY 286
 DB 241 FPK-----WKPTDLETF---VPLNDPDGVDLLSKMLMDPTKINARAALAEHYF 287

RESULT 15
 A29539

protein kinase (EC 2.7.1.37) cdc2 - human
 N:Alternate names: cell division control protein 2 (CDC2)
 C:Species: Homo sapiens (man)
 C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
 C:Accession: A29539

R:Lee, M.G.; Nurse, P.
 Nature 327, 31-35, 1987
 A:Title: Complementation used to clone a human homologue of the fission yeast cell cycle
 A:Reference number: A29539; PMID:87201915; PMID:3553962
 A:Accession: A29539
 A:Molecule type: mRNA
 A:Residues: 1-297 <LEE>
 A:Cross-references: UNIPROT:P06493; GB:X05360; NID:g29838; PIDN:CAA28963.1; PID:g29839
 C:Genetics:
 A:Gene: GDB: CDC2
 A:Cross-references: GDB:119052; OMIM:116940
 A:Map position: 10q21.1-10q21.1
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; cell cycle control; mitosis; phosphoprotein; phosphotransferase; serine
 F:2-256/Domain: protein kinase homology <KIN>
 F:10-18/Region: protein kinase ATP-binding motif
 F:14,161/Binding site: phosphate (Thr) (covalent) #status predicted
 F:15/Binding site: phosphate (Tyr) (covalent) #status predicted
 F:33,51,128,130/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 33.5%; Score 556; DB 2; Length 297;
 Best Local Similarity 39.4%; Pred. No. 2.7e-19;
 Matches 123; Conservative 61; Mismatches 96; Indels 32; Gaps 8;

Qy	1	MEYKELAKTCEGSGYGVVFKCRNKTSGOVAVKXF-VESEDDPVVKIALREIRMKQLK	59
Db	1	MEDYTKIEKIGEGTYGVVYKGRHKTTGQVAMKKIRLESEEG-VPSTAIRISLLKELR	59
Qy	60	HPNLVNLIEVFRKRKMHVPEYCDHTLLNELERNPG--VADGVIKSLMOTLQALNFC	117
Db	60	HPNIVSLQDVLQMDSRLYLIFEFLSMDLKKYLDLIPFGQYWDSSLVKSXYLIQLQGI VFC	119
Qy	118	HIHNCIHRDIKPNILITKQGIKICDFGAQIL-IFGDAYTDYVATRWYRAPELLVGD	176
Db	120	HSRRVLHRLKPNLLIDDKGTIKLADFGLARAFGIPRVVYTHEVVTWYRSPEVLGSA	179
Qy	177	QYSSVDIWAIGCVFAELLTCQPLWPGKSDVDQYLIIRTLGKLI PRHQSFKSNGFHG	236
Db	180	RYSTPVDIWSIGTIFAEELATKKPLFHGDSEIDQLFRIFRALG--TPNNE-----	226
Qy	237	ISIPEPEDEMETLEKFSQDVHVA-----LNFMKGLKMNPDRLTCSQLLESS	284
Db	227	-VMFEVESLQDYKNTFPKWKFGSLASHVKVKNLDENGLDLSKMLIYDPAKRISGKMLNHP	285
Qy	285	YFDSFQEAQIKR	296
Db	286	YFNDL-DNQIKK	296

Search completed: April 22, 2005, 06:51:40
 Job time : 26.6949 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 01:29:40 ; Search time 82.7946 Seconds
(without alignments)
1948.255 Million cell updates/sec

Title: US-10-766-691-12
Perfect score: 1562
Sequence: 1 MEKYEKLAKTGESYGVFK.....RKARNEGRRRQOVLPLKS 315

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1209.5	72.8	350	Q6AXJ9	Q6axj9 brachydanio
2	1206	72.6	352	Q8CEQ0	Q8ceq0 mus musculus
3	1188.5	71.5	358	Q6QUA0	Q6qua0 homo sapien
4	1184	71.2	352	Q66HE7	Q66he7 rattus norv
5	1183.5	71.2	358	1 KIA_HUMAN	Q00532 homo sapien
6	1035.5	62.3	367	Q7QBG7	Q7qbg7 anopheles g
7	1027.5	61.8	353	Q9U2H1	Q9u2h1 caenorhabdi
8	1027.5	61.8	392	Q9VMN3	Q9vmn3 drosophila
9	967.5	58.2	566	Q9TTK0	Q9ttk0 oryctolagus
10	958	57.6	385	Q675R9	Q675r9 oikopleura
11	941.5	56.6	493	Q9QY12	Q9qy12 mus musculus
12	930.5	56.0	564	Q9QUR0	Q9quk0 mus musculus
13	930.5	56.0	568	Q9QY11	Q9qy11 mus musculus
14	928	55.8	329	Q675R9	Q6gmd6 xenopus lae
15	924	55.6	320	Q6GMD6	Q6txh3 rattus norv
16	919.5	55.3	651	Q6TXH3	Q6pl14 homo sapien
17	784.5	47.2	455	Q6PL14	Q6l1v4 homo sapien
18	784.5	47.2	592	Q6IVW4	Q6bm92 trypanosoma
19	781	47.0	657	Q9BMG2	Q8kl34 mus musculus
20	770	46.3	353	Q8KL34	Q9grt9 leishmania
21	769.5	46.3	1106	Q9GRT9	Q8bkr2 mus musculus
22	767.5	46.2	457	Q8BKR2	Q8b149 mus musculus
23	764.5	46.0	585	Q8BL49	Q8jmo2 rattus norv
24	763.5	45.9	457	Q9JMO2	Q8jfm01 rattus norv
25	763.5	45.9	505	Q9JMO1	Q8blf2 mus musculus
26	759.5	45.7	595	Q8BLF2	Q8bw18 mus musculus
27	720.5	43.4	783	Q8BWT8	Q8lvc7 homo sapien
28	720.5	43.4	831	Q8LYC7	Q76039 homo sapien
29	720.5	43.4	1030	1 STK9_HUMAN	Q8wxq5 homo sapien
30	708	42.6	993	Q8WXQ5	Q8bve0 mus musculus
31	702.5	42.3	578	Q8BVE0	

32	644	38.7	1104	2	Q9W6R6	Q9w6r6 fugu rubrip
33	581.5	35.0	289	2	Q7RM49	Q7rm49 plasmodium
34	581	35.0	305	1	CDK3_HUMAN	Q00526 homo sapien
35	579.5	34.9	294	2	Q9ZRI1	Q9zri1 triticum ae
36	574.5	34.6	292	1	CC2H_DICDI	P34117 dictyosteli
37	571.5	34.4	297	1	CDK2_XENLA	P23437 xenopus lae
38	570.5	34.3	297	2	Q66IH7	Q66ih7 xenopus tro
39	570.5	34.3	302	1	CDK2_CARAU	P51958 carassius a
40	570.5	34.3	302	2	Q7T3L7	Q7t3l7 brachydanio
41	568.5	34.2	294	1	CC21_ORYSA	P29618 oryza sativ
42	567.5	34.1	303	1	CDK2_ORYJA	Q49ga2 oryzias jav
43	567	34.1	298	1	CDK2_HUMAN	P24941 homo sapien
44	566.5	34.1	294	1	CDK2_MAIZE	P23111 zea mays (m
45	564	33.9	288	2	Q9XZD6	Q9xz d6 plasmodium

ALIGNMENTS

RESULT 1	
Q6AXJ9	PRELIMINARY; PRT; 350 AA.
AC Q6AXJ9;	
DT 25-OCT-2004 (TrEMBLrel. 28, Created)	
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)	
DE Zgc:101002 protein.	
GN Name=zgc:101002;	
OS Brachydanio rerio (Zebrafish) (Danio rerio).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;	
OC Cyprinidae; Danio.	
OX NCBI_TaxID=7955;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=Singapore local strain; TISSUE=Embryo;	
RC PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heih F.,	
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA Scapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,	
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,	
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,	
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,	
RA Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,	
RA Jones S.J., Marra M.A.;	
RT "Generation and initial analysis of more than 15,000 full-length human	
RT and mouse cDNA sequences."	
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RN [2]	
RP SEQUENCE FROM N.A.	
RC STRAIN=Singapore local strain; TISSUE=Embryo;	
RC Director MGC Project;	
RC Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.	
RL EMBL; BC079506; AAH79506.1; -	
DR GO; GO:0005524; F:ATP binding; IEA.	
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.	
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.	
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.	
DR InterPro; IPR000719; Kinase like.	
DR InterPro; IPR000719; Prot kinase.	
DR InterPro; IPR002290; Ser Thr kinase.	
DR InterPro; IPR008271; Ser Thr_pkin_AS.	
DR InterPro; IPR001245; Tyr_pkinase.	
DR Pfam; PF00069; Pkinase; 1.	

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DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR NCBI; SMO0219; TTKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
DR ATP-binding; Kinase; Transferase.
SQ SEQUENCE 350 AA; 40810 MW; 9B04440EE0E38BE1 CRC64;

Query Match 72.8%; Score 1209.5; DB 2; Length 350;
Best Local Similarity 69.9%; Pred. No. 1.5e-77;
Matches 220; Conservative 47; Mismatches 45; Indels 3; Gaps 2;

QY 1 MEKYEKLAKTGSGYGVVFKCRNKTSGOVAVKVFVESEDDPVVKKIALREIRMLKQLKH 60
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 60
QY 61 PNLVNLIEVFRKRKQHLVFEYCDHTLNELEPNNGVADGVKSVLWQTLQALNFCFH 120
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 120
QY 61 PNLVNLMEVFRKRRLHLVFEYCDHTLNELEPNNGVADGVKSVLWQTLQALNFCFH 120
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 120
QY 121 NCIHREDIKPENLITKQGIKICDFGFAQILI-PCDAVTDVYATRWYRAPELLVGD 179
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 179
QY 121 NCIHREDVAPENLITKHQVILKCDGEPARILTGPCDYTDCCVATRWYRAPELLV 180
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 180
QY 180 SSVDTIAGTCVPAELLTGQPLWPGKSDVDQLYLIIRTLGKLIPRHQSIFKSNPFH 239
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 239
QY 181 PPVDVWAVGCVFAELLSGAPLWPGKSDVDQLYLIIRTLGKLIPRHQVFSNF 240
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 240
QY 240 PEPEDMETLEKFSVDVHVALFMKGLKMPDDRLTCSLLESYFDSFQF--AQIKRK 297
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 297
QY 241 PEPQMEPELEKYPNLSYOALSIMKGLRMDPAERLSCEQLLEQPYFDSLRESESV 300
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 300
QY 298 ARNEGRNRRRQQLVP 312
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 312
QY 301 LDRKKTKTQPRKHL 315
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 315

RESULT 2
ID Q8CEQ0 PRELIMINARY; PRT; 352 AA.
AC Q8CEQ0;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4933411017 product:cyclin-dependent kinase-like 1
DE (CDC2-related kinase), full insert sequence.
GN Name=Cdk1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of

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RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Testis;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Testis;
RC STRAIN=C57BL/6J; TISSUE=Testis;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK016781; BAC25497.1; -.
DR HSSP; Q00535; 1H4L.
DR MGD; MGI:1918341; Cdk1.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Cyclin; Kinase; Transferase.
SQ SEQUENCE 352 AA; 41023 MW; 639F56C8080F35E0 CRC64;

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Query Match 72.6%; Score 1206; DB 2; Length 352;
Best Local Similarity 68.9%; Pred. No. 2.7e-77;
Matches 222; Conservative 42; Mismatches 48; Indels 10; Gaps 3;

QY 1 MEKYEKLAKTGSGYGVVFKCRNKTSGOVAVKVFVESEDDPVVKKIALREIRMLKQLKH 60
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 60
QY 61 PNLVNLIEVFRKRKQHLVFEYCDHTLNELEPNNGVADGVKSVLWQTLQALNFCFH 120
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 120
QY 61 PNLVNLMEVFRKRRLHLVFEYCDHTLNELEPNNGVADGVKSVLWQTLQALNFCFH 120
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 120
QY 121 NCIHREDIKPENLITKQGIKICDFGFAQILI-PCDAVTDVYATRWYRAPELLVGD 179
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 179

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Db 121 NCIRHDKPENILITKSAIKLDFGPARLITGSDYDDVATRWTRSPPELLVGDYQY 180
Qy 180 SSVDIWAIGCVFABELLTGQPLWPKGSDVDQYLIRTLGKLIPIRHQSIKSNFGFHGISI 239
Db 181 PPVDVWAIGCVFABELLGVLWPKGSDVDQYLIRTLGKLIPIRHQSVFNQVFSGVKI 240
Qy 240 PEPEDMETLEKFSVDHPVVALNFMWGLKKNPDDRLTCSOLLESSYFDSFQEA-----QI 294
Db 241 PEPEDMETLEKFFNISYSALGFLKGLCHMDPAERLTCEQLLQHPYFDSIREVGELTROH 300
Qy 295 KRKARNEGRNRRO----QVLP 312
Db 301 DKPARKTLRQSRKHLTGLOLPL 322

RESULT 3
Q6QUAO PRELIMINARY; PRT; 358 AA.
AC Q6QUAO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cyclin-dependent kinase-like 1 (CDC2-related kinase).
GN Name=CDK1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
RA Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,
RA Sherwood J.K., Sherwood A.M., Leithausen B.J., Nickerson D.A.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY525548; AAS000095.1; --
DR HSP; P24941; 1838.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase_1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Cyclin; Kinase; Transferase.
SQ SEQUENCE 358 AA; 41833 MW; 823E432BF84B77C6 CRC64;

Query Match
Best Local Similarity 71.5%; Score 1188.5; DB 2; Length 358;
Matches 213; Conservative 42; Mismatches 46; Indels 1; Gaps 1;

Qy 1 MEKYEKLAKTGSGYGVVFKCRNKTSGQVAVKXFESEDDPVVKYKIALREIRMLKQLKH 60
Db 2 MEKYEKIGKSGYGVVFKCRNRDTCQIVAKKFESEDDPVVKYKIALREIRMLKQLKH 61
Qy 61 PNLVNLLEVERKRRKMLVPEYCDHTLLNELERNPNGVADGVKSVLWOTLQALNFCIH 120
Db 62 PNLVNLLEVERKRRRLHLVPEYCDHTLVLHEDRYQGVPEHLVKSITWTQLQAVNFCXH 121
Qy 121 NCIRHDKPENILITKGIKICDFGAQILI-PCDGYDVATRWTRAPPELLVGDYQY 179
Db 122 NCIRHDKPENILITKHSVKICLDFGPARLITGSDYDDVATRWTRSPPELLVGDYQY 181

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Qy 180 SSVDIWAIGCVFABELLTGQPLWPKGSDVDQYLIRTLGKLIPIRHQSIKSNFGFHGISI 239
Db 182 PPVDVWAIGCVFABELLGVLWPKGSDVDQYLIRTLGKLIPIRHQSVFNQVFSGVKI 241
Qy 240 PEPEDMETLEKFSVDHPVVALNFMWGLKKNPDDRLTCSOLLESSYFDSFQEAQIKRKAR 299
Db 242 PEPEDMEPLEKFPNISYPALGKGLCHMDPTERLTCEQLLHHPYFENIREIEDLAKEH 301
Qy 300 NE 301
Db 302 NK 303

RESULT 4
Q66HE7 PRELIMINARY; PRT; 352 AA.
AC Q66HE7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC081896; AAH81896.1; --
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase_1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 352 AA; 40899 MW; DB9CDF5464E66E24 CRC64;

Query Match
Best Local Similarity 71.2%; Score 1184; DB 2; Length 352;
Matches 214; Conservative 45; Mismatches 49; Indels 2; Gaps 2;

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[illegible]

RESULT 8
Q9VMN3 PRELIMINARY; PRT; 392 AA.
AC Q9VMN3;
DT 01-MAY-2000 (TReMBUrel. 13, Created)
DT 01-MAY-2000 (TReMBUrel. 13, Last sequence update)
DT 01-MAR-2004 (TReMBUrel. 26, Last annotation update)
DE CG7236-PA.
GN ORFNames=CG7236;
OS *Drosophila melanogaster* (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blaise R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.C., Holt R.A., Andrews-Frannkoch C., Baldwin D.,
RA April J.F., Agbayani A., An H.J., Andrews-Frannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Besley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.

Db 1 MEKYNLGVGSGVMKCNKDSGRIVAKKFELESDDDKMKVKIAMREIKLLKQLRH 60
Qy 61 PNLVNLIEVFRKRKRMHLVYFCOHTLLNELRNPNGVADGVKSVLWQTLQALNFCCHI 120
Db 61 ENLVNLIEVCKKRWYLVFEVDHTLDDLEFPNGLDDQVQKYLFOIINGIGFCHSH 120
Qy 121 NCIRDIKPENILITKQGIKICDGFPAQIL-IPGDAYTDVATRWYRAPELLVGDQY 179
Db 121 NIHRDIKPENILVSQSGVVKLCDFGFARTLAAPGEVYTDVATRWYRAPELLVGDVKY 180
Qy 180 SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIIRHOSIFKSNGFPHGSI 239
Db 181 KAVDVWALGCLVTEMLGEPFPGSDIDQLYLWRCLGNLIPRQELFYKNPFAVRL 240
Qy 240 PEPEDMETLEKFSVDVHPVAFNMFKGLKMNPPDRLLTCSQLLESSYF--DSF-----QEA 292
Db 241 PEIKESPELRRYPKLSVWIDLAKCLHVPDKRPFCAELLHDDFFQMDGFAERFSQEL 300
Qy 293 QIK--RKARN-----EGNRRRQ 309
Db 301 QMKVQKQARNISLSKKSQNRKKEK 324

RESULT 10

Q675R9 PRELIMINARY; PRT; 385 AA.
AC Q675R9;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Cyclin-dependent kinase-like 1.
GN ORFNames=006-03;
OS Oikopleura dioica.
OC Eukaryota; Metazoa; Chordata; Urochordata; Appendicularia;
OC Oikopleuridae; Oikopleura.
OX NCBI_TaxID=34765;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15343333; DOI=10.1038/nature02709;
RA Seo H.C., Edvardsen R.B., Maeland A.D., Bjordal M., Jensen M.F.,
RA Hansen A., Flaatt M., Weissenbach J., Lehrach H., Wincker P.,
RA Reinhardt R., Chourrout D.;
RT "Hox cluster disintegration with persistent anteroposterior order of
RT expression in Oikopleura dioica.";
RL Nature 431:67-71(2004).
DR EMBL; AY449462; AAS21447.1; -
DR GO; GO:0016301; F-kinase activity; IEA.
DR InterPro; IPR011009; Kinase-like.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR01245; Tyr_kinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW Cyclin; Kinase.
SQ SEQUENCE 385 AA; 45512 MW; 059F814421ACADAI CRC64;

Query Match 57.6%; Score 958; DB 2; Length 385;
Best Local Similarity 57.9%; Pred. No. 1e-59;
Matches 168; Conservative 58; Mismatches 62; Indels 2; Gaps 1;

Qy 2 EYKELAKTGEISGVVFKCRNKTSGQVAVKVFESDDPVVKIALREIMLKQLKHP 61
Db 4 DKYEKIESRSGSIVYKCNRETRAIVAKRFIESEELNIKKIAMREIMLKSLKHQ 63
Qy 62 NLVNLIEVFRKRKRMHLVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCCHI 121
Db 64 NLVNLIEVYKRRKRLHLVFEYCDHTLVLTLEQNPHGLPEQSIKRITVQVLKGLSFCHAQK 123

Qy 122 CIHRDIKPENILITKQGIKICDGFPAQILIPGDAYTDVATRWYRAPELLVGDQYSS 181
Db 124 CIHRDVPENILITKQGOIKLDFGFAIRILIPGDDLTDDYVATRWYRAPELLVGDLYNSA 183
Qy 182 VDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIIRHOSIFKSNGFPHG--ISI 239
Db 184 VDIWAIGCVFAGELLNGQPIWPGKSELQDLHKIKTCCGELLIOHKKLIQTNKYLGRQHLH 243
Qy 240 PEPEDMETLEKFSVDVHPVAFNMFKGLKMNPPDRLLTCSQLLESSYFDSF 289
Db 244 TSPRERVIEALYKAPSHTSIFLKNCLQMDPTWRLDCVELLDHAYFDY 293
RESULT 11
Q92772 PRELIMINARY; PRT; 493 AA.
AC Q92772;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE P56 KKIAMRE protein kinase.
GN Name=KKIAMRE;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97152547; PubMed=9000130;
RA Taglienti C.A., Wysk M., Davis R.J.;
RT "Molecular cloning of the epidermal growth factor-stimulated protein
RT kinase p56 KKIAMRE.";
RL Oncogene 13:2563-2574(1996).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; U35146; AAC50918.1; -
DR HSSP; P24941; IH00
DR Genew; HGNC:1782; CDKL2.
DR GO; GO:0004672; F-protein kinase activity; TAS.
DR GO; GO:0007548; P:sex differentiation; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 493 AA; 56018 MW; 5CC20A91CBF89EFE CRC64;

Query Match 56.6%; Score 941.5; DB 2; Length 493;
Best Local Similarity 53.1%; Pred. No. 1.9e-58;
Matches 172; Conservative 68; Mismatches 69; Indels 15; Gaps 5;

Qy 1 MEKYEKLAKTGEISGVVFKCRNKTSGQVAVKVFESDDPVVKIALREIMLKQLKH 60
Db 1 MEKYNLGVGSGVMKCNKDSGRIVAKKFELESDDDKMKVKIAMREIKLLKQLRH 60
Qy 61 PNLVNLIEVFRKRKRMHLVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCCHI 120
Db 61 ENLVNLIEVCKKRWYLVFEVDHTLDDLEFPNGLDDQVQKYLFOIINGIGFCHSH 120
Qy 121 NCIRDIKPENILITKQGIKICDGFPAQIL-IPGDAYTDVATRWYRAPELLVGDQY 179
Db 121 NIHRDIKPENILVSQSGVVKLCDFGFARTLAAPGEVYTDVATRWYRAPELLVGDVKY 180
Qy 180 SSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLIIRHOSIFKSNGFPHGSI 239
Db 181 KAVDVWALGCLVTEMLGEPFPGSDIDQLYLWRCLGNLIPRQELFYKNPFAVRL 240
Qy 240 PEPEDMETLEKFSVDVHPVAFNMFKGLKMNPPDRLLTCSQLLESSYF--DSF-----QEA 292
Db 241 PEIKEREPLRRYPKLSVWIDLAKCLHVPDKRPFCAELLHDDFFQMDGFAERFSQEL 300

RESULT 14

Q9QY11 PRELIMINARY; PRT; 329 AA.
 AC Q9QY11;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Ser/Thr kinase KIAA0842.1 (Fragment).
 GN Name=Cdk12; Synonyms=Kcm;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Sassa T., Gomi H., Sun W., Ikeda T., Thompson R.F., Itoharu S.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AB029067; BAA8429.1; -;
 DR HSP; P24941; 101Q.
 DR MGD; MGI:1185827; Cdk12.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser Thr pkinase.
 DR InterPro; IPR008271; Ser Thr pkin AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NON TER 329
 SQ SEQUENCE 329 AA; 38023 MW; F72EB8965AE8585 CRC64;

Query Match 55.8%; Score 928; DB 2; Length 329;
 Best Local Similarity 53.9%; Pred. No. 1.1e-57;
 Matches 173; Conservative 63; Mismatches 73; Indels 12; Gaps 5;
 Qy 1 MEKYEKLAKTGEQSYGVVFKCRNKTSGQVAVKFKVESEDDPVVKIALREIRMLKQLKH 60
 Db 1 MEKYNLGLVGEQSYGVVFKCRNKTSGRIVAIKFKFLESDDDKWKVKIAMREIKLKLQRH 60
 Qy 61 PNLVNLLEVRKRMHVLVEYCDHTLLNELRNPNVGVGVKSVLQALNFCFHH 120
 Db 61 ENLVNLLEVCCKRWYLVFEVDHTLLDLKLPNGLDYQVQKYLFOIINGIGFCHSH 120
 Qy 121 NCHRDIKPENILTKGIIKICDFGPAQLL-IPGDAYTDVATRWVRAPELLVGDYQYG 179
 Db 121 NIHRDILPENILVSQGVKCLDFGFARTLAPEVITDVTATRWVRAPELLVGDYQYG 180
 Qy 180 SSVDAWAGCVFALLTCQPLWPGKSDVDQLYLIRTLGLKIPRHQISFGKSGFFHGISI 239
 Db 181 KAVDIWAGCLVLEWMLGQPLPFGESIDQLHMTCLGNLIPRQELFYKNPVPAGVRL 240
 Qy 240 PEPEDMET--LEEKFSVDVHVALNFMKGLKMNPDRLTCSQLLESYF--DSF-----Q 290
 Db 241 PEVKDAEAPLESYPKLPFAVSLAKCLHIDDPKPFCAIDLRLHDFQMDGFAERFSQ 300
 Qy 291 EAQIK--RKARNEGRNRQQ 309
 Db 301 ELQKIEKADNNSLPKKSQK 321

RESULT 15

Q6GMD6 PRELIMINARY; PRT; 320 AA.
 ID Q6GMD6

Q6GMD6; 2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE LOC443693 protein (Fragment).
 GN Name=LOC443693;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 initiative.";
 RL Dev. Dyn. 225:384-391 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; BC074132; AAH74132.1; -;
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR002290; Ser Thr pkinase.
 DR InterPro; IPR008271; Ser Thr pkin AS.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TyrKc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 FT NON TER 320
 SQ SEQUENCE 320 AA; 37063 MW; 4CD2189603F9115F CRC64;

Query Match

55.8%; Score 924; DB 2; Length 320;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 01:23:15 ; Search time 96.4471 Seconds
(without alignments)
1391.497 Million cell updates/sec

Title: US-10-766-691-10
Perfect score: 1820
Sequence: 1 MEKYEKLAKTGEYSYGVFK.....RKARNEGRRRRQQVLPLKS 347

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1820	100.0	347	4	AAE00494 Human kin
2	1796	98.7	356	4	AAE00491 Human kin
3	1636	89.9	315	4	AAE00495 Human kin
4	1613	88.6	342	5	AAE19152 Human kin
5	1612	88.6	324	4	AAE00492 Human kin
6	1593	87.5	360	4	AAU03525 Human pro
7	1270.5	69.8	296	4	AAE00494 Novel pro
8	1270.5	69.8	296	4	AAE00494 Novel pro
9	1162.5	63.9	358	5	ABP62954 Human cyc
10	1157.5	63.6	358	8	ADO01538 Human kin
11	1134	62.3	228	5	AAE00494 Human kin
12	1123	61.7	247	4	AAE00494 Human kin
13	1123	61.7	247	8	ADI29249 Human MAR
14	1001.5	55.0	392	4	ABB63118 Drosophila
15	948	52.1	197	6	ABU11689 Human MDD
16	941.5	51.7	566	3	AAE00494 Human kin
17	915.5	50.3	493	7	ADU77659 Human 162
18	915.5	50.3	493	8	ADU77659 Human 162
19	911.5	50.1	362	6	ABP6087 Human pro
20	829.5	45.6	183	8	ADI40875 Human kin
21	791	43.5	187	4	AAE00494 Human kin
22	791	43.5	198	4	AAE00493 Human kin
23	791	43.5	205	8	ADK71868 Human kin
24	758.5	41.7	455	3	AAE00494 Human kin
25	758.5	41.7	455	8	ADI57233 NKIAMRE d

26	758.5	41.7	455	8	ADI57214 Human NKI
27	758.5	41.7	455	8	ADI57236 CDK3 domi
28	758.5	41.7	591	4	AAU03524 Human pro
29	737.5	40.5	457	3	AAE00494 Rat lost
30	737.5	40.5	505	3	AAE00494 Rat lost
31	712.5	39.1	154	6	ABU05290 Human dia
32	699	38.4	562	8	ABM83922 Human dia
33	666	36.6	534	4	AAE00494 Novel pro
34	666	36.6	534	8	ADI29252 Human MAR
35	569	31.3	224	4	ABG06142 Novel hum
36	565	31.0	305	7	ADU45039 Human kin
37	565	31.0	305	7	ADU45039 Human kin
38	565	31.0	305	8	ADI57200 Human CDK
39	565	31.0	305	8	ADI57237 CDK3 domi
40	565	31.0	333	4	AAE00494 Human pol
41	563	30.9	544	2	AAE00494 CDK2-gree
42	558	30.7	352	4	AAE00494 Human pol
43	557	30.6	298	2	AAE00494 Homo sapi
44	557	30.6	544	2	AAE00494 Green flu
45	556	30.5	298	7	ADD21390 Human cyc

ALIGNMENTS

RESULT 1
AAE00494
ID AAE00494 standard; protein; 347 AA.
AC AAE00494;
XX
DT 19-JUN-2001 (first entry)
XX
DE Human kinase #5.
XX
KW Human; kinase; gene therapy; bioreactor; mental disorder;
KW biological disorder.
XX
OS Homo sapiens.
XX
PN WO200123579-A1.
XX
PD 05-APR-2001.
XX
PF 27-SEP-2000; 2000WO-US026621.
XX
PR 28-SEP-1999; 99US-0156511P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
PI Sands AT;
XX
DR WPI; 2001-266166/27.
DR N-FSDB; AAD03816.
XX
XX New isolated human kinase polynucleotide useful for generating
PT antibodies, as reagents in diagnostic assays and for screening for
PT compounds useful for treating mental, biological or medical diseases.
XX
PS Claim 2; Page 32-33; 39pp; English.
XX
CC The present sequence is novel human protein (NHP) known as human kinase.
CC The human kinases share structural similarity with animal kinases, more
CC particularly serine or threonine protein kinases. Human kinase cDNA is
CC useful for the detection of mutant human kinase for the diagnosis of
CC disease, and also as a therapeutic. It is useful for screening drugs
CC effective in the treatment of symptomatic or phenotypic manifestations
CC perturbing the normal function of NHP in the body. The NHP nucleotide
CC sequences are useful for generation of antibodies, as reagents in
CC diagnostic assays, for the identification of other cellular gene products
CC related to human kinases, and as reagents in assays for screening
CC compounds that are useful for treating mental, biological or medical

disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression

Sequence 347 AA;
Query Match 100.0%; Score 1820; DB 4; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.6e-186;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEKYEKLAKTSGSYGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
Db 1 MEKYEKLAKTSGSYGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCCHI 120
Db 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCCHI 120
QY 121 NCIHRIKPENILITKQGIKIICDFGPAQLIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
Db 121 NCIHRIKPENILITKQGIKIICDFGPAQLIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
QY 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
Db 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
QY 241 VASQAGITGKLIIPRHQSIKSNFGFHGISIPEPEMETLEEKFSVDHPVALNFMKGCLK 300
Db 241 VASQAGITGKLIIPRHQSIKSNFGFHGISIPEPEMETLEEKFSVDHPVALNFMKGCLK 300
QY 301 MNPDDLTCQLLESSYFDSFQEAQIKRKARNEGRRRRRQOVLPLKS 347
Db 301 MNPDDLTCQLLESSYFDSFQEAQIKRKARNEGRRRRRQOVLPLKS 347

RESULT 2
AAE00491
ID AAE00491 standard; protein; 356 AA.
AC AAE00491;
XX 19-JUN-2001 (first entry)
DT Human kinase #2.
DE Human; kinase; gene therapy; bioreactor; mental disorder;
KW biological disorder.
XX Homo sapiens.
OS WO200123579-A1.
FN 05-APR-2001.
PD 27-SEP-2000; 2000WO-US026621.
PF 28-SEP-1999; 99US-0156511P.
PR (LEXI-) LEXICON GENETICS INC.
PA Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
PI Sands AT;
XX WPI; 2001-266166/27.
XX N-PSDB; AAD03813.
XX New isolated human kinase polynucleotide useful for generating

antibodies, as reagents in diagnostic assays and for screening for compounds useful for treating mental, biological or medical diseases.
Disclosure; Page 28-29; 38pp; English.
The present sequence is novel human protein (NHP) known as human kinase. The human kinases share structural similarity with animal kinases, more particularly serine or threonine protein kinases. Human kinase cDNA is useful for the detection of mutant human kinase for the diagnosis of disease, and also as a therapeutic. It is useful for screening drugs effective in the treatment of symptomatic or phenotypic manifestations perturbing the normal function of NHP in the body. The NHP nucleotide sequences are useful for generation of antibodies, as reagents in diagnostic assays, for the identification of other cellular gene products related to human kinases, and as reagents in assays for screening compounds that are useful for treating mental, biological or medical disorders. NHP oligonucleotides are used as probes. The labelled NHP probes are useful for screening human genomic library for identifying polymorphisms and as primers in amplification assays to detect mutations within the exons, introns and splice sites that can be used in diagnostics and pharmacogenomics. Nucleotide construct encoding NHP products are used to genetically engineer cells in vivo that functions as bioreactors in the body delivering a continuous supply of NHP to the body. Nucleotide constructs encoding functional NHPs are used in gene therapy for the modulation of NHP expression

Sequence 356 AA;
Query Match 98.7%; Score 1796; DB 4; Length 356;
Best Local Similarity 100.0%; Pred. No. 6.5e-184;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEKYEKLAKTSGSYGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
Db 1 MEKYEKLAKTSGSYGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCCHI 120
Db 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCCHI 120
QY 121 NCIHRIKPENILITKQGIKIICDFGPAQLIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
Db 121 NCIHRIKPENILITKQGIKIICDFGPAQLIPGDAYTDYVATRWYRAPELLVGDTOYGS 180
QY 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
Db 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
QY 241 VASQAGITGKLIIPRHQSIKSNFGFHGISIPEPEMETLEEKFSVDHPVALNFMKGCLK 300
Db 241 VASQAGITGKLIIPRHQSIKSNFGFHGISIPEPEMETLEEKFSVDHPVALNFMKGCLK 300
QY 301 MNPDDLTCQLLESSYFDSFQEAQIKRKARNEGRRRRRQOVLPLKS 342
Db 301 MNPDDLTCQLLESSYFDSFQEAQIKRKARNEGRRRRRQOVLPLKS 342

RESULT 3
AAE00495
ID AAE00495 standard; protein; 315 AA.
AC AAE00495;
XX 19-JUN-2001 (first entry)
DT Human kinase #6.
DE Human; kinase; gene therapy; bioreactor; mental disorder;
KW biological disorder.
XX Homo sapiens.
OS WO200123579-A1.

XX 05-APR-2001.
XX 27-SEP-2000; 2000WO-US026621.
XX 28-SEP-1999; 99US-0156511P.
XX (LEXI-) LEXICON GENETICS INC.
XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
XX Sands AT;
XX WPI; 2001-266166/27.
XX N-PSDB; AAD03817.
XX New isolated human kinase polynucleotide useful for generating
XX antibodies, as reagents in diagnostic assays and for screening for
XX compounds useful for treating mental, biological or medical diseases.
XX Claim 3; Page 33-34; 38pp; English.
XX The present sequence is novel human protein (NHP) known as human kinase.
XX The human kinases share structural similarity with animal kinases, more
XX particularly serine or threonine protein kinases. Human kinase cDNA is
XX useful for the detection of mutant human kinase for the diagnosis of
XX disease, and also as a therapeutic. It is useful for screening drugs
XX effective in the treatment of symptomatic or phenotypic manifestations
XX perturbing the normal function of NHP in the body. The NHP nucleotide
XX sequences are useful for generation of antibodies, as reagents in
XX diagnostic assays, for the identification of other cellular gene products
XX related to human kinases, and as reagents in assays for screening
XX compounds that are useful for treating mental, biological or medical
XX disorders. NHP oligonucleotides are used as probes. The labelled NHP
XX probes are useful for screening human genomic library for identifying
XX polymorphisms and as primers in amplification assays to detect mutations
XX within the exons, introns and splice sites that can be used in
XX diagnostics and pharmacogenomics. Nucleotide construct encoding NHP
XX products are used to genetically engineer cells in vivo that functions as
XX bioreactors in the body delivering a continuous supply of NHP to the
XX body. Nucleotide constructs encoding functional NHPs are used in gene
XX therapy for the modulation of NHP expression
XX Sequence 315 AA;
Query Match 89.9%; Score 1636; DB 4; Length 315;
Best Local Similarity 90.8%; Pred. No. 9e-167;
Matches 315; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
Qy 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKOLKH 60
Db 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKOLKH 60
Qy 61 PNLVNLIEVFRKRMHLVFEYDHTLLNELRPNPGVADGVKSVLWOTLQALNFCIH 120
Db 61 PNLVNLIEVFRKRMHLVFEYDHTLLNELRPNPGVADGVKSVLWOTLQALNFCIH 120
Qy 121 NCIRHDIKPENILITKQGIKICDFGAQILIPGDAYTDYVATRYRAPELLVGDTOYGS 180
Db 121 NCIRHDIKPENILITKQGIKICDFGAQILIPGDAYTDYVATRYRAPELLVGDTOYGS 180
Qy 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYIIRTLVETGFRHVDQAGLELLTSSDPPA 240
Db 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYIIRTLVETGFRHVDQAGLELLTSSDPPA 240
Qy 241 VASQAGITGKLIIRHOSIFKSNCFEFGISIPEDMETLEKFSVDHPVALNFMKGLK 300
Db 241 VASQAGITGKLIIRHOSIFKSNCFEFGISIPEDMETLEKFSVDHPVALNFMKGLK 300
Qy 301 MNPDRLTCSQLLESSYFDSFQEAQIKKARNEGRRRRQOVLPLKS 347
Db 269 MNPDRLTCSQLLESSYFDSFQEAQIKKARNEGRRRRQOVLPLKS 315

RESULT 4
AAE19152
ID AAE19152 standard; protein; 342 AA.
XX
AC AAE19152;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human kinase polypeptide (PKIN-10).
XX
KW Human, kinase polypeptide; PKIN-10; gene therapy; Addison's disease;
KW leukaemia; immune disorder; lymphoma; melanoma; developmental disorder;
KW acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension;
KW asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis;
KW cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer;
KW cholelithiasis; cardiac; cardiovascular disorder; Niemann-Pick's disease;
KW lipid disorder; fatty liver; Gaucher's disease; myocardial infarction;
KW drug screening; transgenic animal; antiinflammatory; hepatotropic;
KW hypotensive; anti-HIV; enzyme.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 4. .286
XX /note= "Eukaryotic protein kinase domain"
XX
XX WO200208399-A2.
XX
XX 31-JAN-2002.
XX
XX 20-JUL-2001; 2001WO-US023092.
XX
XX 21-JUL-2000; 2000US-0220038P.
XX 28-JUL-2000; 2000US-0222112P.
XX 04-AUG-2000; 2000US-0222831P.
XX 11-AUG-2000; 2000US-0224729P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX (THOR-) THORNTON M.
XX
XX Thornton M, Yue H, Khan FA, Gururajan R, Hafalia AJA, Walla NK;
XX Patterson C, Ramkumar J, Gandhi AR, Policky JL, Baughn MR;
XX Tribouley CM, Bandman O, Nguyen DE, Lu Y, Burford N, Lal P, Ding L;
XX Yao MG, Elliott VS, Recipon SA, Kearney L, Lu DAM, Greenwald SR;
XX Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J, Hillman JL;
XX
XX WPI: 2002-206083/26.
XX N-PSDB; AAD30557.
XX
XX New human kinase polypeptide, useful in diagnosis, prevention and
XX treatment of cancer, immune disorder, growth and developmental disorder,
XX cardiovascular disorder and lipid disorder.
XX
XX Claim 1; Page 147-148; 196pp; English.
XX
XX The present invention relates to an isolated human kinase polypeptide
XX (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is
XX useful for diagnosing, treating and preventing cancer (e.g., leukaemia,
XX lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency
XX syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's
XX disease, rheumatoid arthritis), a growth and developmental disorder (e.g.,
XX bursitis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a
XX cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial
XX infarction), and a lipid disorder (e.g., fatty liver, cholelithiasis,
XX Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of
XX drug screening techniques and to analyse the proteome of a tissue or cell
XX type. PKIN is useful for creating knockin humanised animals or transgenic
XX animals to model human diseases, in somatic or germline gene therapy, to
XX generate a transcript image of a tissue or cell type, for detecting
XX differences in the chromosomal location due to translocation, inversion,
XX etc., among normal, carrier or affected individuals, and as hybridisation
XX probes for mapping naturally occurring genomic sequences. PKIN is useful
XX in southern or northern analysis, dot blot or other membrane-based

CC technologies, in PCR technologies, in dipstick, pin, multiformat enzyme
 CC linked immunosorbent (ELISA)-like assays and in microarrays utilising
 CC fluids or tissues from patients to detect altered PKIN expression. The
 CC present sequence is human PKIN-10
 XX
 SQ Sequence 342 AA;
 Query Match 88.6%; Score 1613; DB 5; Length 342;
 Best Local Similarity 89.9%; Pred. No. 3.1e-164;
 Matches 312; Conservative 1; Mismatches 0; Indels 34; Gaps 2;
 QY 1 MEKYEKLAKTSGSYGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
 DB 1 MEKYEKLAKTSGSYGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
 QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPGVADGVKSVLWQTLQALNFCIH 120
 DB 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPGVADGVKSVLWQTLQALNFCIH 120
 QY 121 NCIHRIKPENILITKQGIKICDFGFAQLIPGDYTDYVATRWYRAPELLVGDTOYGS 180
 DB 121 NCIHRIKPENILITKQGIKICDFGFAQLIPGDYTDYVATRWYRAPELLVGDTOYGS 180
 QY 181 SVDIWAIGCVFAELLTGQPLWPKSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 DB 181 SVDIWAIGCVFAELLTGQPLWPKSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 QY 241 VASQAGITGKLI PRHOSIFKSNFGFHGISIPEDMETLEEKFSVHPVAFNFMKGCLK 300
 DB 241 VASQAGITGKLI PRHOSIFKSNFGFHGISIPEDMETLEEKFSVHPVAFNFMKGCLK 300
 QY 301 MNPDRLTCSQLLESSYFDSFOEAQIKRKARNEGRRRRQV--QVLPL 345
 DB 269 MNPDRLTCSQLLESSYFDSFOEAQIKRKARNEGRRRRQV--QVLPL 315
 RESULT 5
 ID AA00492 standard; protein; 324 AA.
 AC AA00492;
 DT 19-JUN-2001 (first entry)
 DE Human kinase #3.
 KW Human; kinase; gene therapy; bioreactor; mental disorder;
 KW biological disorder.
 XX Homo sapiens.
 XX WO200123579-A1.
 XX 05-APR-2001.
 XX 27-SEP-2000; 2000WO-US026621.
 XX 28-SEP-1999; 99US-0156511P.
 XX (LEXI-) LEXICON GENETICS INC.
 XX Donoho G, Turner CA, Nehls M, Friedrich G, Zambrowicz B;
 XX Sands AT;
 XX WPI; 2001-266166/27.
 XX N-PSDB; AAD03814.
 XX New isolated human kinase polynucleotide useful for generating
 XX antibodies, as reagents in diagnostic assays and for screening for
 XX compounds useful for treating mental, biological or medical diseases.
 XX Disclosure; Page 30; 38pp; English.

CC The present sequence is novel human protein (NHP) known as human kinase.
 CC The human kinases share structural similarity with animal kinases, more
 CC particularly serine or threonine protein kinases. Human kinase cDNA is
 CC useful for the detection of mutant human kinase for the diagnosis of
 CC disease, and also as a therapeutic. It is useful for screening drugs
 CC effective in the treatment of symptomatic or phenotypic manifestations
 CC perturbing the normal function of NHP in the body. The NHP nucleotide
 CC sequences are useful for generation of antibodies, as reagents in
 CC diagnostic assays, for the identification of other cellular gene products
 CC related to human kinases, and as reagents in assays for screening
 CC compounds that are useful for treating mental, biological or medical
 CC disorders. NHP oligonucleotides are used as probes. The labelled NHP
 CC probes are useful for screening human genomic library for identifying
 CC polymorphisms and as primers in amplification assays to detect mutations
 CC within the exons, introns and splice sites that can be used in
 CC diagnostics and pharmacogenomics. Nucleotide construct encoding NHP
 CC products are used to genetically engineer cells in vivo that functions as
 CC bioreactors in the body delivering a continuous supply of NHP to the
 CC body. Nucleotide constructs encoding functional NHPs are used in gene
 CC therapy for the modulation of NHP expression
 XX
 SQ Sequence 324 AA;
 Query Match 88.6%; Score 1612; DB 4; Length 324;
 Best Local Similarity 90.6%; Pred. No. 3.6e-164;
 Matches 310; Conservative 0; Mismatches 0; Indels 32; Gaps 1;
 QY 1 MEKYEKLAKTSGSYGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
 DB 1 MEKYEKLAKTSGSYGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
 QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPGVADGVKSVLWQTLQALNFCIH 120
 DB 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPGVADGVKSVLWQTLQALNFCIH 120
 QY 121 NCIHRIKPENILITKQGIKICDFGFAQLIPGDYTDYVATRWYRAPELLVGDTOYGS 180
 DB 121 NCIHRIKPENILITKQGIKICDFGFAQLIPGDYTDYVATRWYRAPELLVGDTOYGS 180
 QY 181 SVDIWAIGCVFAELLTGQPLWPKSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 DB 181 SVDIWAIGCVFAELLTGQPLWPKSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 QY 241 VASQAGITGKLI PRHOSIFKSNFGFHGISIPEDMETLEEKFSVHPVAFNFMKGCLK 300
 DB 241 VASQAGITGKLI PRHOSIFKSNFGFHGISIPEDMETLEEKFSVHPVAFNFMKGCLK 300
 QY 301 MNPDRLTCSQLLESSYFDSFOEAQIKRKARNEGRRRRQV 342
 DB 269 MNPDRLTCSQLLESSYFDSFOEAQIKRKARNEGRRRRQV 310
 RESULT 6
 ID AA003525 standard; protein; 360 AA.
 AC AA003525;
 DT 12-SEP-2001 (first entry)
 DE Human protein kinase #25.
 KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
 KW metabolic disorder; immune related disease; neurological disorder;
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;
 KW reproductive disorder.
 XX Homo sapiens.
 XX WO200138503-A2.
 XX 31-MAY-2001.

QY 226 DQAGLELLTSSDPPAVASQSAGITGKLI PRHQSI FKSNGFFHGISTPEPEDMETLEEKFS 285
 Db 172 -----GKLI PRHQSI FKSNGFFHGISTPEPEDMETLEEKFS 207

QY 286 DVHPVALNFMKGLKKNPDDRLTCSOLLESSYFDSFOEAQIKRKARNEGRNRRO--QVL 343
 Db 208 NVQPVALSFMKGLKKNPDDRLTCAQLDSAYFESFOEDQMKRKARSEGRSRRRQOQLL 267

QY 344 PL 345
 Db 268 PL 269

RESULT 8
 ADI29250
 ID ADI29250 standard; protein; 296 AA.
 AC ADI29250;
 XX 22-APR-2004 (first entry)
 DT Mouse MARK3-associated protein #12.
 DE
 XX Mouse; antisense gene therapy; MARK3;
 KW MAP/microtubule affinity-regulating kinase 3; cancer;
 KW Alzheimer's disease; neurodegenerative disorder;
 KW hyperproliferative disorder; cytostatic.
 XX
 OS Mus musculus.
 XX
 FN US2003232771-A1.
 XX
 PD 18-DEC-2003.
 XX
 PF 17-JUN-2002; 2002US-00174319.
 XX
 PR 17-JUN-2002; 2002US-00174319.
 XX
 XX (ISIS-) ISIS PHARM INC.
 PA
 XX Ward DT, Freier SM, Dobie KW;
 PI WPI; 2004-052188/05.
 DR N-PSDB; ADI29368.
 XX
 PT New antisense compound targeted to a nucleic acid molecule encoding
 PT microtubule-affinity-regulating kinases (MARK3), useful for modulating
 PT expression of MARK3 or for treating cancer or Alzheimer's disease.
 XX
 PS Disclosure; SEQ ID NO 170; 233pp; English.
 XX
 CC The invention relates to a compound comprising a sequence comprising 8-80
 CC base pairs (bp) targeted to a nucleic acid encoding MARK3
 CC (MAP/microtubule affinity-regulating kinase 3), that specifically
 CC hybridizes with the nucleic acid encoding MARK3 and inhibits expression
 CC of MARK3, i.e. is an antisense oligonucleotide (AO). Also included are a
 CC composition comprising the compound and a carrier or diluent, inhibiting
 CC the expression of MARK3 in cells or tissues, treating an animal having or
 CC suspected of having a disease or condition associated with MARK3 and
 CC screening for an antisense compound. The antisense oligonucleotide is
 CC useful for preparing a composition for treating hyperproliferative
 CC disorder, particularly cancer and neurodegenerative diseases e.g.
 CC Alzheimer's disease. The present sequence is a MARK3 associated protein
 CC included in the figures but not mentioned anywhere else in the
 CC specification.
 XX
 SQ Sequence 296 AA;

Query March 69.8%; Score 1270.5; DB 8; Length 296;
 Best Local Similarity 80.5%; Pred. No. 1.8e-127;
 Matches 243; Conservative 19; Mismatches 5; Indels 35; Gaps 3;

QY 46 KIALREIRMLKQLKHPNLVNLIEVFRKRKXKHLVFEYCDHTLLNELEARNPNVADGVIKS 105
 Db 1 KIALREIRMLK-LKHPNLVNLIEVFRKRKXKHLVFEYCDHTLLNELEARNPNVADGVIKS 59

QY 106 VLWOTLQALNFECHTHNCIHRDIKBNILITKQGIKICDQFGAQLIPGDAYTYVATRW 165
 Db 60 VLWOTLQALNFECHTHNCIHRDVKPENILITKQGMKICDQGFARILIPGDAYTYVATRW 119

QY 166 YRAPELLVGDYQYSSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIRTLVETGRHV 225
 Db 120 YRAPELLVGDYQYSSVDVWAVGCVFAELLTGQPLWPKSDVDQLYLIRTL 171

QY 226 DQAGLELLTSSDPPAVASQSAGITGKLI PRHQSI FKSNGFFHGISTPEPEDMETLEEKFS 285
 Db 172 -----GKLI PRHQSI FKSNGFFHGISTPEPEDMETLEEKFS 207

QY 286 DVHPVALNFMKGLKKNPDDRLTCSOLLESSYFDSFOEAQIKRKARNEGRNRRO--QVL 343
 Db 208 NVQPVALSFMKGLKKNPDDRLTCAQLDSAYFESFOEDQMKRKARSEGRSRRRQOQLL 267

QY 344 PL 345
 Db 268 PL 269

RESULT 9
 ABP62954
 ID ABP62954 standard; protein; 358 AA.
 AC ABP62954;
 XX 14-OCT-2002 (first entry)
 DT Human polypeptide SEQ ID NO 391.
 XX
 DE Human; vulnery; dermatological; neuroprotective; nootropic; cancer;
 KW antiparkinsonian; immunostimulant; cytostatic; immunosuppressive;
 KW antidiabetic; antiallergic; gene therapy; wound healing; tissue repair;
 KW burn; central nervous system disorder; Alzheimer's disease;
 KW Parkinson's disease; Huntington's disease; immune disorder;
 KW autoimmune disorder; multiple sclerosis; diabetes; allergy.
 XX
 OS Homo sapiens.
 XX
 FN WO200218424-A2.
 XX
 PD 07-MAR-2002.
 XX
 PF 31-AUG-2001; 2001WO-US027093.
 XX
 PR 01-SEP-2000; 2000US-00654935.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;
 PI Zhao QA, Wang D, Liu C, Drmanac RT, Wehrman T;
 XX WPI; 2002-583321/62.
 DR N-PSDB; ABQ93433.
 XX
 PT New polynucleotide and polypeptides, useful for treatment and diagnosis
 PT of Alzheimer's, Parkinson's, Huntington's, amyotrophic lateral
 PT sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple
 PT sclerosis, diabetes and allergies.
 XX
 PS Claim 20; SEQ ID NO 391; 284pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated polynucleotide (I) comprising one of
 CC 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising
 CC administering to a mammalian subject a composition comprising the protein
 CC (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).
 CC (I), (II) and (III) are useful for diagnostic evaluation of disorders.
 CC (I) is useful for gene therapy of diseases and (II) can be used for

CC therapeutic treatment. Diseases that may be treated include wound healing
 CC and tissue repair, burns, central nervous system disorders (e.g.
 CC Alzheimer's, Parkinson's, Huntington's and amyotrophic lateral
 CC sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple
 CC sclerosis, diabetes and allergies. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 358 AA;

Query Match 63.9%; Score 1162.5; DB 5; Length 358;
 Best Local Similarity 63.8%; Pred. No. 1e-115;
 Matches 213; Conservative 42; Mismatches 46; Indels 33; Gaps 2;
 Qy 1 MEKYEKAKTGEISYGVVFKCRNKTSGQVAVKFESEDDPVVKIALRMLKQLKH 60
 Db 2 MEKYEKIGKIGESYGVVFKCRNRTGQIVAKKFESEDDPVVKIALRMLKQLKH 61
 Qy 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELRNPNVGADVIVKSVLWQTLQALNFCIH 120
 Db 62 PNLVNLIEVFRKRRLHLVFEYCDHTVLHBLDRYQGVPEHLVKSITWQTLQAVNFCCHK 121
 Qy 121 NCIRHDIKPENILITKQGIKICDFGPAQILI - PGDAYTDVATRWYRAPPELLVGDTOYG 179
 Db 122 NCIRHDVAPENILITKHSVILKCLDFGPAQLTGTGSDDYTDVATRWTRSPPELLVGDTOYG 181
 Qy 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIRTLVETGFRHVDQAGLELLTSSDPP 239
 Db 182 PPVDVWAIGCVFAELLSGVPLWPKSDVDQLYLIRKTL----- 219
 Qy 240 AVASQSGITGKLIPIRHSQIFKNGFHHGISIPEDMETLEKFSVHPVAFMKGCL 299
 Db 220 -----GDLIPRHQQVSTNQYFSGVKIPDPEDMEPLEKFPNISYPALGLKGL 269
 Qy 300 KMPDRLTCSOLLESSYFDSFQEAQ 333
 Db 270 HMDPTERTCEQLLHPYFNIRIEDLAKHNK 303

RESULT 10
 AD001538
 ID AD001538 standard; protein; 358 AA.
 XX
 AC AD001538;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Human cyclin-dependent kinase like 1 (CDKL1) protein SEQ ID NO:4.
 XX human; cyclin-dependent kinase like 1; CDKL1; branching morphogenesis;
 KW branching morphogenesis modulator; angiogenic disorder;
 KW apoptotic disorder; proliferation disorder; chromosome 14.
 XX
 OS Homo sapiens.
 XX
 PN WO2004038372-A2.
 XX
 PD 06-MAY-2004.
 XX
 PF 22-OCT-2003; 2003WO-US033483.
 XX
 PR 23-OCT-2002; 2002US-0420554P.
 XX
 PA (EXEL-) EXELIXIS INC.
 XX
 PI Plowman GD, Karim FD, Swimmer C, Habeck HA, Koblizek TI;
 PI Schulte-Werker S, Langheinrich U, Stott GM, Trowe T, Vogel AM;
 PI Odenthal JH, Scheel JK, Will TT, Jin Y, Hai B;
 XX
 DR WPI; 2004-365563/34.
 DR N-PSDB; ADO01535.
 XX

PT Use of cyclin-dependent kinase like 1 polypeptides or nucleic acids for
 PT modulating branching morphogenesis in a mammalian cell or for diagnosing
 PT a disease e.g. angiogenic, apoptotic or proliferation disorder in a
 PT patient.
 XX
 PS Example; SEQ ID NO 4; 52pp; English.

XX
 CC The present invention describes the use of a cyclin-dependent kinase like
 CC 1 (CDKL1) polypeptide or nucleic acid for modulating branching
 CC morphogenesis in a mammalian cell or for diagnosing a disease in a
 CC patient. Also described: (1) identifying a candidate branching
 CC morphogenesis modulating agent; (2) modulating branching morphogenesis in
 CC a mammalian cell comprising contacting the cell with an agent that
 CC specifically binds a CDKL1 polypeptide or nucleic acid; and (3) a method
 CC for diagnosing a disease in a patient. The CDKL1 polypeptide or nucleic
 CC acid is useful for modulating branching morphogenesis in a mammalian
 CC cell. It is also useful for diagnosing a disease, e.g. angiogenic,
 CC apoptotic or proliferation disorder in a patient. The present sequence
 CC represents human CDKL1, which is used in the exemplification of the
 CC present invention. The human CDKL1 gene is located on chromosome 14, more
 CC specifically to 14q22.1.
 XX

SQ Sequence 358 AA;

Query Match 63.8%; Score 1157.5; DB 8; Length 358;
 Best Local Similarity 64.7%; Pred. No. 3.6e-115;
 Matches 211; Conservative 41; Mismatches 41; Indels 33; Gaps 2;
 Qy 1 MEKYEKAKTGEISYGVVFKCRNKTSGQVAVKFESEDDPVVKIALRMLKQLKH 60
 Db 2 MEKYEKIGKIGESYGVVFKCRNRTGQIVAKKFESEDDPVVKIALRMLKQLKH 61
 Qy 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELRNPNVGADVIVKSVLWQTLQALNFCIH 120
 Db 62 PNLVNLIEVFRKRRLHLVFEYCDHTVLHBLDRYQGVPEHLVKSITWQTLQAVNFCCHK 121
 Qy 121 NCIRHDIKPENILITKQGIKICDFGPAQILI - PGDAYTDVATRWYRAPPELLVGDTOYG 179
 Db 122 NCIRHDVAPENILITKHSVILKCLDFGPAQLTGTGSDDYTDVATRWTRSPPELLVGDTOYG 181
 Qy 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIRTLVETGFRHVDQAGLELLTSSDPP 239
 Db 182 PPVDVWAIGCVFAELLSGVPLWPKSDVDQLYLIRKTL----- 219
 Qy 240 AVASQSGITGKLIPIRHSQIFKNGFHHGISIPEDMETLEKFSVHPVAFMKGCL 299
 Db 220 -----GDLIPRHQQVSTNQYFSGVKIPDPEDMEPLEKFPNISYPALGLKGL 269
 Qy 300 KMPDRLTCSOLLESSYFDSFQEAQ 325
 Db 270 HMDPTERTCEQLLHPYFNIRIE 295

RESULT 11

AAG78547
 ID AAG78547 standard; protein; 228 AA.
 XX
 AC AAG78547;
 XX
 DT 08-MAR-2002 (first entry)
 XX
 DE Human kinase 14257 amino acid sequence.

Protein kinase; enzyme; cytostatic; osteopathic; hepatotropic;
 KW antidiabetic; neuroprotective; antiarthritic; dermatological;
 KW immunosuppressive; antiinflammatory; antithyroid; antipsoriatic;
 KW ophthalmological; antiallergic; antiasthmatic; anticholesterolic;
 KW hypotensive; vasotropic; antiarrhythmic; virucide; anorectic; metabolic;
 KW immunomodulator; analgesic; cellular proliferative disorder; cancer;
 KW acute lymphoblastic leukaemia; Hodgkin's disease;
 KW bone metabolism disorder; osteoporosis; immune system disorder;
 KW inflammatory; diabetes mellitus; osteoarthritis; asthma;
 KW cardiovascular disorder; hypertension; coronary artery disease;

XX WPI; 2001-656860/75.
 DR N-PSDB; ABL07221.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 XX Disclosure; SEQ ID NO 16146; 21pp + Sequence Listing; English.
 PS
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 392 AA;
 XX
 Query Match 55.0%; Score 1001.5; DB 4; Length 392;
 Best Local Similarity 53.0%; Pred. No. 2.6e-98;
 Matches 184; Conservative 65; Mismatches 61; Indels 37; Gaps 3;
 QY 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGOVAVKFESEDDPVVKKIALREIRMLKOLKH 60
 Db 1 MDREYKLSLGGSGYGVVFKCRNKTSGOVAVKFESEDDPVVKKIALREIRMLKOLKH 60
 QY 61 PNLVNLIEVFRKRKRLHLVFEYCDHTLNLNERNPENGADVGVKSVLWQTLQALNFCFH 120
 Db 61 PNLVNLIEVFRKRKRLHLVFEYCDHTLNLNERNPENGADVGVKSVLWQTLQALNFCFH 120
 QY 121 NCIHREDIKPENLITKQGIKICDFGFAQIIPGDAYTDYATWYRAPELLVGTQYGS 180
 Db 121 GCLHRDIPENLITKQGIKICDFGFAQIIPGDAYTDYATWYRAPELLVGTQYGS 180
 QY 181 SVDIWAICVFAELTGOPLWFGSDVDQLYLIRTVETGFRHVDQAGLELLTSSDPPA 240
 Db 181 PVDVWAIGCLFAELVGRGALWFGSDVDQLYLIRKTL----- 217
 QY 241 VASQSGITGKLIPIHQISFKNSGFFHGISTPEPEDMETLEEF---SDVHPVALNFMKG 297
 Db 218 -----GDLPRHIQIFQNEYFKGITLPVPTLEPLEDKMPAKSQQNPLTIDFLK 268
 QY 298 CLKWNPDDRLTCSOLLESSYFDSF--OEAQIKRKARNEGRRRQOV 342
 Db 269 CLDKDPTKWSCEKLTKHSYFDDYIAKQRELEHVNLSLEAANLROOQL 315
 RESULT 15
 ABU11689
 ID ABU11689 standard; protein; 197 AA.
 XX
 AC ABU11689;
 XX
 DT 13-FEB-2003 (first entry)
 XX
 DE Human MDDT polypeptide SEQ ID 636.
 XX
 KW MDDT: human; disease detection and treatment molecule polypeptide;
 KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;
 KW haemostatic; nephrotropic; antianemic; antiproliferative; hepatotropic;
 KW gene therapy; protein replacement therapy; cell proliferative disorder;
 KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;
 KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;
 KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;
 KW psoriasis; hepatitis.
 OS Homo sapiens.
 XX

PN WO200279449-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 27-MAR-2002; 2002WO-US009944.
 XX
 PR 28-MAR-2001; 2001US-0279619P.
 PR 29-MAR-2001; 2001US-0280067P.
 PR 29-MAR-2001; 2001US-0280068P.
 PR 16-MAY-2001; 2001US-0291280P.
 PR 17-MAY-2001; 2001US-0291829P.
 PR 17-MAY-2001; 2001US-0291849P.
 PR 19-JUN-2001; 2001US-0293428P.
 PR 20-JUN-2001; 2001US-0299776P.
 PR 20-JUN-2001; 2001US-0300001P.
 XX (INCY-) INCYTE GENOMICS INC.
 PA Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshay SR;
 PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;
 DR WPI; 2003-058431/05.
 DR N-PSDB; ABX34679.
 XX
 XX New purified disease detection and treatment molecule proteins and
 PT polynucleotides, useful for diagnosing, treating or preventing cancers
 PT (e.g. leukemia or sarcoma), anaemia, Crohn's disease, AIDS, osteoporosis
 PT or hepatitis.
 XX
 PS Claim 27; SEQ ID NO 636; 339pp + Sequence Listing; English.
 XX
 CC This invention describes a novel disease detection and treatment molecule
 CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,
 CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,
 CC antianemic, antiproliferative and hepatotropic activity. The polynucleotides
 CC and the polypeptides of the invention can be used for gene therapy,
 CC protein replacement therapy and are useful for treating a variety of
 CC diseases or conditions. These polypeptides or polynucleotides are
 CC particularly useful for diagnosing, treating or preventing cell
 CC proliferative disorders (e.g. cancers including adenocarcinoma,
 CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's
 CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's
 CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or
 CC hepatitis. ABU11450-ABU11845 represent the MDDT polynucleotides encoded
 CC by ABU11450-ABU11845, described in the disclosure of the invention. NOTE:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 197 AA;

Query Match 52.1%; Score 948; DB 6; Length 197;
 Best Local Similarity 98.9%; Pred. No. 5e-93;
 Matches 180; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGOVAVKFESEDDPVVKKIALREIRMLKOLKH 60
 Db 6 MEKYEKLAKTGGSGYGVVFKCRNKTSGOVAVKFESEDDPVVKKIALREIRMLKOLKH 65
 QY 61 PNLVNLIEVFRKRKRLHLVFEYCDHTLNLNERNPENGADVGVKSVLWQTLQALNFCFH 120
 Db 66 PNLVNLIEVFRKRKRLHLVFEYCDHTLNLNERNPENGADVGVKSVLWQTLQALNFCFH 125
 QY 121 NCIHREDIKPENLITKQGIKICDFGFAQIIPGDAYTDYATWYRAPELLVGTQYGS 180
 Db 126 NCIHREDIKPENLITKQGIKICDFGFAQIIPGDAYTDYATWYRAPELLVGTQYGS 185
 QY 181 SV 182
 Db 186 SV 187

Search completed: April 22, 2005, 06:47:31
Job time : 101.447 secs

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OM protein - protein search, using sw model

Run on: April 22, 2005, 04:37:19 ; Search time 34.071 Seconds
(without alignments)
760.272 Million cell updates/sec

Title: US-10-766-691-10

Perfect score: 1820

Sequence: 1 MEKYEKLAKTGEISGVVFK.....RKARNEGRRRQVLPKLS 347

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1820	100.0	347	4	US-09-671-050-10
2	1796	98.7	356	4	US-09-671-050-4
3	1636	89.9	315	4	US-09-671-050-12
4	1612	88.6	324	4	US-09-671-050-6
5	1162.5	63.9	367	4	US-09-949-016-7552
6	1157.5	63.6	358	4	US-09-411-628-11
7	1157.5	63.6	358	4	US-10-174-794-11
8	941.5	51.7	566	4	US-09-411-628-4
9	941.5	51.7	566	4	US-10-174-794-4
10	915.5	50.3	475	4	US-09-949-016-7954
11	915.5	50.3	493	4	US-09-411-628-10
12	915.5	50.3	493	4	US-10-174-794-10
13	791	43.5	187	4	US-09-671-050-2
14	791	43.5	198	4	US-09-671-050-8
15	565	31.0	305	4	US-09-538-092-1236
16	565	31.0	305	4	US-09-949-016-6052
17	565	31.0	334	4	US-09-949-016-10777
18	563	30.9	544	4	US-09-417-197-113
19	557	30.6	298	2	US-08-874-347-25
20	557	30.6	298	2	US-08-969-106-2
21	557	30.6	298	3	US-09-093-522-25
22	557	30.6	298	4	US-09-338-125-2
23	557	30.6	298	4	US-09-266-225D-14
24	557	30.6	544	4	US-09-417-197-115
25	556	30.5	298	4	US-09-411-628-13
26	556	30.5	298	4	US-10-174-794-13
27	554	30.4	297	1	US-08-176-620A-16

28	554	30.4	297	2	US-08-461-985-16	Sequence 16, Appl
29	554	30.4	298	3	US-09-457-040B-29	Sequence 29, Appl
30	554	30.4	298	4	US-09-538-092-1006	Sequence 1006, Ap
31	554	30.4	354	4	US-09-949-016-8025	Sequence 8025, Ap
32	551.5	30.3	294	2	US-08-874-347-26	Sequence 26, Appl
33	551.5	30.3	294	3	US-09-093-522-26	Sequence 26, Appl
34	547.5	30.1	270	2	US-07-857-224B-31	Sequence 31, Appl
35	545	29.9	297	2	US-08-874-347-24	Sequence 24, Appl
36	545	29.9	297	3	US-09-093-522-24	Sequence 24, Appl
37	545	29.9	297	4	US-09-411-628-12	Sequence 12, Appl
38	545	29.9	297	4	US-10-174-794-12	Sequence 12, Appl
39	541	29.7	297	2	US-08-874-347-23	Sequence 23, Appl
40	541	29.7	297	3	US-09-093-522-23	Sequence 23, Appl
41	540	29.7	274	1	US-08-318-947A-20	Sequence 20, Appl
42	540	29.7	274	2	US-08-795-303-20	Sequence 20, Appl
43	540	29.7	299	4	US-09-949-016-10673	Sequence 10673, A
44	538.5	29.6	300	2	US-08-874-347-10	Sequence 10, Appl
45	538.5	29.6	300	3	US-09-093-522-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-671-050-10
; Sequence 10, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/671,050
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 347
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-671-050-10

Query Match	100.0%;	Score 1820;	DB 4;	Length 347;
Best Local Similarity	100.0%;	Pred. No. 2.4e-186;		
Matches 347;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MEKYEKLAKTGEISGVVFKCRNKTSGQVAVKFFVSEDDPVVKKTALREIRMLKQLKH	60	
Db	1	MEKYEKLAKTGEISGVVFKCRNKTSGQVAVKFFVSEDDPVVKKTALREIRMLKQLKH	60	
Qy	61	PNLVNLLEVFRRKRKMHLPVEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCIH	120	
Db	61	PNLVNLLEVFRRKRKMHLPVEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCIH	120	
Qy	121	NCIHRDIKPENILTKQGIKICDFGPAQLIPGDAYTDVYVATRYRAPELLVGDQYGS	180	
Db	121	NCIHRDIKPENILTKQGIKICDFGPAQLIPGDAYTDVYVATRYRAPELLVGDQYGS	180	
Qy	181	SVDIWAIGCVPAELLTQGPLWPGSKSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPPA	240	
Db	181	SVDIWAIGCVPAELLTQGPLWPGSKSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPPA	240	
Qy	241	VASQASGITGKLI PRHOSIFKSNFGFFHGISIPEDMETLEEKFSVDHPVAINFMKGLK	300	
Db	241	VASQASGITGKLI PRHOSIFKSNFGFFHGISIPEDMETLEEKFSVDHPVAINFMKGLK	300	

QY 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOVLPLKS 347
Db 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOVLPLKS 347

RESULT 2

US-09-671-050-4
; Sequence 4, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 356
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-671-050-4

Query Match 98.7%; Score 1796; DB 4; Length 356;
Best Local Similarity 100.0%; Pred. No. 9.2e-184;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
Db 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
QY 61 PNLVNLIEVFRFRKRMHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCCHI 120
Db 61 PNLVNLIEVFRFRKRMHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCCHI 120
QY 121 NCIHRIKPNILITKQGIKICDGFQAQILIPGDAYTDVATRWYRAPELLVGDTOYGS 180
Db 121 NCIHRIKPNILITKQGIKICDGFQAQILIPGDAYTDVATRWYRAPELLVGDTOYGS 180
QY 181 SVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
Db 181 SVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
QY 241 VASQSAGITGKLI PRHQSIFKSNFGFFHGISIPEPEMETLEEKFSVHPVALNFMKGCLK 300
Db 241 VASQSAGITGKLI PRHQSIFKSNFGFFHGISIPEPEMETLEEKFSVHPVALNFMKGCLK 300
QY 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOVLPLKS 342
Db 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOVLPLKS 342

RESULT 3

US-09-671-050-12
; Sequence 12, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; FILE OF INVENTION: Polynucleotides Encoding the Same

; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 315
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-671-050-12

Query Match 89.9%; Score 1636; DB 4; Length 315;
Best Local Similarity 90.8%; Pred. No. 1.1e-166;
Matches 315; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
Db 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
QY 61 PNLVNLIEVFRFRKRMHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCCHI 120
Db 61 PNLVNLIEVFRFRKRMHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCCHI 120
QY 121 NCIHRIKPNILITKQGIKICDGFQAQILIPGDAYTDVATRWYRAPELLVGDTOYGS 180
Db 121 NCIHRIKPNILITKQGIKICDGFQAQILIPGDAYTDVATRWYRAPELLVGDTOYGS 180
QY 181 SVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
Db 181 SVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
QY 241 VASQSAGITGKLI PRHQSIFKSNFGFFHGISIPEPEMETLEEKFSVHPVALNFMKGCLK 300
Db 241 VASQSAGITGKLI PRHQSIFKSNFGFFHGISIPEPEMETLEEKFSVHPVALNFMKGCLK 300
QY 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOVLPLKS 315
Db 269 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOVLPLKS 315

RESULT 4

US-09-671-050-6
; Sequence 6, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; FILE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 324
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-671-050-6

Query Match 88.6%; Score 1612; DB 4; Length 324;
Best Local Similarity 90.6%; Pred. No. 4.2e-164;
Matches 310; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

QY 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60

Db 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKPFVSEDDPVVKKIALREIRMLKQLKH 60
Qy 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCCHI 120
Db 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCCHI 120
Qy 121 NCIRDIKPENILITKOGIIKICDFGFAQILI-PGDAYTYDVATRWYRAPELLVGDTOYGS 180
Db 121 NCIRDIKPENILITKOGIIKICDFGFAQILI-PGDAYTYDVATRWYRAPELLVGDTOYGS 180
Qy 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDOLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
Db 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDOLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
Qy 241 VASQSAGITGKLIIPRHOSIFKSNFGFHGISIPEPEDMETLEEKFSVHPVAFNMFKGCLK 300
Db 218 -----GKLIIPRHOSIFKSNFGFHGISIPEPEDMETLEEKFSVHPVAFNMFKGCLK 268
Qy 301 MNPDDLRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOV 342
Db 269 MNPDDLRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOV 310

RESULT 5
US-09-949-016-7552
; Sequence 7552, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYHUMANISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7552
; LENGTH: 367
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7552

Query Match 63.9%; Score 1162.5; DB 4; Length 367;
Best Local Similarity 63.8%; Pred. No. 7.7e-116;
Matches 213; Conservative 42; Mismatches 46; Indels 33; Gaps 2;
Qy 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKPFVSEDDPVVKKIALREIRMLKQLKH 60
Db 11 MEKYEKIGKIGSGYGVVFKCRNRTDGTQIVAIKKFLESEDDPVVKKIALREIRMLKQLKH 70
Qy 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCCHI 120
Db 71 PNLVNLIEVFRKRKMLHVFYCDHTLVHLDYRGVPEHLVKSITWQTLQAVNFCCHK 130
Qy 121 NCIRDIKPENILITKOGIIKICDFGFAQILI-PGDAYTYDVATRWYRAPELLVGDTOYGS 179
Db 131 NCIRDIKPENILITKOGIIKICDFGFAQILI-PGDAYTYDVATRWYRAPELLVGDTOYGS 190
Qy 180 SVDIWAIGCVFAELLTGQPLWPKGSDVDOLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 191 PPVDWAIGCVFAELLTGQPLWPKGSDVDOLYLIIRTLVETGFRHVDQAGLELLTSSDPP 228
Qy 240 AVASQSAGITGKLIIPRHOSIFKSNFGFHGISIPEPEDMETLEEKFSVHPVAFNMFKGCL 299
Db 229 -----GDLIPRHQQVSTNQYFSGVKIPDPEDMEPELEKFPNISYPALGGLKGL 278

Qy 300 KMPDDLRLTCSQLLESSYFDSFQEAQIKRKARNE 333
Db 279 HMDPTELRITCEQLLHHPYFENIREIEDLAKENK 312
RESULT 6
US-09-411-628-11
; Sequence 11, Application US/09411628
; Patent No. 6428994
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; FILE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/09/411,628
; CURRENT FILING DATE: 1999-10-01
; EARLIER FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-411-628-11

Query Match 63.6%; Score 1157.5; DB 4; Length 358;
Best Local Similarity 64.7%; Pred. No. 2.6e-115;
Matches 211; Conservative 41; Mismatches 41; Indels 33; Gaps 2;
Qy 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKPFVSEDDPVVKKIALREIRMLKQLKH 60
Db 2 MEKYEKIGKIGSGYGVVFKCRNRTDGTQIVAIKKFLESEDDPVVKKIALREIRMLKQLKH 61
Qy 61 PNLVNLIEVFRKRKMLHVFYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCCHI 120
Db 62 PNLVNLIEVFRKRKMLHVFYCDHTLVHLDYRGVPEHLVKSITWQTLQAVNFCCHK 121
Qy 121 NCIRDIKPENILITKOGIIKICDFGFAQILI-PGDAYTYDVATRWYRAPELLVGDTOYGS 179
Db 122 NCIRDIKPENILITKOGIIKICDFGFAQILI-PGDAYTYDVATRWYRAPELLVGDTOYGS 181
Qy 180 SVDIWAIGCVFAELLTGQPLWPKGSDVDOLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 182 PPVDWAIGCVFAELLTGQPLWPKGSDVDOLYLIIRTLVETGFRHVDQAGLELLTSSDPP 219
Qy 240 AVASQSAGITGKLIIPRHOSIFKSNFGFHGISIPEPEDMETLEEKFSVHPVAFNMFKGCL 299
Db 220 -----GDLIPRHQQVSTNQYFSGVKIPDPEDMEPELEKFPNISYPALGGLKGL 269
Qy 300 KMPDDLRLTCSQLLESSYFDSFQEAQ 325
Db 270 HMDPTELRITCEQLLHHPYFENIREIE 295

RESULT 7
US-10-174-794-11
; Sequence 11, Application US/10174794
; Patent No. 6664086
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; FILE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11

; LENGTH: 358
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-174-794-11

 Query Match 63.6%; Score 1157.5; DB 4; Length 358;
 Best Local Similarity 64.7%; Pred. No. 2.6e-115;
 Matches 211; Conservative 41; Mismatches 41; Indels 33; Gaps 2;

 QY 1 MEKYEKLAKTGEISYGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
 DB 2 MEKYEKIGTGEGSYGVVFKCRNRTDQIIVAIKKFLESEDDPVVKKIALREIRMLKQLKH 61
 QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNVADGVKSVLWQTLQALNFCCHI 120
 DB 62 PNLVNLIEVFRKRKMHVFEYCDHTLVHLDYRQGVPEHLVKSITWTLQAVNFCCHK 121
 QY 121 NCHRDIKPENILITKQGIKICDFGFAQIL-IPGDAYTDYVATRYRAPELLVGTQYG 179
 DB 122 NCHRDIKPENILITKHSVVKLCDFGFAQLLTGSPDYDDYVATRYRSPPELLVGTQYG 181
 QY 180 SSVDIWAIGCVFAELLTGOPLWPKGSDVDQYLIITLVTETGFRHVDQAGLELLTSSDPP 239
 DB 182 PPVDVWAIGCVFAELLTGOPLWPKGSDVDQYLIITLVTETGFRHVDQAGLELLTSSDPP 219
 QY 240 AVASQAGITGKLIPIRHQSIKSNFGFHGISIPEDEMTELEKPSDVHPVALNFMKGCL 299
 DB 220 -----GDLIPRHQSVFSTNOVFSGVKIPDPEDMEPLKFPNISYPALGLKQL 269
 QY 300 KNPDPDLTCSOLLESSYFDSQEAQ 325
 DB 270 HMDPTERTCEQLLHHHPYENIREIE 295

RESULT 8

US-09-411-628-4
 ; Sequence 4, Application US/09411628
 ; Patent No. 6428994
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Southern California
 ; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
 ; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
 ; FILE REFERENCE: 13761-707
 ; CURRENT APPLICATION NUMBER: US/09/411,628
 ; CURRENT FILING DATE: 1999-10-01
 ; EARLIER APPLICATION NUMBER: US 60/102,906
 ; EARLIER FILING DATE: 1998-10-02
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 566
 ; TYPE: PRT
 ; ORGANISM: Orcytolagus cuniculus
 US-09-411-628-4

Query Match 51.7%; Score 941.5; DB 4; Length 566;
 Best Local Similarity 49.7%; Pred. No. 7.4e-92;
 Matches 177; Conservative 67; Mismatches 65; Indels 47; Gaps 6;

 QY 1 MEKYEKLAKTGEISYGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
 DB 1 MEKYEKIGTGEGSYGVVFKCRNRTDQIIVAIKKFLESEDDPVVKKIALREIRMLKQLKH 60
 QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNVADGVKSVLWQTLQALNFCCHI 120
 DB 62 PNLVNLIEVFRKRKMHVFEYCDHTLVHLDYRQGVPEHLVKSITWTLQAVNFCCHK 121
 QY 121 NCHRDIKPENILITKQGIKICDFGFAQIL-IPGDAYTDYVATRYRAPELLVGTQYG 179
 DB 122 NCHRDIKPENILITKHSVVKLCDFGFAQLLTGSPDYDDYVATRYRSPPELLVGTQYG 180
 QY 180 SSVDIWAIGCVFAELLTGOPLWPKGSDVDQYLIITLVTETGFRHVDQAGLELLTSSDPP 239

DB 181 KAVDVWAIGCLVTEMLMGEPLFPFGSDIDQLYLMRCL----- 218
 QY 240 AVASQAGITGKLIPIRHQSIKSNFGFHGISIPEDEMTELEKPSDVHPVALNFMKGCL 299
 DB 219 -----GNLIPRHQELFYKNPVFAGVRLPEIKSESEPLERRYPKLSEVVIDLAKKCL 268
 QY 300 KNPDPDLTCSOLLESSYF--DSF-----QEAQIK--RKARN-----EGRNRRQO 341
 DB 269 HVDPDKRPFCAELLHHDFFQMDGFAERFSQBLQMKVQKDAENISLSKKSQNRKKEK 324

RESULT 9

US-10-174-794-4
 ; Sequence 4, Application US/10174794
 ; Patent No. 6664086
 ; GENERAL INFORMATION:
 ; APPLICANT: University of Southern California
 ; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
 ; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
 ; FILE REFERENCE: 13761-707
 ; CURRENT APPLICATION NUMBER: US/10/174,794
 ; CURRENT FILING DATE: 2002-06-18
 ; PRIOR APPLICATION NUMBER: US/09/411,628
 ; PRIOR FILING DATE: 1999-10-01
 ; PRIOR APPLICATION NUMBER: US 60/102,906
 ; PRIOR FILING DATE: 1998-10-02
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 566
 ; TYPE: PRT
 ; ORGANISM: Orcytolagus cuniculus
 US-10-174-794-4

Query Match 51.7%; Score 941.5; DB 4; Length 566;
 Best Local Similarity 49.7%; Pred. No. 7.4e-92;
 Matches 177; Conservative 67; Mismatches 65; Indels 47; Gaps 6;

 QY 1 MEKYEKLAKTGEISYGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
 DB 1 MEKYEKIGTGEGSYGVVFKCRNRTDQIIVAIKKFLESEDDPVVKKIALREIRMLKQLKH 60
 QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNVADGVKSVLWQTLQALNFCCHI 120
 DB 62 PNLVNLIEVFRKRKMHVFEYCDHTLVHLDYRQGVPEHLVKSITWTLQAVNFCCHK 121
 QY 121 NCHRDIKPENILITKQGIKICDFGFAQIL-IPGDAYTDYVATRYRAPELLVGTQYG 179
 DB 122 NCHRDIKPENILITKHSVVKLCDFGFAQLLTGSPDYDDYVATRYRSPPELLVGTQYG 180
 QY 180 SSVDIWAIGCVFAELLTGOPLWPKGSDVDQYLIITLVTETGFRHVDQAGLELLTSSDPP 239
 DB 181 KAVDVWAIGCLVTEMLMGEPLFPFGSDIDQLYLMRCL----- 218
 QY 240 AVASQAGITGKLIPIRHQSIKSNFGFHGISIPEDEMTELEKPSDVHPVALNFMKGCL 299
 DB 219 -----GNLIPRHQELFYKNPVFAGVRLPEIKSESEPLERRYPKLSEVVIDLAKKCL 268
 QY 300 KNPDPDLTCSOLLESSYF--DSF-----QEAQIK--RKARN-----EGRNRRQO 341
 DB 269 HVDPDKRPFCAELLHHDFFQMDGFAERFSQBLQMKVQKDAENISLSKKSQNRKKEK 324

RESULT 10

US-09-949-016-7954
 ; Sequence 7954, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016

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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7954
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-7954

Query Match          50.3%; Score 915.5; DB 4; Length 475;
Best Local Similarity 48.3%; Pred. No. 3.4e-89;
Matches 172; Conservative 68; Mismatches 69; Indels 47; Gaps 6;

Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKIATLREIRMLKOLKH 60
Db 3 MEKYNLGLVGECSYGMVKCRNKDTGRIVAIAKKFLESDDDDKMKVKIAMREIKLLKOLRH 62

Qy 61 PNLVNLIEVFRRRKMHVPEYCDHTLLNELRNPNGVADGVIKSVLWOTLQALNFCCHI 120
Db 63 ENLVNLLEVCKKKRWYLVFEVDHTLLDLELFPNGLDYQVQVKYLFQIINGIGFCHSH 122

Qy 121 NCIHRIKPENILITKQGIKICDFGPAQIL-IPGDAYTDYVATRWYRAPELLVGDTOYG 179
Db 123 NIIHRDIKPENILVSQSGVVKLCDFGFARTLAARGEVYTDYVATRWYRAPELLVGDVKYG 182

Qy 180 SSVDIWAIGCVFABLLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 183 KAVDVWAIGCLVTEMFMGEPFLPGDSIDQLYHMMCL-----EGRNRRRQ 220

Qy 240 AVASQASAGITGKLI PRHOSIFKSNPFHGHSIPEPEMETLEKFSVDVHPVALNFMKGCL 299
Db 221 -----GNLIPRHOELFNKNPVFAGVRLPEIKEREPLERRYPKLSSEVIDLAKKCL 270

Qy 300 KMPDRLTCSQLESSEYF--DSF-----QEAQIK--RKARN-----EGRNRRRQ 341
Db 271 HIDPKRPFCAELLHDDFFQMDGFAERFSQELQLKVQKDARNVSLSKKSQNRKKEK 326

RESULT 11
US-09-411-628-10
; Sequence 10, Application US/09411628
; Patent No. 6428994
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/09/411,628
; CURRENT FILING DATE: 1999-10-01
; EARLIER FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-411-628-10

Query Match          50.3%; Score 915.5; DB 4; Length 493;
Best Local Similarity 48.3%; Pred. No. 3.7e-89;
Matches 172; Conservative 68; Mismatches 69; Indels 47; Gaps 6;

Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKIATLREIRMLKOLKH 60
Db 1 MEKYNLGLVGECSYGMVKCRNKDTGRIVAIAKKFLESDDDDKMKVKIAMREIKLLKOLRH 60

Qy 61 PNLVNLIEVFRRRKMHVPEYCDHTLLNELRNPNGVADGVIKSVLWOTLQALNFCCHI 120
Db 61 ENLVNLLEVCKKKRWYLVFEVDHTLLDLELFPNGLDYQVQVKYLFQIINGIGFCHSH 120

Qy 121 NCIHRIKPENILITKQGIKICDFGPAQIL-IPGDAYTDYVATRWYRAPELLVGDTOYG 179
Db 121 NIIHRDIKPENILVSQSGVVKLCDFGFARTLAARGEVYTDYVATRWYRAPELLVGDVKYG 180

Qy 180 SSVDIWAIGCVFABLLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 KAVDVWAIGCLVTEMFMGEPFLPGDSIDQLYHMMCL-----EGRNRRRQ 218

Qy 240 AVASQASAGITGKLI PRHOSIFKSNPFHGHSIPEPEMETLEKFSVDVHPVALNFMKGCL 299
Db 219 -----GNLIPRHOELFNKNPVFAGVRLPEIKEREPLERRYPKLSSEVIDLAKKCL 268

Qy 300 KMPDRLTCSQLESSEYF--DSF-----QEAQIK--RKARN-----EGRNRRRQ 341
Db 269 HIDPKRPFCAELLHDDFFQMDGFAERFSQELQLKVQKDARNVSLSKKSQNRKKEK 324
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Qy 61 PNLVNLIEVFRRRKMHVPEYCDHTLLNELRNPNGVADGVIKSVLWOTLQALNFCCHI 120
Db 61 ENLVNLLEVCKKKRWYLVFEVDHTLLDLELFPNGLDYQVQVKYLFQIINGIGFCHSH 120

Qy 121 NCIHRIKPENILITKQGIKICDFGPAQIL-IPGDAYTDYVATRWYRAPELLVGDTOYG 179
Db 121 NIIHRDIKPENILVSQSGVVKLCDFGFARTLAARGEVYTDYVATRWYRAPELLVGDVKYG 180

Qy 180 SSVDIWAIGCVFABLLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 KAVDVWAIGCLVTEMFMGEPFLPGDSIDQLYHMMCL-----EGRNRRRQ 218

Qy 240 AVASQASAGITGKLI PRHOSIFKSNPFHGHSIPEPEMETLEKFSVDVHPVALNFMKGCL 299
Db 219 -----GNLIPRHOELFNKNPVFAGVRLPEIKEREPLERRYPKLSSEVIDLAKKCL 268

Qy 300 KMPDRLTCSQLESSEYF--DSF-----QEAQIK--RKARN-----EGRNRRRQ 341
Db 269 HIDPKRPFCAELLHDDFFQMDGFAERFSQELQLKVQKDARNVSLSKKSQNRKKEK 324

RESULT 12
US-10-174-794-10
; Sequence 10, Application US/10174794
; Patent No. 6664086
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; TITLE OF INVENTION: SEQUENCES OF LEARNING-INDUCED KINASES
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-174-794-10

Query Match          50.3%; Score 915.5; DB 4; Length 493;
Best Local Similarity 48.3%; Pred. No. 3.7e-89;
Matches 172; Conservative 68; Mismatches 69; Indels 47; Gaps 6;

Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKIATLREIRMLKOLKH 60
Db 1 MEKYNLGLVGECSYGMVKCRNKDTGRIVAIAKKFLESDDDDKMKVKIAMREIKLLKOLRH 60

Qy 61 PNLVNLIEVFRRRKMHVPEYCDHTLLNELRNPNGVADGVIKSVLWOTLQALNFCCHI 120
Db 61 ENLVNLLEVCKKKRWYLVFEVDHTLLDLELFPNGLDYQVQVKYLFQIINGIGFCHSH 120

Qy 121 NCIHRIKPENILITKQGIKICDFGPAQIL-IPGDAYTDYVATRWYRAPELLVGDTOYG 179
Db 121 NIIHRDIKPENILVSQSGVVKLCDFGFARTLAARGEVYTDYVATRWYRAPELLVGDVKYG 180

Qy 180 SSVDIWAIGCVFABLLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 KAVDVWAIGCLVTEMFMGEPFLPGDSIDQLYHMMCL-----EGRNRRRQ 218

Qy 240 AVASQASAGITGKLI PRHOSIFKSNPFHGHSIPEPEMETLEKFSVDVHPVALNFMKGCL 299
Db 219 -----GNLIPRHOELFNKNPVFAGVRLPEIKEREPLERRYPKLSSEVIDLAKKCL 268

Qy 300 KMPDRLTCSQLESSEYF--DSF-----QEAQIK--RKARN-----EGRNRRRQ 341
Db 269 HIDPKRPFCAELLHDDFFQMDGFAERFSQELQLKVQKDARNVSLSKKSQNRKKEK 324
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RESULT 13

US-09-671-050-2
; Sequence 2, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 187
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-671-050-2

Query Match 43.5%; Score 791; DB 4; Length 187;
Best Local Similarity 100.0%; Pred. No. 1.8e-76;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEKYELAKTGGSGYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKQLKH	60
DB	1	MEKYELAKTGGSGYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKQLKH	60
QY	61	PNLVNLIIEVFRKRKMHVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCIH	120
DB	61	PNLVNLIIEVFRKRKMHVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCIH	120
QY	121	NCIHRDIKPNILITKQGIKICDFGFAQIL	151
DB	121	NCIHRDIKPNILITKQGIKICDFGFAQIL	151

RESULT 14

US-09-671-050-8
; Sequence 8, Application US/09671050
; Patent No. 6716616
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6716616el Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/671,050
; CURRENT FILING DATE: 2001-06-11
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 198
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-671-050-8

Query Match 43.5%; Score 791; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 2e-76;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEKYELAKTGGSGYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKQLKH	60
DB	1	MEKYELAKTGGSGYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKQLKH	60
QY	61	PNLVNLIIEVFRKRKMHVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCIH	120
DB	61	PNLVNLIIEVFRKRKMHVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCIH	120
QY	121	NCIHRDIKPNILITKQGIKICDFGFAQIL	151
DB	121	NCIHRDIKPNILITKQGIKICDFGFAQIL	151

RESULT 15

US-09-538-092-1236
; Sequence 1236, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapSeqFormatter Version 0.9
; SEQ ID NO 1236
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number Q00526
US-09-538-092-1236

Query Match 31.0%; Score 565; DB 4; Length 305;
Best Local Similarity 36.8%; Pred. No. 6.5e-52;
Matches 124; Conservative 66; Mismatches 99; Indels 48; Gaps 9;

QY	1	MEKYELAKTGGSGYGVVFKCRNKTSGQVAVKFP---VESEDDPVVKKIALREIRMLKQ	57
DB	1	MDMFQKEKIGEGTYGVVYKAKNRETGQVAVKIRLDLEMEGVP---STAIRISLLKE	57
QY	58	LKHPNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNNG-VADGVKSVLWQTLQALNF	116
DB	58	LKHPNIVRLLDVVHNERKLYLVFEFLSQDLKKYMDSTPGSELPLHLIKSYLFQLQGVSF	117
QY	117	CHHNCHIRDIRPENILITKQGIKICDFGFAQIL-IPGDAYTDYVATRWYRAPPVLLVD	175
DB	118	CHSHRVHHRDLKPNLLINELGAILADPLARAFGVLRTYTHEVVTILWYRAPPVLLGS	177
QY	176	TOYGSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIRTLVETGFRHVDQAGLELTS	235
DB	178	KYTTAVDIWSIGCIFAEWVTRKALFPGDSELDQIFRFRML-----	219
QY	236	SDPPAVASQSA--GITGLIPRHQSIFKNGPFGHGISIPEPE-DMETLEEKFSVDVHPVAL	292
DB	220	-----GTPSEDTPGVT--QLPDYKGSF-----PKWTRKGLEEIVPNLEPGR	260
QY	293	NFMKGLKMNPDRLTCSQLLESYSYFDSFQRAQIKRK	329
DB	261	DILMQLQLQDPSQRITAKTALAHYPFSSPSPAPARQ	297

Search completed: April 22, 2005, 06:52:56
Job time : 36.071 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 06:50:50 ; Search time 859.637 Seconds
(without alignments)
134.334 Million cell updates/sec

Title: US-10-766-691-10

Perfect score: 1820

Sequence: 1 MEKYEKLAKTGGSGYGVVFK.....RKARNGRRRRROOVLPKLS 347

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1820	100.0	347	17	US-10-766-691-10
2	1796	98.7	356	17	US-10-766-691-4
3	1636	89.9	315	17	US-10-766-691-12
4	1613	88.6	342	15	US-10-333-314-10
5	1612	88.6	324	17	US-10-766-691-6
6	1162.5	63.9	358	15	US-10-363-616-391
7	1160.5	63.8	338	16	US-10-664-421-97
8	1157.5	63.6	358	14	US-10-174-794-11
9	1134	62.3	228	9	US-09-834-496A-2
10	941.5	51.7	566	14	US-10-174-794-4
11	915.5	50.3	493	14	US-10-174-794-10
12	915.5	50.3	493	15	US-10-369-022-22
13	915.5	50.3	493	16	US-10-757-262-108

14	791	43.5	187	17	US-10-766-691-2	Sequence 2, Appli
15	791	43.5	198	17	US-10-766-691-8	Sequence 8, Appli
16	758.5	41.7	455	16	US-10-620-052A-34	Sequence 34, Appl
17	712.5	39.1	154	16	US-10-250-889-62	Sequence 62, Appl
18	565	31.0	305	15	US-10-394-322A-8	Sequence 8, Appli
19	565	31.0	305	16	US-10-408-765A-544	Sequence 544, App
20	565	31.0	305	16	US-10-620-052A-20	Sequence 20, Appl
21	563	30.9	544	14	US-10-072-036-113	Sequence 113, App
22	557	30.6	298	9	US-09-771-161A-187	Sequence 187, App
23	557	30.6	544	14	US-10-072-036-115	Sequence 115, App
24	556	30.5	298	14	US-10-174-794-13	Sequence 13, Appl
25	556	30.5	298	14	US-10-295-681-27	Sequence 27, Appl
26	555	30.5	297	14	US-10-295-681-51	Sequence 51, Appl
27	554	30.4	298	11	US-09-969-034-4493	Sequence 4493, Ap
28	554	30.4	298	15	US-10-394-322A-7	Sequence 7, Appli
29	554	30.4	298	16	US-10-620-052A-55	Sequence 55, Appl
30	554	30.4	298	16	US-10-664-421-14	Sequence 14, Appl
31	554	30.4	298	16	US-10-664-421-51	Sequence 51, Appl
32	551.5	30.3	294	15	US-10-389-566-1333	Sequence 1333, Ap
33	551	30.3	294	15	US-10-334-143-181	Sequence 181, App
34	550	30.2	298	14	US-10-295-681-31	Sequence 31, Appl
35	550	30.2	298	14	US-10-295-681-39	Sequence 39, Appl
36	548	30.1	298	14	US-10-295-681-29	Sequence 29, Appl
37	548	30.1	298	14	US-10-295-681-43	Sequence 43, Appl
38	546.5	30.0	294	15	US-10-389-566-1030	Sequence 1030, Ap
39	546	30.0	298	14	US-10-295-681-35	Sequence 35, Appl
40	545.5	30.0	294	15	US-10-389-566-1087	Sequence 1087, Ap
41	545	29.9	297	14	US-10-060-065-11	Sequence 11, Appl
42	545	29.9	297	14	US-10-059-585-32	Sequence 32, Appl
43	545	29.9	297	14	US-10-177-293-41	Sequence 41, Appl
44	545	29.9	297	14	US-10-174-794-12	Sequence 12, Appl
45	545	29.9	297	14	US-10-204-041-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-10-766-691-10
; Sequence 10, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0046-USA
; CURRENT APPLICATION NUMBER: US/10766,691
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 347
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-766-691-10

Query Match 100.0%; Score 1820; DB 17; Length 347;
Best Local Similarity 100.0%; Pred. No. 3.66-143;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKFFVESEDDPVVKIALREIRMLKQLKH 60
Db 1 MEKYEKLAKTGGSGYGVVFKCRNKTSGQVAVKFFVESEDDPVVKIALREIRMLKQLKH 60

QY 61 PNLVNLIEVFRKRKXHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCIH 120
 DB 61 PNLVNLIEVFRKRKXHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCIH 120
 QY 121 NCIHRDIKPENILITKQGIKICDFGFAQILIPGDATDYVATRWYRAPELLVGDTOYGS 180
 DB 121 NCIHRDIKPENILITKQGIKICDFGFAQILIPGDATDYVATRWYRAPELLVGDTOYGS 180
 QY 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGRHVDQAGLELLTSSDPPA 240
 DB 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGRHVDQAGLELLTSSDPPA 240
 QY 241 VASQAGITGKLIPIRHSIFKSNFGFHGISIPEPEMETLEEKFSVHPVAFNFMKGCLK 300
 DB 241 VASQAGITGKLIPIRHSIFKSNFGFHGISIPEPEMETLEEKFSVHPVAFNFMKGCLK 300
 QY 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOVLPLKS 347
 DB 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOVLPLKS 347
 RESULT 2
 US-10-766-691-4
 ; Sequence 4, Application US/10766691
 ; Publication No. US20050042626A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: Novel Human Kinase Proteins and
 ; FILE REFERENCE: LEX-0046-USA
 ; CURRENT APPLICATION NUMBER: US/10/766.691
 ; PRIOR FILING DATE: 2004-01-28
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 356
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-766-691-4

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 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 QY 61 PNLVNLIEVFRKRKXHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCIH 120
 DB 61 PNLVNLIEVFRKRKXHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCIH 120
 QY 121 NCIHRDIKPENILITKQGIKICDFGFAQILIPGDATDYVATRWYRAPELLVGDTOYGS 180
 DB 121 NCIHRDIKPENILITKQGIKICDFGFAQILIPGDATDYVATRWYRAPELLVGDTOYGS 180
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 DB 241 VASQAGITGKLIPIRHSIFKSNFGFHGISIPEPEMETLEEKFSVHPVAFNFMKGCLK 300

QY 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOVLPLKS 342
 DB 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOVLPLKS 342
 RESULT 3
 US-10-766-691-12
 ; Sequence 12, Application US/10766691
 ; Publication No. US20050042626A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: Novel Human Kinase Proteins and
 ; FILE REFERENCE: LEX-0046-USA
 ; CURRENT APPLICATION NUMBER: US/10/766.691
 ; PRIOR FILING DATE: 2004-01-28
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 315
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-766-691-12

Query Match 89.9%; Score 1636; DB 17; Length 315;
 Best Local Similarity 90.8%; Pred. No. 6.7e-128;
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 DB 1 MEKYEKLAKTGEISGVVFKCRNKTSGQVAVKVFVESEDDPVVKKIALREIRMLKOLKH 60
 QY 61 PNLVNLIEVFRKRKXHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCIH 120
 DB 61 PNLVNLIEVFRKRKXHLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCIH 120
 QY 121 NCIHRDIKPENILITKQGIKICDFGFAQILIPGDATDYVATRWYRAPELLVGDTOYGS 180
 DB 121 NCIHRDIKPENILITKQGIKICDFGFAQILIPGDATDYVATRWYRAPELLVGDTOYGS 180
 QY 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGRHVDQAGLELLTSSDPPA 240
 DB 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGRHVDQAGLELLTSSDPPA 240
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 DB 241 VASQAGITGKLIPIRHSIFKSNFGFHGISIPEPEMETLEEKFSVHPVAFNFMKGCLK 300
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 DB 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQOVLPLKS 347

RESULT 4
 US-10-333-314-10
 ; Sequence 10, Application US/10333314
 ; Publication No. US20030211093A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.; YUE, Henry
 ; APPLICANT: KHAN, Farrah A.; GURURAJAN, Rajagopal
 ; APPLICANT: HAFALIA, April J.A.; CHAWLA, Narinder K.
 ; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
 ; APPLICANT: GANDHI, Ameena R.; POLICKY, Jennifer L.
 ; APPLICANT: BAUGHN, Mariah R.; TRIBOULEY, Catherine M.

```

; APPLICANT: THORNTON, Michael B.; BANDMAN, Olga
; APPLICANT: NGUYEN, Daniel B.; LU, Yan
; APPLICANT: BURFORD, Neil; LAL, Preeti G.
; APPLICANT: DING, Li; YAO, Monique G.
; APPLICANT: ELIOTT, Vicki S.; RECIPON, Shirley A.
; APPLICANT: KEARNEY, Liam; LU, Dyung Aina M.
; APPLICANT: GREENWALD, Sara R.; TANG, Y. Tom
; APPLICANT: XU, Yuming; WALSH, Roderick T.
; APPLICANT: GIETZEN, Kimberly J.; YANG, Junming
; APPLICANT: JACKSON, Jennifer L.
; TITLE OF INVENTION: HUMAN KINASES
; FILE REFERENCE: PI-0162 USN
; CURRENT APPLICATION NUMBER: US/10/333,314
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: PCT/US01/23092
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/220,038
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: US 60/222,112
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,831
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: US 60/224,729
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1698381CD1
US-10-333-314-10

Query Match      88.6%; Score 1613; DB 15; Length 342;
Best Local Similarity 89.9%; Pred. No. 6e-126;
Matches 312; Conservative 1; Mismatches 0; Indels 34; Gaps 2;

Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
Db 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60

Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCIH 120
Db 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCIH 120

Qy 121 NCIHRIKPNILITKGGIIKICDFGPAQLIPGDATDYVATRYRAPELLVGDTOYGS 180
Db 121 NCIHRIKPNILITKGGIIKICDFGPAQLIPGDATDYVATRYRAPELLVGDTOYGS 180

Qy 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
Db 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240

Qy 241 VASOSAGITGKLI PRHOSIFKSGFFHGISIPEDMETLEEKFSVDHPVVALNFMKGLK 300
Db 241 VASOSAGITGKLI PRHOSIFKSGFFHGISIPEDMETLEEKFSVDHPVVALNFMKGLK 300

Qy 218 -----GKLI PRHOSIFKSGFFHGISIPEDMETLEEKFSVDHPVVALNFMKGLK 268
Db 218 -----GKLI PRHOSIFKSGFFHGISIPEDMETLEEKFSVDHPVVALNFMKGLK 268

Qy 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQV 345
Db 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQV 345

Qy 269 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQV 315
Db 269 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQV 315

RESULT 5
US-10-766-691-6
; Sequence 6, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn

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; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/10/766,691
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US/09/671,050
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US 60/156,511
; PRIOR FILING DATE: 1999-09-28
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 324
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-766-691-6

Query Match      88.6%; Score 1612; DB 17; Length 324;
Best Local Similarity 90.6%; Pred. No. 6.9e-126;
Matches 310; Conservative 0; Mismatches 0; Indels 32; Gaps 1;

Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
Db 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60

Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCIH 120
Db 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNGVADGVIKSVLWQTLQALNFCIH 120

Qy 121 NCIHRIKPNILITKGGIIKICDFGPAQLIPGDATDYVATRYRAPELLVGDTOYGS 180
Db 121 NCIHRIKPNILITKGGIIKICDFGPAQLIPGDATDYVATRYRAPELLVGDTOYGS 180

Qy 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
Db 181 SVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240

Qy 241 VASOSAGITGKLI PRHOSIFKSGFFHGISIPEDMETLEEKFSVDHPVVALNFMKGLK 300
Db 241 VASOSAGITGKLI PRHOSIFKSGFFHGISIPEDMETLEEKFSVDHPVVALNFMKGLK 300

Qy 218 -----GKLI PRHOSIFKSGFFHGISIPEDMETLEEKFSVDHPVVALNFMKGLK 268
Db 218 -----GKLI PRHOSIFKSGFFHGISIPEDMETLEEKFSVDHPVVALNFMKGLK 268

Qy 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQV 342
Db 301 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQV 342

Qy 269 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQV 310
Db 269 MNPDRLTCSQLLESSYFDSFQEAQIKRKARNEGRRRRQV 310

RESULT 6
US-10-363-616-391
; Sequence 391, Application US/10363616
; Publication No. US20040044181A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-113 (793)
; CURRENT APPLICATION NUMBER: US/10/363,616
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 09/654,935
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 490
; SEQ ID NO 391
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-616-391

Query Match      63.9%; Score 1162.5; DB 15; Length 358;
Best Local Similarity 63.8%; Pred. No. 2e-88;
Matches 213; Conservative 42; Mismatches 46; Indels 33; Gaps 2;

Qy 1 MEKYEKLAKTGECSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60

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Db 2 MEKYEKIGKIGEGSYGVVFKCRNRDTGQIVAIKKFLESEDDPVIKKIALREIRMLKQLKH 61
Qy 61 PNLVNLLEVEFRKKRMLHVFYCDHTLLNELERNPNGVADGVTKSVLWOTLQALNFCCHI 120
Db 62 PNLVNLLEVEFRKKRMLHVFYCDHTVLHEDRYQGVPEHLVKSITWOTLQAVNFCCHK 121
Qy 121 NCIHRIKIPENILITKGIKIICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGTQYG 179
Db 122 NCIHROVKPENILITKHSVILKCLDFGARLLTGPSDYTDYVATRWYRSPPELLVGTQYG 181
Qy 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQYLILIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 182 PPVDVWAIGCVFAELLSGVPLWPKSDVDQYLIRKTL----- 219
Qy 240 AVASQAGITGKLI PRHQSIKSNFGFHGISIPEDMETLEKFSDVHPVAFNFMKGCL 299
Db 220 -----GDLIPRHQQVFTNQYFSGVKIPDPEDMEPLKFPNISYPALGGLKGCL 269
Qy 300 KMPDRLTCSQLLESSYFDSFOEAQIKRKARNE 333
Db 270 HMDPTERTLTCQELLHHPYFENIREIDLAKEHNK 303
RESULT 7
US-10-664-421-97
; Sequence 97, Application US/10664421
; Publication No. US20040142864A1
; GENERAL INFORMATION:
; APPLICANT: BREMER, RYAN
; APPLICANT: IBRAHIM, PRABHA
; APPLICANT: KOMAR, ABHINAV
; APPLICANT: MANDIYAN, VALSAN
; APPLICANT: MILBURN, MICHAEL V.
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE
; FILE REFERENCE: 039363/0703
; CURRENT APPLICATION NUMBER: US/10/664,421
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/412,341
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/411,398
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 169
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 97
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-664-421-97

Query Match 63.8%; Score 1160.5; DB 16; Length 338;
Best Local Similarity 63.8%; Pred. No. 2.8e-88;
Matches 213; Conservative 41; Mismatches 47; Indels 33; Gaps 2;
Qy 1 MEKYEKLAKTGEYSYGVVFKCRNKTSGQVAVKVFSEDDPVYKVKIALREIRMLKQLKH 60
Db 2 MEKYEKIGKIGEGSYGVVFKCRNRDTGQIVAIKKFLESEDDPVIKKIALREIRMLKQLKH 61
Qy 61 PNLVNLLEVEFRKKRMLHVFYCDHTLLNELERNPNGVADGVTKSVLWOTLQALNFCCHI 120
Db 62 PNLVNLLEVEFRKKRMLHVFYCDHTVLHEDRYQGVPEHLVKSITWOTLQAVNFCCHK 121
Qy 121 NCIHRIKIPENILITKGIKIICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGTQYG 179
Db 122 NCIHROVKPENILITKHSVILKCLDFGARLLTGPSDYTDYVATRWYRSPPELLVGTQYG 181
Qy 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQYLILIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 182 PPVDVWAIGCVFAELLSGVPLWPKSDVDQYLIRKTL----- 219
Qy 240 AVASQAGITGKLI PRHQSIKSNFGFHGISIPEDMETLEKFSDVHPVAFNFMKGCL 299
Db 220 -----GDLIPRHQQVFTNQYFSGVKIPDPEDMEPLKFPNISYPALGGLKGCL 269

Qy 300 KMPDRLTCSQLLESSYFDSFOEAQIKRKARNE 333
Db 270 HMDPTERTLTCQELLHHPYFENIREIDLAKEHNK 303
RESULT 8
US-10-174-794-11
; Sequence 11, Application US/10174794
; Publication No. US20030166220A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US/09/411,628
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 60/102,906
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-794-11

Query Match 63.6%; Score 1157.5; DB 14; Length 358;
Best Local Similarity 64.7%; Pred. No. 5.2e-88;
Matches 211; Conservative 41; Mismatches 41; Indels 33; Gaps 2;
Qy 1 MEKYEKLAKTGEYSYGVVFKCRNKTSGQVAVKVFSEDDPVYKVKIALREIRMLKQLKH 60
Db 2 MEKYEKIGKIGEGSYGVVFKCRNRDTGQIVAIKKFLESEDDPVIKKIALREIRMLKQLKH 61
Qy 61 PNLVNLLEVEFRKKRMLHVFYCDHTLLNELERNPNGVADGVTKSVLWOTLQALNFCCHI 120
Db 62 PNLVNLLEVEFRKKRMLHVFYCDHTVLHEDRYQGVPEHLVKSITWOTLQAVNFCCHK 121
Qy 121 NCIHRIKIPENILITKGIKIICDFGFAQILI-PGDAYTDYVATRWYRAPELLVGTQYG 179
Db 122 NCIHROVKPENILITKHSVILKCLDFGARLLTGPSDYTDYVATRWYRSPPELLVGTQYG 181
Qy 180 SSVDIWAIGCVFAELLTGQPLWPKSDVDQYLILIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 182 PPVDVWAIGCVFAELLSGVPLWPKSDVDQYLIRKTL----- 219
Qy 240 AVASQAGITGKLI PRHQSIKSNFGFHGISIPEDMETLEKFSDVHPVAFNFMKGCL 299
Db 220 -----GDLIPRHQQVFTNQYFSGVKIPDPEDMEPLKFPNISYPALGGLKGCL 269

Qy 300 KMPDRLTCSQLLESSYFDSFOEAQ 325
Db 270 HMDPTERTLTCQELLHHPYFENIREIE 295
RESULT 9
US-09-834-496A-2
; Sequence 2, Application US/09834496A
; Patent No. US20020090701A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann
; TITLE OF INVENTION: 14257 NOVEL PROTEIN KINASE MOLECULES AND
; FILE REFERENCE: 381552000900
; CURRENT APPLICATION NUMBER: US/09/834,496A
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/196,910
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2

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; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-496A-2

Query Match      62.3%; Score 1134; DB 9; Length 228;
Best Local Similarity 98.2%; Pred. No. 2.8e-86;
Matches 213; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MEKYEKLAKTGEQGVVFKCRNKTSGQVAVKVFVESEDDPVVKIATLREIRMLKQLKH 60
Db 1 MGKYEKLAKTGEQGVVFKCRNKTSGQVAVKVFVESEDDPVVKIATLREIRMLKQLKH 60
Qy 61 PNLVNLIEVFRKRKMLVFEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCCHI 120
Db 61 PNLVNLIEVFRKRKMLVFEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCCHI 120
Qy 121 NCIHRIKPENILITKOGIIKICDFGFAQILIPGDATYDVATRWYRAPELLVGDTOYGS 180
Db 121 NCIHRIKPENILITKOGIIKICDFGFAQILIPGDATYDVATRWYRAPELLVGDTOYGS 180
Qy 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTL 217
Db 181 SVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTL 217

RESULT 10
US-10-174-794-4
; Sequence 4, Application US/10174794
; Publication No. US20030166220A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; PRIOR FILING DATE: 2002-06-18
; PRIOR FILING DATE: 1999-10-01
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Orcytolagus cuniculus
US-10-174-794-4

Query Match      51.7%; Score 941.5; DB 14; Length 566;
Best Local Similarity 49.7%; Pred. No. 8.7e-70;
Matches 177; Conservative 67; Mismatches 65; Indels 47; Gaps 6;

Qy 1 MEKYEKLAKTGEQGVVFKCRNKTSGQVAVKVFVESEDDPVVKIATLREIRMLKQLKH 60
Db 1 MEKYEKLAKTGEQGVVFKCRNKTSGQVAVKVFVESEDDPVVKIATLREIRMLKQLKH 60
Qy 61 PNLVNLIEVFRKRKMLVFEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCCHI 120
Db 61 ENLVNLIEVCKKRWLVFEYCDHTLLDELFPNGLDQVQVYLFQINGIFGCHSH 120
Qy 121 NCIHRIKPENILITKOGIIKICDFGFAQILIPGDATYDVATRWYRAPELLVGDTOY 179
Db 121 NCIHRIKPENILITKOGIIKICDFGFAQILIPGDATYDVATRWYRAPELLVGDTOY 179
Qy 180 SVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 KAVDVAIGCLVTEMFMGEPLFGDSDDIDQLXIMMCL----- 218
Qy 240 AVASQAGITCKLIPRHSIFKSNPFHGISPEPEMETLEEKFSVDHPVAFNMKGCL 299
Db 219 -----GNLIPRHOELFKNPVFAGVRLPEIKEREPLRRYPKLSSEVVIDLAKKCL 268

Qy 300 KMPDDRLTCSQLLESSYF--DSF-----QEAQIK--RKARN-----EGNRNRQ 341
Db 269 HIDPDKRPFCAELLHDDFFQMDGFAERFSQELQKVKQKDRNVSLSKSKSQRKKEK 324

RESULT 12
US-10-369-022-22
; Sequence 22, Application US/10369022
; Publication No. US20030203847A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Beth
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS IN USING 9949, 14230, 760, 62553,
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44372,
; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
; TITLE OF INVENTION: 13424 MOLECULES
; FILE REFERENCE: MF102-027PIRNMNM
; CURRENT APPLICATION NUMBER: US/10/369,022
```

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Qy 300 KMPDDRLTCSQLLESSYF--DSF-----QEAQIK--RKARN-----EGNRNRQ 341
Db 269 HIDPDKRPFCAELLHDDFFQMDGFAERFSQELQKVKQKDRNVSLSKSKSQRKKEK 324

RESULT 11
US-10-174-794-10
; Sequence 10, Application US/10174794
; Publication No. US20030166220A1
; GENERAL INFORMATION:
; APPLICANT: University of Southern California
; TITLE OF INVENTION: CDNA, GENOMIC, AND PREDICTED PROTEIN
; FILE REFERENCE: 13761-707
; CURRENT APPLICATION NUMBER: US/10/174,794
; PRIOR FILING DATE: 2002-06-18
; PRIOR FILING DATE: 1999-10-01
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-174-794-10

Query Match      50.3%; Score 915.5; DB 14; Length 493;
Best Local Similarity 48.3%; Pred. No. 1.1e-67;
Matches 172; Conservative 68; Mismatches 69; Indels 47; Gaps 6;

Qy 1 MEKYEKLAKTGEQGVVFKCRNKTSGQVAVKVFVESEDDPVVKIATLREIRMLKQLKH 60
Db 1 MEKYEKLAKTGEQGVVFKCRNKTSGQVAVKVFVESEDDPVVKIATLREIRMLKQLKH 60
Qy 61 PNLVNLIEVFRKRKMLVFEYCDHTLLNELRPNPGVADGVKSVLWQTLQALNFCCHI 120
Db 61 ENLVNLIEVCKKRWLVFEYCDHTLLDELFPNGLDQVQVYLFQINGIFGCHSH 120
Qy 121 NCIHRIKPENILITKOGIIKICDFGFAQILIPGDATYDVATRWYRAPELLVGDTOY 179
Db 121 NCIHRIKPENILITKOGIIKICDFGFAQILIPGDATYDVATRWYRAPELLVGDTOY 179
Qy 180 SVDIWAIGCVFAELLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 KAVDVAIGCLVTEMFMGEPLFGDSDDIDQLXIMMCL----- 218
Qy 240 AVASQAGITCKLIPRHSIFKSNPFHGISPEPEMETLEEKFSVDHPVAFNMKGCL 299
Db 219 -----GNLIPRHOELFKNPVFAGVRLPEIKEREPLRRYPKLSSEVVIDLAKKCL 268

Qy 300 KMPDDRLTCSQLLESSYF--DSF-----QEAQIK--RKARN-----EGNRNRQ 341
Db 269 HIDPDKRPFCAELLHDDFFQMDGFAERFSQELQKVKQKDRNVSLSKSKSQRKKEK 324

RESULT 12
US-10-369-022-22
; Sequence 22, Application US/10369022
; Publication No. US20030203847A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Rosenfeld, Julie Beth
; APPLICANT: Silos-Santiago, Immaculada
; TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
; TITLE OF INVENTION: PAIN AND PAINFUL DISORDERS IN USING 9949, 14230, 760, 62553,
; TITLE OF INVENTION: 12216, 17719, 41897, 47174, 33408, 10002, 16209, 314, 636,
; TITLE OF INVENTION: 27410, 33260, 619, 15985, 69112, 2158, 224, 615, 44372,
; TITLE OF INVENTION: 95431, 22245, 2387, 16658, 55054, 16314, 1613, 1675, 9569 OR
; TITLE OF INVENTION: 13424 MOLECULES
; FILE REFERENCE: MF102-027PIRNMNM
; CURRENT APPLICATION NUMBER: US/10/369,022
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; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US 60/360,495
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/370,121
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/373,010
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/373,908
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/377,717
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US 60/379,949
; PRIOR FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/382,409
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/385,280
; PRIOR FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/386,879
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/387,536
; PRIOR FILING DATE: 2002-06-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-369-022-22

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```

Query Match      50.3%; Score 915.5; DB 15; Length 493;
Best Local Similarity 48.3%; Pred. No. 1.1e-67;
Matches 172; Conservative 68; Mismatches 69; Indels 47; Gaps 6;

QY 1 MEKYEKLAKTGEGSYGVFKCRNKTSGQVAVKVFVESEDDPVVKKALREIMLKQLKH 60
Db 1 MEKYENGLVGEISYGVWVKCRNKTGRIVAKKFESEDDDKVKKAMREIKLKLQLRH 60

QY 61 PNLVNLIEVFRKRKHVFEYCDHTLNLNELRNPNGVADGVKISVLWQTLQALNFCIH 120
Db 61 ENLVNLLEVCCKRWYLVFEVDHTILDLELFPNGLDYQVQVKYLFQIINGIFGCHSH 120

QY 121 NCIRHDIKPENILITKQGIKIICDPGFAQIL-IPGDAYTDVATWYRAPPELLVGTQYG 179
Db 121 NIHRDIKPENILVSQSGVVKCLDFGFAARTLAAPGEVYTDVATWYRAPPELLVGTQYG 180

QY 180 SSVDIWAICGVFAELLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 KAVDVWAICLVTEMFMGEPLFGSDSDIDQLYHMMCL-----218

QY 240 AVASQAGITKGLIPRHQSIFKSNGFHGISIPEDMETLEKFSVHPVVALNFMKGL 299
Db 219 -----GNLIPRHQELFNKNPVFAGVRLPEIKEREPLERYPKLSEVVIDLAKKCL 268

QY 300 KNPDPDLTCSQLLESSYF--DSF-----QBAQIK--RKARN-----EGNRRRQ 341
Db 269 HIDPKRPFCAELLHHDFQMDGFAERFSQELQLKVQKDARNVLSKSNRRKKEK 324

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RESULT 13

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US-10-757-262-108
; Sequence 108, Application US/10757262
; Publication No. US20040197825A1
; GENERAL INFORMATION:
; APPLICANT: Karicheti, Venkateswarlu
; APPLICANT: Eliasoof, Scott D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 44390, 54181, 211, 5687, 884,
; TITLE OF INVENTION: 1405, 636, 4421, 5410, 30905, 2045, 16405, 18560, 2047,
; TITLE OF INVENTION: 33751, 52872, 14063, 20739, 32544, 43239, 44373, 51164,
; TITLE OF INVENTION: 53010, 16852, 1587, 2207, 22445, 2387, 52908, 69112, 14990,
; TITLE OF INVENTION: 18547, 115, 579, 15985, 15625, 760, 18603, 2395, 2554, 8675,

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RESULT 14

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US-10-766-691-2
; Sequence 2, Application US/10766691
; Publication No. US20050042626A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn

```

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; TITLE OF INVENTION: 32720, 4809, 14303, 16816, 17827, 32620, 577, 619, 1423,
; TITLE OF INVENTION: 2158, 8263, 15402, 16209, 16386, 21165, 30911, 41897, 1643,
; TITLE OF INVENTION: 2543, 9626, 13231, 32409, 84260, 2882, 8203, 32678 OR
; FILE REFERENCE: MPI03-007PIRNMNMIM
; CURRENT APPLICATION NUMBER: US/10/757,262
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US 60/440,318
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/444,783
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: US 60/457,901
; PRIOR FILING DATE: 2003-03-27
; PRIOR APPLICATION NUMBER: US 60/468,775
; PRIOR FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/471,614
; PRIOR FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: US 60/478,742
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/488,529
; PRIOR FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 60/491,156
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/499,594
; PRIOR FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US 60/506,332
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-757-262-108

```

```

Query Match      50.3%; Score 915.5; DB 16; Length 493;
Best Local Similarity 48.3%; Pred. No. 1.1e-67;
Matches 172; Conservative 68; Mismatches 69; Indels 47; Gaps 6;

QY 1 MEKYEKLAKTGEGSYGVFKCRNKTSGQVAVKVFVESEDDPVVKKALREIMLKQLKH 60
Db 1 MEKYENGLVGEISYGVWVKCRNKTGRIVAKKFESEDDDKVKKAMREIKLKLQLRH 60

QY 61 PNLVNLIEVFRKRKHVFEYCDHTLNLNELRNPNGVADGVKISVLWQTLQALNFCIH 120
Db 61 ENLVNLLEVCCKRWYLVFEVDHTILDLELFPNGLDYQVQVKYLFQIINGIFGCHSH 120

QY 121 NCIRHDIKPENILITKQGIKIICDPGFAQIL-IPGDAYTDVATWYRAPPELLVGTQYG 179
Db 121 NIHRDIKPENILVSQSGVVKCLDFGFAARTLAAPGEVYTDVATWYRAPPELLVGTQYG 180

QY 180 SSVDIWAICGVFAELLTGQPLWPKGSDVDQYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 KAVDVWAICLVTEMFMGEPLFGSDSDIDQLYHMMCL-----218

QY 240 AVASQAGITKGLIPRHQSIFKSNGFHGISIPEDMETLEKFSVHPVVALNFMKGL 299
Db 219 -----GNLIPRHQELFNKNPVFAGVRLPEIKEREPLERYPKLSEVVIDLAKKCL 268

QY 300 KNPDPDLTCSQLLESSYF--DSF-----QBAQIK--RKARN-----EGNRRRQ 341
Db 269 HIDPKRPFCAELLHHDFQMDGFAERFSQELQLKVQKDARNVLSKSNRRKKEK 324

```

; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: Novel Human Kinase Proteins and
 ; FILE REFERENCE: Polynucleotides Encoding the Same
 ; CURRENT APPLICATION NUMBER: US-0046-USA
 ; CURRENT FILING DATE: 2004-01-28
 ; PRIOR APPLICATION NUMBER: US/09/671,050
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 187
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-766-691-2

Query Match 43.5%; Score 791; DB 17; Length 187;
 Best Local Similarity 100.0%; Pred. No. 7.7e-58;
 Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MEKYEKLAKTGGSGVGVFKCRNKTSGQVAVKKFVESEDDPVVKKIALREIRMLKQLKH 60
 Db 1 MEKYEKLAKTGGSGVGVFKCRNKTSGQVAVKKFVESEDDPVVKKIALREIRMLKQLKH 60
 Qy 61 PNLVNLIEVFRKRKRMHLVFEYCDHTLLNELERNPNVGADGVKSVLWQTLQALNFCIH 120
 Db 61 PNLVNLIEVFRKRKRMHLVFEYCDHTLLNELERNPNVGADGVKSVLWQTLQALNFCIH 120
 Qy 121 NCIRHDIKPENILITKQGIKICDFGFAQIL 151
 Db 121 NCIRHDIKPENILITKQGIKICDFGFAQIL 151

RESULT 15
 US-10-766-691-8
 ; Sequence 8, Application US/10766691
 ; Publication No. US20050042626A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Gregory
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Nehls, Michael
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: Novel Human Kinase Proteins and
 ; FILE REFERENCE: Polynucleotides Encoding the Same
 ; CURRENT APPLICATION NUMBER: US/10/766,691
 ; CURRENT FILING DATE: 2004-01-28
 ; PRIOR APPLICATION NUMBER: US/09/671,050
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: US 60/156,511
 ; PRIOR FILING DATE: 1999-09-28
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 198
 ; TYPE: PRT
 ; ORGANISM: homo sapiens
 US-10-766-691-8

Query Match 43.5%; Score 791; DB 17; Length 198;
 Best Local Similarity 100.0%; Pred. No. 8.3e-58;
 Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MEKYEKLAKTGGSGVGVFKCRNKTSGQVAVKKFVESEDDPVVKKIALREIRMLKQLKH 60
 Db 1 MEKYEKLAKTGGSGVGVFKCRNKTSGQVAVKKFVESEDDPVVKKIALREIRMLKQLKH 60
 Qy 61 PNLVNLIEVFRKRKRMHLVFEYCDHTLLNELERNPNVGADGVKSVLWQTLQALNFCIH 120

Db 61 PNLVNLIEVFRKRKRMHLVFEYCDHTLLNELERNPNVGADGVKSVLWQTLQALNFCIH 120
 Qy 121 NCIRHDIKPENILITKQGIKICDFGFAQIL 151
 Db 121 NCIRHDIKPENILITKQGIKICDFGFAQIL 151

Search completed: April 22, 2005, 07:36:42
 Job time : 860.637 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 03:32:53 ; Search time 28.3051 Seconds
(without alignments)
1179.546 Million cell updates/sec

Title: US-10-766-691-10
Perfect score: 1820
Sequence: 1 MEKYEKLAKTGEISYGVVFK.....RKARNEGRRRRQVLPKLS 347

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1157.5	63.6	358	2 S23383	protein kinase (EC
2	1149.5	63.2	376	2 S22745	serine/threonine p
3	565	31.0	305	2 S23382	protein kinase (EC
4	563	30.9	302	1 I50474	protein kinase (EC
5	558.5	30.7	292	2 S40021	protein kinase (EC
6	555	30.5	297	2 A37871	protein kinase (EC
7	554	30.4	298	2 A41227	protein kinase (EC
8	552.5	30.4	294	2 B40444	protein kinase (EC
9	551.5	30.3	294	2 S22440	protein kinase (EC
10	551.5	30.3	294	2 S23095	protein kinase (EC
11	546.5	30.0	294	1 A40444	protein kinase (EC
12	546.5	30.0	294	2 T49271	CELL DIVISION CONT
13	545	29.9	297	2 A29539	protein kinase (EC
14	545	29.9	298	1 A44878	protein kinase (EC
15	542	29.8	297	2 I45977	cyclin-dependent k
16	541	29.7	297	1 S24913	protein kinase (EC
17	540.5	29.7	297	1 S12009	protein kinase cdc
18	540.5	29.7	302	2 B43439	protein kinase (EC
19	540	29.7	302	1 A43439	protein kinase (EC
20	539	29.6	303	1 S06011	protein kinase (EC
21	537	29.5	288	1 S42566	protein kinase (EC
22	536.5	29.5	311	2 S36619	protein kinase (EC
23	535.5	29.4	294	1 S79928	protein kinase (EC
24	535.5	29.4	294	1 J02243	protein kinase (EC
25	535.5	29.4	294	1 S42049	protein kinase (EC
26	532	29.2	301	1 S19209	protein kinase (EC
27	531	29.2	292	1 A46365	protein kinase (EC
28	530.5	29.1	294	1 S31332	protein kinase (EC
29	529	29.1	292	1 A45091	protein kinase (EC

30	529	29.1	292	1 I49592	protein kinase (EC
31	527.5	29.0	308	1 S53538	protein kinase (EC
32	527	29.0	297	1 A36074	protein kinase (EC
33	527	29.0	301	1 S42101	protein kinase (EC
34	526.5	28.9	291	2 S23386	protein kinase (EC
35	526	28.9	293	2 JE0374	cyclin-dependent k
36	526	28.9	294	2 S51008	protein kinase (EC
37	526	28.9	296	2 S24386	protein kinase (EC
38	524	28.8	302	1 OKBY85	protein kinase PHO
39	521.5	28.7	302	2 T17115	protein kinase cdc
40	519.5	28.5	346	2 A54820	CDK-activating pro
41	518	28.5	292	2 S22441	protein kinase (EC
42	517.5	28.4	346	2 A56231	MO15/CDK-activatin
43	516.5	28.4	314	1 S12007	protein kinase (EC
44	514	28.2	293	2 T02922	protein kinase (EC
45	514	28.2	346	1 I78840	protein kinase (EC

ALIGNMENTS

RESULT 1

S23383
protein kinase (EC 2.7.1.37) cdc2-related KKIALRE - human
C/Species: Homo sapiens (man)
C/Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C/Accession: S23383; S22744
R/Meyerson, M.; Enders, G.H.; Wu, C.L.; Su, L.K.; Gorka, C.; Nelson, C.; Harlow, E.; Tsai
EMBO J. 11, 2909-2917, 1992
A/Title: A family of human cdc2-related protein kinases.
A/Reference number: S23382; MUID:92347325; PMID:1639063
A/Accession: S23383
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-358 <MEY>
A/Cross-references: UNIPROT:Q00532; EMBL:X66358; NID:g36614; PIDN:CAA47002.1; PID:g36615
C/Superfamily: kinase-related transforming protein; protein kinase homology
C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F/3-278/Domain: protein kinase homology <KIN>
F/11-19/Region: protein kinase ATP-binding motif
F/34,52,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match	63.6%	Score	1157.5	DB	2	Length	358
Best Local Similarity	64.7%	Pred. No.	2.4e-45				
Matches	211	Conservative	41	Mismatches	41	Indels	33
Gaps	2						
Qy	1	MEKYEKLAKTGEISYGVVFKCRNKTSGQVAVKXFESEDDPVVVKIALREIRMLKQLKH	60				
Db	2	MEKYEKLGKIGEGSYGVVFKCRNRTDQIVAKKFESEDDPVVVKIALREIRMLKQLKH	61				
Qy	61	PNLVNLLIEVFRKRKMHVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCIH	120				
Db	62	PNLVNLLIEVFRKRKMHVFEYCDHTLVHLDYRGVPEHLVKSITWQTLQAVNFCIKH	121				
Qy	121	NCIHRDKPENILITKOGIKICDFGFAQLI-PCDAYTDYVATRWYRAPELLVGDQYQ	179				
Db	122	NCIHRDKPENILITKHSVKLCDFGFARLLTGESDYTDYVATRWYRSPPELLVGDQYQ	181				
Qy	180	SSVDIWAIGCVFAELLTGQPLWPKSDVDQLYLIRTLVETGFRHVDQAGLELLTSSDPP	239				
Db	182	PPVDVWAIGCVFAELLTGQPLWPKSDVDQLYLIRKTL-----	219				
Qy	240	AVASQSGAGITKGLIPRHQSIFKSNFGFHGISIPPEDEMETLEEKFSVDVHPVALNFMKGL	299				
Db	220	-----GDLIPRQQVFTNQYFSGVKIPDPEDMEPLEKFPNITSYPALGLLKGL	269				
Qy	300	KMNPPDRLTCSOLLESYFDSFQEAQ	325				
Db	270	HMDPTERTLCEQLLHHPYFENIRIE	295				

RESULT 2

S22745

serine/threonine protein kinase KIALRE (EC 2.7.1.1) - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 19-Dec-1997
 C:Accession: S22745
 R:Meyerson, M.L.
 submitted to the EMBL Data Library, May 1992
 A:Reference number: S22743
 A:Accession: S22745
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-376 <MEY>
 A:Cross-references: EMBL:X66359
 C:Genetics:
 A:Introns: 152/3; 170/3
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F;3-296/Domain: protein kinase homology <KIN>
 F;11-19/Region: protein kinase ATP-binding motif

Query Match 63.2%; Score 1149.5; DB 2; Length 376;
 Best Local Similarity 61.3%; Pred. No. 5.7e-45; Indels 51; Gaps 2;
 Matches 211; Conservative 41; Mismatches 41

Qy 1 MEKYEKLAKTGEQSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
 Dd 2 MEKYEKIGKIGESYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 61
 Qy 61 PNLVNLLEVFRRKRKMLHVFYCDHTLLNELRNPNQVADGVKSVLWQTLQALNFC 120
 Dd 62 PNLVNLLEVFRRKRKMLHVFYCDHTLLNELRNPNQVADGVKSVLWQTLQALNFC 121
 Qy 121 NCIRHDKPENILITKQIIKICDFGFAQIL - - - - - PGDAYTDYV 161
 Dd 122 NCIRHDKPENILITKQIIKICDFGFAQIL - - - - - PGDAYTDYV 181
 Qy 162 ATRWYRAPELLVGTQYGVSSVDIWAICGVFAELLTGQPLWPGKSDVDQLYLIIRTLVETG 221
 Dd 182 ATRWYRPELLVGTQYGVSSVDIWAICGVFAELLTGQPLWPGKSDVDQLYLIIRTLVETG 237
 Qy 222 FRHVDQAGLELLTSSDPPAVASQASGITKGLIPHQSIKSNFGHGISIPEPEDMETLE 281
 Dd 238 - - - - - GDLIPHQVQVSTNQYFSGVKIPDPEDMEPL 269
 Qy 282 EKFSVDHPVAFNMKGLKMPDRLTCSQLLESSYFDSFOEAQ 325
 Dd 270 LKPNISYPALGKLGKLDHDPFRLICEQLLHPYFENIREIE 313

RESULT 3
 S23382
 protein kinase (EC 2.7.1.37) cdk3 - human
 C:Species: Homo sapiens (man)
 C:Date: 18-Jun-1993 #sequence_revision 18-Jun-1993 #text_change 09-Jul-2004
 C:Accession: S23382; S22743
 R:Meyerson, M.; Enders, G.H.; Wu, C.L.; Su, L.K.; Gorka, C.; Nelson, C.; Harlow, E.; Tsai
 EMBO J. 11, 2909-2917, 1992
 A:Title: A family of human cdc2-related protein kinases.
 A:Reference number: S23382; MUID:92347325; PMID:1639063
 A:Accession: S23382
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-305 <MEY>
 A:Cross-references: UNIPROT:Q00526; EMBL:X66357; NID:G36612; PID:G36613
 C:Genetics:
 A:Gene: GDB:CDK3
 A:Cross-references: GDB:283456
 A:Map position: 12q13-12q13
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein kinase
 F;2-255/Domain: protein kinase homology <KIN>
 F;10-18/Region: protein kinase ATP-binding motif
 F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 31.0%; Score 565; DB 2; Length 305;
 Best Local Similarity 36.8%; Pred. No. 5.5e-19;
 Matches 124; Conservative 66; Mismatches 99; Indels 48; Gaps 9;

Qy 1 MEKYEKLAKTGEQSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 57
 Dd 1 MDMFQKVEKIGETGYGVVYKAKNRETQGLVALKIRLDLEMEGVP - - - STAIRISILLKE 57
 Qy 58 LKHPNLVNLLEVFRRKRKMLHVFYCDHTLLNELRNPNQVADGVKSVLWQTLQALNFC 116
 Dd 58 LKHPNLVNLLEVFRRKRKMLHVFYCDHTLLNELRNPNQVADGVKSVLWQTLQALNFC 117
 Qy 117 CHHNCIHRDKPENILITKQIIKICDFGFAQIL - - - - - IPGDYTDYVATRWYRAPELLVGD 175
 Dd 118 CHHNCIHRDKPENILITKQIIKICDFGFAQIL - - - - - IPGDYTDYVATRWYRAPELLVGD 177
 Qy 176 TOYGVSSVDIWAICGVFAELLTGQPLWPGKSDVDQLYLIIRTLVETGPRHVDQAGLELLT 235
 Dd 178 KFTVTAVIDWSIGICFAEMVTRKALFGDSEIDQLFRFRL - - - - - 219
 Qy 236 SDPPAVASQSA - - - GITKGLIPHQSIKSNFGHGISIPEPEDMETLEBKFSVDHPVAL 292
 Dd 220 - - - - - GTPSEDTPGVT - - - QLPDYKGSF - - - - - PKWTRKGLLEIIVNLEPEGR 260
 Qy 293 NFMKGCGLKMPDRLTCSQLLESSYFDSFOEAQIKRK 329
 Dd 261 DLMLQLLOYDPSORITAKTALAHYPSSPEPSAARQ 297

RESULT 4
 I50474
 protein kinase (EC 2.7.1.37) cdc2 [similarity] - goldfish
 C:Species: Carassius auratus (goldfish)
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C:Accession: I50474
 R:Kajiura, H.; Yamashita, M.; Katsu, Y.; Nagahama, Y.
 Dev. Growth Differ. 35, 647-654, 1993
 A:Title: Isolation and characterization of goldfish cdc2, a catalytic component of mature
 A:Reference number: I50474
 A:Accession: I50474
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-302 <RAJ>
 A:Cross-references: UNIPROT:P51958; GB:D17758; NID:G471097; PID:BA04605.1; PID:G471098
 C:Superfamily: kinase-related transforming protein; protein kinase homology
 C:Keywords: ATP; phosphotransferase
 F;2-256/Domain: protein kinase homology <KIN>
 F;10-18/Region: protein kinase ATP-binding motif
 F;33,51,128,130/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 30.9%; Score 563; DB 1; Length 302;
 Best Local Similarity 41.2%; Pred. No. 6.7e-19;
 Matches 117; Conservative 60; Mismatches 71; Indels 36; Gaps 6;

Qy 1 MEKYEKLAKTGEQSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 59
 Dd 1 MDDYKIEKIGETGYGVVYKGRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 59
 Qy 60 HPNLVNLLEVFRRKRKMLHVFYCDHTLLNELRNPNQVADGVKSVLWQTLQALNFC 117
 Dd 60 HPNLVNLLEVFRRKRKMLHVFYCDHTLLNELRNPNQVADGVKSVLWQTLQALNFC 119
 Qy 118 HIHNCIHRDKPENILITKQIIKICDFGFAQIL - - - - - IPGDYTDYVATRWYRAPELLVGD 176
 Dd 120 HCRVLRHDKPENILITKQIIKICDFGFAQIL - - - - - IPGDYTDYVATRWYRAPELLVGD 179
 Qy 177 QYGVSSVDIWAICGVFAELLTGQPLWPGKSDVDQLYLIIRTL - - - - - 217
 Dd 180 RYSTPVDVWSIGITFAELATKKPLPHGDSIDQLFRITLGTPTNNEVWDVESLPDYN 239
 Qy 218 - - - - - VETGFRHVDQAGLELLTSS - - - - - DPPAVASQASGIT 249
 Dd 240 TFPKWSGNLASTVKNLKNGIDLLTKMLIYDPPKRIARQAMT 283

RESULT 5

S40021
protein kinase (EC 2.7.1.37) cdc2 homolog - slime mold (Dictyostelium discoideum)
C/Species: Dictyostelium discoideum
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S40021; S39071
R/Michaelis, C.E.; Weeks, G.
submitted to the EMBL Data Library, August 1992
A/Description: The unicellular organism Dictyostelium discoideum possesses a highly related protein kinase.
A/Reference number: S40021
A/Accession: S40021
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-292 <MIC>
A/Cross-references: UNIPROT:P34117; EMBL:L00652; NID:g167695; PIDN:AAA16056.1; PID:g167695
R/Michaelis, C.; Weeks, G.
Biochim. Biophys. Acta 1179, 117-124, 1993
A/Title: The isolation from a unicellular organism, Dictyostelium discoideum, of a highly related protein kinase.
A/Reference number: S39071; MUID:94032415; PMID:8218353
A/Accession: S39071
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-18, 'Y', 20-188, 'G', 190-292 <MI2>
A/Cross-references: EMBL:L00652
C/Complex: In various organisms, cdc2 has been identified as a component of the M-phase
C/Superfamily: kinase-related transforming protein; protein kinase homology
C/Keywords: ATP; cell cycle control; phosphoprotein; phosphotransferase; serine/threonine
F/2-254/Domain: protein kinase homology <KIN>
F/10-18/Region: protein kinase ATP-binding motif
F/33,51,126,128/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 30.7%; Score 558.5; DB 2; Length 292;
Best Local Similarity 35.0%; Pred. No. 1e-18;
Matches 115; Conservative 66; Mismatches 101; Indels 47; Gaps 6;
Qy 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
Db 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
Qy 61 PNLVNLLEVFRRKKRMLHVFYCDHTLLNELE-RNPNGVADGVKSVLWQTLQALNFCIH 120
Db 61 PNLVNLLEVFRRKKRMLHVFYCDHTLLNELE-RNPNGVADGVKSVLWQTLQALNFCIH 120
Qy 121 NCIRHDKPENILITKQIIKICDFGPAQL-IPGDAYTDVATRWYRAPELLVGDTOY 179
Db 121 RVLHRLKPKQNLINRKGELKADFGARAFIPWRTYSHEVVTWYRAPELLVGDTOY 180
Qy 180 SSVDIWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 TPDIWSALCIFAEMWGRPLFGSGTSDQLFRIFKILGTP-----NEESWP 227
Qy 240 AVASQSGAGITKGLIPRHOSIF-----KSNQFFHGISTPEPEDEMETLEEKFSVDHVPALN 293
Db 228 SITE-----LPFYKTFDFVHPAQLSSIVHG-----LDEK-----GLN 260
Qy 294 FMKGLKXNPPDLTCSQLLESSYFDSFQ 322
Db 261 LLSKMLQYDPNQRITAAALAKHPYFDGLE 289

RESULT 6

A37871
protein kinase (EC 2.7.1.37) cdk2 - African clawed frog
N/Alternate names: cell division control protein CDC2 homolog Egl
C/Species: Xenopus laevis (African clawed frog)
C/Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 09-Jul-2004
C/Accession: A37871; S15866; I51662; S14410
R/Paris, J.; Le Guellec, R.; Couturier, A.; Le Guellec, K.; Omilli, F.; Camonis, J.; Mac
Proc. Natl. Acad. Sci. U.S.A. 88, 1039-1043, 1991
A/Title: Cloning by differential screening of a Xenopus cDNA coding for a protein highly
A/Reference number: A37871; MUID:91126051; PMID:1704128

A/Accession: A37871
A/Molecule type: mRNA
A/Residues: 1-297 <PAR>
A/Cross-references: UNIPROT:P23437; UNIPROT:Q9PSU0; GB:X14227
R/le Guellec, R.
submitted to the EMBL Data Library, January 1989
A/Reference number: S15866
A/Accession: S15866
A/Molecule type: mRNA
A/Residues: 1-92, 'R', '94-297 <LEA>
A/Cross-references: EMBL:X14227; NID:g64665; PIDN:CAA32443.1; PID:g64666
R/Olive, M.; Theze, N.; Philippe, M.; Le Pennec, J.P.; Lerivray, H.
Gene 151, 81-88, 1994
A/Title: Cloning of the Xenopus laevis cdk2 promoter and functional analysis in oocytes

A/Reference number: S151662
A/Accession: S151662
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-39 <OLI>
A/Cross-references: EMBL:U07979; NID:g473584; PIDN:AAA82123.1; PID:g473585
C/Genetics:
A/Gene: cdk2

C/Superfamily: kinase-related transforming protein; protein kinase homology
C/Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific
F/2-255/Domain: protein kinase homology <KIN>
F/10-18/Region: protein kinase ATP-binding motif
F/33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
Query Match 30.5%; Score 555; DB 2; Length 297;
Best Local Similarity 37.8%; Pred. No. 1.5e-18;
Matches 115; Conservative 59; Mismatches 90; Indels 40; Gaps 6;

Qy 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
Db 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKVFSEDDPVVKKIALREIRMLKQLKH 60
Qy 61 PNLVNLLEVFRRKKRMLHVFYCDHTLLNELE-RNPNGVADGVKSVLWQTLQALNFCIH 119
Db 61 PNLVNLLEVFRRKKRMLHVFYCDHTLLNELE-RNPNGVADGVKSVLWQTLQALNFCIH 120
Qy 120 HNCIRHDKPENILITKQIIKICDFGPAQL-IPGDAYTDVATRWYRAPELLVGDTOY 178
Db 121 HRVLRDLKPKQNLINRKGELKADFGARAFIPWRTYSHEVVTWYRAPELLVGDTOY 180
Qy 179 GSSVDIWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTL----- 217
Db 181 STAVDIWSALCIFAEMITRRALPGDSEIDQLFRITLGTDPDSVSGVVTMPDYKSTF 240
Qy 218 ---VETGFRHV-----DOAGLELLTSSDPPAVASQSGAGITKGLIPRHOSIFKSNQFFHGIS 270
Db 241 PKWIRQDFSKVVPPLDEGRDLAQM---LOYDSNKRISAKVALTHP-----FFRDVS 290
Qy 271 IPEP 274
Db 291 RPTP 294

RESULT 7

A41227
protein kinase (EC 2.7.1.37) cdk2 - human
N/Alternate names: Egl homolog; protein kinase p34
C/Species: Homo sapiens (man)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C/Accession: A41227; S17873; S16520
R/Ninomiya-Tsuji, J.; Nomoto, S.; Yasuda, H.; Reed, S.I.; Matsumoto, K.
Proc. Natl. Acad. Sci. U.S.A. 88, 9006-9010, 1991
A/Title: Cloning of a human cDNA encoding a CDC2-related kinase by complementation of a
A/Reference number: A41227; MUID:92020980; PMID:1717994
A/Accession: A41227
A/Molecule type: mRNA

A/Residues: 1-298 <NIN>
A/Cross-references: UNIPROT:P24941; GB:M68520; NID:g180177; PIDN:AAA35667.1; PID:g180178
R/Tsai, L.H.; Harlow, E.; Meyerson, M.

Nature 353, 174-177, 1991
A;Title: Isolation of the human cdk2 gene that encodes the cyclin A- and adenovirus E1A-
A;Reference number: S17873; MUID:91367262; PMID:1653904
A;Accession: S17873
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-298 <TGA>
A;Cross-references: GB:X62071; NID:g312802; PIDN:CAA43985.1; PID:g312803
R;Elledge, S.J.; Spottswood, M.R.
EMBO J. 10, 2653-2659, 1991
A;Title: A new human p34 protein kinase, CDK2, identified by complementation of a cdc28
A;Reference number: S16520; MUID:91330891; PMID:1714386
A;Accession: S16520
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-176, 'S', 178-298 <ELL>
A;Cross-references: EMBL:X61622; NID:g29848; PIDN:CAA43807.1; PID:g29849
C;Genetics:
A;Gene: GDB:CDK2
A;Cross-references: GDB:128984; OMIM:116953
A;Map position: 12q13-12q13
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; cell cycle control; mitosis; phosphoprotein; phosphotransferase; serine
F;2-255/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;14,160/Binding site: phosphate (Thr) (covalent) #status predicted
F;15/Binding site: phosphate (Tyr) (covalent) #status predicted
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
Query Match 30.4%; Score 554; DB 2; Length 298;
Best Local Similarity 38.4%; Pred. No. 1.7e-18;
Matches 118; Conservative 54; Mismatches 89; Indels 46; Gaps 6;
QY 1 MEKYELAKTGEISGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
DB 1 MENFQKEKIGEGTYGVVYKARNKLTGEVVALKIRLDTETEGVPSTAIRISILLKELNH 60
QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLN-----ELERNPVGADVGVKSVLWOTLQALNFC 119
DB 61 PNLVNLIEVFRKRKMHVFEYCDHTLLN-----ELERNPVGADVGVKSVLWOTLQALNFC 120
QY 120 HNCIHRDIPKPNILITKQGIKICDFGAQIL-IPGDAYTDYVATRWYRAPELLVGD 178
DB 121 HRVLRDLKPNLLINTEGAIKLADFLARAFGVVVRTYTHEVVTWYRAPELLGCKY 180
QY 179 GSSVDIWAICGVFAELLTGQPLWPKSDVDQLYLIIRTL----- 217
DB 181 STAVDIWSLGCIFAEWVTRRALFPDSEIDQLFRIFRTLGPDEVWVPGVTSMPDYKPSF 240
QY 218 ---VETGFRHV---DQAGLELLTSS---DPPAVASQASGITGKLI PRHQSIFKNSGFFH 267
DB 241 PKWARQDFSVKVPVLDDEGRSLLSQMLHYDNPKNRISAKAAL-----AHFFQ 287
QY 268 GISIPEP 274
DB 288 DVTKPVP 294
RESULT 8
B40444
protein kinase (EC 2.7.1.37) cdc2 homolog B - maize (fragment)
C;Species: Zea mays (maize)
C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 28-Feb-1997
R;Colasanti, J.; Tyers, M.; Sundaresan, V.
Proc. Natl. Acad. Sci. U.S.A. 88, 3377-3381, 1991
A;Title: Isolation and characterization of cDNA clones encoding a functional p34 (cdc2) h
A;Reference number: A40444; MUID:91195354; PMID:2014258
A;Accession: B40444
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-294 <GB>
A;Cross-references: GB:M60526

C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase
F;2-256/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
Query Match 30.4%; Score 552.5; DB 2; Length 294;
Best Local Similarity 35.4%; Pred. No. 1.9e-18;
Matches 119; Conservative 66; Mismatches 98; Indels 53; Gaps 9;
QY 1 MEKYELAKTGEISGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
DB 1 MEQYKEKIGEGTYGVVYKALDKTANETIALKKIRLEQDEGVSPSTAIRISILLKEMNH 60
QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLN-----ELERNPVGADVGVKSVLWOTLQAL 114
DB 61 GNIVLRHDVHSEKIRYLVEFYLDLKKFMDSCPEFAKNPT-----LIKSYLYQILRGV 115
QY 115 NFIHNCIHRDIPKPNILITKQ-GIIKICDFGAQIL-IPGDAYTDYVATRWYRAPELL 172
DB 116 AYCHSHRVLRDLKPNLLIDRNNALKLADFLARAFGIPVFTTHEVVTWYRAPELL 175
QY 173 VGDYQYSSVDIWAICGVFAELLTGQPLWPKSDVDQLYLIIRTL---VETGFRHVDQAG 229
DB 176 LGARQYSTPVDVMSVGCIFAEWVQKPLFPDSEIDELFKIFRVLGTPNEQGW----- 228
QY 230 LELLTSSDPPAVASQASGITGKLI PRHQSIFKNSGFFHISIPEDMETLEEKFSVDHP 289
DB 229 -----PGVSCLPDFKTA--FPRWQA-----QDLATI---VPLNEP 258
QY 290 VALNFMKGCILKMPDRLTCSQLLESYFDSFOBAQ 325
DB 259 AGDLLSKMLRYEFSKEITARQALEHVEYFKDLEWVQ 294
RESULT 9
S22440
protein kinase (EC 2.7.1.37) cdc2 homolog 1 - rice
C;Species: Oryza sativa (rice)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S22440
R;Hashimoto, J.; Hirabayashi, T.; Hayano, Y.; Hata, S.; Ohashi, Y.; Suzuki, I.; Utsugi, J.
Mol. Gen. Genet. 233, 10-16, 1992
A;Title: Isolation and characterization of cDNA clones encoding cdc2 homologues from Oryz
A;Reference number: S22440; MUID:92293101; PMID:1376401
A;Accession: S22440
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-294 <HAS>
A;Cross-references: UNIPROT:P29618; EMBL:X60374; NID:g20342; PIDN:CAA42922.1; PID:g20343
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein ki
F;2-256/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted
Query Match 30.3%; Score 551.5; DB 2; Length 294;
Best Local Similarity 34.8%; Pred. No. 2.2e-18;
Matches 116; Conservative 68; Mismatches 102; Indels 47; Gaps 8;
QY 1 MEKYELAKTGEISGVVFKCRNKTSGQVAVKVFESDDPVVKKIALREIRMLKQLKH 60
DB 1 MEQYKEKIGEGTYGVVYKARDKVTNETIALKKIRLEQDEGVSPSTAIRISILLKEMNH 60
QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLN-----ELERNPVGADVGVKSVLWOTLQAL 114
DB 61 GNIVLRHDVHSEKIRYLVEFYLDLKKFMDSCPEFAKNPT-----LIKSYLYQILRGV 115
QY 115 NFIHNCIHRDIPKPNILITKQ-GIIKICDFGAQIL-IPGDAYTDYVATRWYRAPELL 172
DB 116 AYCHSHRVLRDLKPNLLIDRNNALKLADFLARAFGIPVFTTHEVVTWYRAPELL 175
QY 173 VGDYQYSSVDIWAICGVFAELLTGQPLWPKSDVDQLYLIIRTLVETGFRHVDQAGLE 232

Db 176 LGSSQYSTPVDWMSVGCIFAEWVQKPLFPDSEIDELFKIFRVLGTP----- 223
 Qy 233 LTSSDPPAVASQASGITGKLIPIRHSQIFKSGNFFHGISIPEDMETLEEKFSVDHPVAL 292
 Db 224 -NEQSWFCVSS-----LPDYKSAPFK-----WQAQDLATI---VPTLDPAGL 261
 Qy 293 NFMKGCLKMPDDRLTCSQLLESSYFDSFQEAQ 325
 Db 262 DLLSKMLRYEPNKRITARQALEHEFYFKDLEMVQ 294

RESULT 10
 S23095
 protein kinase (EC 2.7.1.37) cdc2 - Arabidopsis thaliana
 N;Alternate names: cdc2 protein homolog; CDC2a protein; cell division control protein 2
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 22-Nov-1993 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S23095; A48984; JQ1337; JQ0967; S18202
 R;Imajuku, Y.; Hirayama, T.; Endoh, H.; Oka, A.
 FEBS Lett. 304, 73-77, 1992
 A;Title: Exon-intron organization of the Arabidopsis thaliana protein kinase genes CDC2a
 A;Reference number: S23095; MUID:92316202; PMID:1618302
 A;Accession: S23095
 A;Molecule type: DNA
 A;Residues: 1-294 <IMA>
 A;Cross-references: UNIPROT:P24100; EMBL:D10850; NID:g217848; PIDN:BAA01623.1; PID:g21784
 R;Inze, D.; Ferreira, P.; Hemerly, A.; Van Montagu, M.
 Biochem. Soc. Trans. 20, 80-84, 1992
 A;Title: Control of cell division in plants.
 A;Reference number: A48984; MUID:92339744; PMID:1634002
 A;Accession: A48984
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Residues: 1-294 <INZ>
 A;Experimental source: flower
 A;Note: sequence extracted from NCBI backbone (NCBIP:109461)
 R;Hirayama, T.; Imajuku, Y.; Anai, T.; Matsui, M.; Oka, A.
 Gene 105, 159-165, 1991
 A;Title: Identification of two cell-cycle-controlling cdc2 gene homologs in Arabidopsis
 A;Reference number: JQ1337; MUID:92039027; PMID:1937013
 A;Accession: JQ1337
 A;Molecule type: mRNA
 A;Residues: 1-294 <HIF>
 A;Cross-references: EMBL:X57839; NID:g16218; PIDN:CAA040971.1; PID:g16219
 R;Ferreira, P.C.G.; Hemerly, A.S.; Villarroel, R.; Van Montagu, M.; Inze, D.
 Plant Cell 3, 531-540, 1991
 A;Title: The Arabidopsis functional homolog of the p34cdc2 protein kinase.
 A;Reference number: JQ0967; MUID:93005715; PMID:1840925
 A;Accession: JQ0967
 A;Molecule type: mRNA
 A;Residues: 1-294 <PER>
 A;Cross-references: GB:S45387; NID:g257373; PIDN:AAB23643.1; PID:g257374
 A;Experimental source: flower
 C;Comment: The protein is a key component of the eukaryotic cell cycle.
 C;Genetics:
 A;Gene: cdc2
 A;Introns: 3/3; 65/2; 105/3; 163/3; 218/2; 247/3; 265/3
 C;Function:
 A;Description: phosphotransferase; protein kinase; required for G1 to S-phase transition
 C;Superfamily: kinase-related transforming protein; protein kinase homology
 C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
 F;2-256/Domain: protein kinase homology <KIN>
 F;10-18/Region: protein kinase ATP-binding motif
 F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 30.3%; Score 551.5; DB 2; Length 294;
 Best Local Similarity 35.5%; Pred. No. 2.2e-18;
 Matches 115; Conservative 71; Mismatches 95; Indels 43; Gaps 8;

Qy 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKFESEDDPVVVKTLALREIRMLKQLKH 60
 Db 1 MDQYKVEKIGEGTYGVVYKARDKVTNETIALKIRLEQDEGVFPSTAIRISLLKEMQH 60

Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNVAD-GVIKSVLWQTLQALNECHI 119
 Db 61 SNIVKLDQVHSEKRLYLVEYLDLKGMDSTPDFSKLHMIKTYLQILRGIAYSCHS 120
 Qy 120 HNCIHRDKPENILITKO-GIIKIDFGFAQIL-IPGDAYTDVYVATWYRAPELLVGDQT 177
 Db 121 HRVLRDLKFNQLIDRRTNLSKLADGLARAGIPVRTTHEVVTLYWYRAPELLGSHH 180
 Qy 178 YGSSVDIWAIGCVFAELLTQPLWPKGSDVDQLYLIIR---TLVETGFRHVDQAGLELLT 234
 Db 181 YSTPVDIWSVGCIFAEMISQKPLFGDSEIDQLFKIFRIMGTPYEDTWR----- 229
 Qy 235 SSDPPAVASQASGITGKLIPIRHSQIFKSGNFFHGISIPEDMETLEEKFSVDHPVALNF 294
 Db 230 -----GVTS--LFDYKSAPFK-----WKPTDLETF--VPLNDPDGVDL 263
 Qy 295 MKGCLKMPDDRLTCSQLLESSYF 318
 Db 264 LSKMLMDPTKRINARAALAEHYF 287

RESULT 11
 A40444
 protein kinase (EC 2.7.1.37) cdc2 homolog A - maize
 C;Species: Zea mays (maize)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C;Accession: A40444
 R;Colasanti, J.; Tyers, M.; Sundaresan, V.
 Proc. Natl. Acad. Sci. U.S.A. 88, 3377-3381, 1991
 A;Title: Isolation and characterization of cDNA clones encoding a functional p34 (cdc2) h
 A;Reference number: A40444; MUID:91195354; PMID:2014258
 A;Accession: A40444
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-294 <COL>
 A;Cross-references: GB:M60526
 C;Superfamily: kinase-related transforming protein; protein kinase homology
 C;Keywords: ATP; phosphotransferase
 F;2-256/Domain: protein kinase homology <KIN>
 F;10-18/Region: protein kinase ATP-binding motif
 F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 30.0%; Score 546.5; DB 1; Length 294;
 Best Local Similarity 34.1%; Pred. No. 3.6e-18;
 Matches 117; Conservative 66; Mismatches 93; Indels 67; Gaps 9;

Qy 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKFESEDDPVVVKTLALREIRMLKQLKH 60
 Db 1 MEQYKVEKIGEGTYGVVYKALDKTANETIALKIRLEQDEGVFPSTAIRISLLKEMNH 60
 Qy 61 PNLVNLIEVFRKRKMHVFEYCDHTLLN-----ELERNPNVADGVKISVLWQTLQAL 114
 Db 61 GNIVLRHDVHSEKRIYLVFEYLDLKKFWDSCPEFAKNFT-----LIKSYLQILHGV 115
 Qy 115 NFCHIHNCIHRDKPENILITKO-GIIKIDFGFAQIL-IPGDAYTDVYVATWYRAPELL 172
 Db 116 AYCHSHRVLHDLKPNQLIDRRTNALKADFGLARAFGIPVRTTHEVVTLYWYRAPEIL 175
 Qy 173 VGDYQYSSVDIWAIGCVFAELLTQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLEL 232
 Db 176 LGARQYSTPVDVMSVGCIFAEMVNVQKPLFPDSEIDSLFKIFRLG----- 221
 Qy 233 LTSSDPPAVASQASGITGKLIPIRHSQIFKSGNFFHGIS-IP-----EPEDMETLEE 282
 Db 222 -----TPNEQS-----WPGVSCLPDFKTAFRWQAQDLATV-- 252

Query Match 30.3%; Score 551.5; DB 2; Length 294;
 Best Local Similarity 35.5%; Pred. No. 2.2e-18;
 Matches 115; Conservative 71; Mismatches 95; Indels 43; Gaps 8;

Qy 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKFESEDDPVVVKTLALREIRMLKQLKH 60
 Db 1 MDQYKVEKIGEGTYGVVYKARDKVTNETIALKIRLEQDEGVFPSTAIRISLLKEMQH 60

RESULT 12

T49271
CELL DIVISION CONTROL PROTEIN 2 HOMOLOG A - Arabidopsis thaliana
N;Alternate names: protein T21J18.20
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jun-2000
C;Accession: T49271
R;Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Rudd, S.
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25021
A;Accession: T49271
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-294 <R1E>
A;Cross-references: EMBL:AL132963; GSPDB:GN00061; ATSP:T21J18.20
A;Experimental source: cultivar Columbia; BAC clone T21J18
C;Genetics:
A;Gene: ATSP:T21J18.20
A;Map position: 3
A;Introns: 3/3; 67/3; 105/3; 163/3; 218/2; 247/3; 265/3
C;Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 30.0%; Score 546.5; DB 2; Length 294;
Best Local Similarity 35.2%; Pred. No. 3.6e-18;
Matches 114; Conservative 71; Mismatches 96; Indels 43; Gaps 8;

QY 1 MEKYELAKTSGSYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKOLKH 60
DB 1 MDQYKVEKIGSGYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKOLKH 60

QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNQVAD-GVKSVLVMTQALNFC 119
DB 61 SNIVYDDVHSEKRLVFEYCDHTLLNELRNPNQVAD-GVKSVLVMTQALNFC 120

QY 120 HNCIHRDIKPNILITKQ-GIIKICDFGFAQIL-IPGDAYTDVATRYRAPELLVGD 177
DB 121 HRVLRDLKPNQLIDRTNSLKLADFGARAFGIPRTFHEVTVLWYRAPELLVGS 180

QY 178 YGSSVDIWAIGCVFABLLTGQPLWPKSDVDOLYLIIR---TLVETGFRHVDQAGLE 234
DB 181 YSTPVDIWSGICFAEMISQKPLFGDSEIDQLFRIFALGTPNNEVPEVESLQ 239

QY 235 SSDPPAVASQASAGITGKLIIRHQSIFKSNFGFFHGISPEPEDEMETLEKSDVHP 294
DB 230 -----GVTS--LPDYKAFPK-----WKPTDLETF---VNLDPDQGV 263

QY 295 MKGCLKNPDRRLTCSOLLESSYF 318
DB 264 LSKMLMDPTKRINARAALHEYF 287

RESULT 13
A29539
protein kinase (EC 2.7.1.37) cdc2 - human
N;Alternate names: cell division control protein 2 (CDC2)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1998 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
C;Accession: A29539
R;Lee, M.G.; Nurse, P.
Nature 327, 31-35, 1987
A;Title: Complementation used to clone a human homologue of the fission yeast cell cycle
A;Reference number: A29539; MUID:87201915; PMID:3553962
A;Accession: A29539
A;Molecule type: mRNA
A;Residues: 1-297 <LEE>
A;Cross-references: UNIPROT:P06493; GB:X05360; NID:g29838; PIDN:CAA2983.1; PID:g29839
C;Genetics:
A;Gene: GDB:CDC2
A;Cross-references: GDB:119052; OMIM:116940
A;Map position: 10q21.1-10q21.1
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; cell cycle control; mitosis; phosphoprotein; phosphotransferase; serine
F;2-256/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif

F;14,161/Binding site: phosphate (Thr) (covalent) #status predicted
F;15/Binding site: phosphate (Tyr) (covalent) #status predicted
F;33,51,128,130/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 29.9%; Score 545; DB 2; Length 297;
Best Local Similarity 40.2%; Pred. No. 4.2e-18;
Matches 117; Conservative 58; Mismatches 74; Indels 42; Gaps 7;

QY 1 MEKYELAKTSGSYGVVFKCRNKTSGQVAVKFF-VESEDDPVVKKIALREIRMLKOLKH 59
DB 1 MEDVTKEIGSGYGVVFKCRNKTSGQVAVKFF-VESEDDPVVKKIALREIRMLKOLKH 59

QY 60 HPNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNQVAD-GVKSVLVMTQALNFC 117
DB 60 HPNIVSLQDVLMDQSRLLYFEFLSMDLKKYLDIPFGQYMDSSLVKSXYLIQGLVFC 119

QY 118 HNCIHRDIKPNILITKQGIKICDFGFAQIL-IPGDAYTDVATRYRAPELLVGD 176
DB 120 HSRVLRDLKPNQLIDDKGTIKLADFGARAFGIPRTFHEVTVLWYRAPELLVGS 179

QY 177 QYSSVDIWAIGCVFABLLTGQPLWPKSDVDOLYLIIRTL----- 217
DB 180 RYSTPVDIWSGITFABELATKPLFGDSEIDQLFRIFALGTPNNEVPEVESLQ 239

QY 218 -----VETGFRHVDQAGLELITSS---DPPAVASQASAGITGKLIIRH 256
DB 240 TFPKWKPGSLASHVKNLDENGLOLLSKOLLYDP-----AKRISGRMALNH 284

RESULT 14
A44878
protein kinase (EC 2.7.1.37) cdk2 [validated] - goldfish
C;Species: Carassius auratus (goldfish)
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: A44878
R;Hirai, T.; Yamashita, M.; Yoshikuni, M.; Tokumoto, T.; Kajiuza, H.; Sakai, N.; Nagahama
Dev. Biol. 152, 113-120, 1992
A;Title: Isolation and characterization of goldfish cdk2, a cognate variant of the cell
A;Reference number: A44878; MUID:92331802; PMID:1339336
A;Accession: A44878
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-298 <HIR>
A;Cross-references: UNIPROT:P43450; GB:S40289; NID:g251619; PIDN:AAB22550.1; PID:g251620
A;Experimental source: oocyte
A;Note: sequence extracted from NCBI backbone (NCBIN:108782, NCBI:P:108783)
C;Genetics:
A;Gene: cdk2
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; cell cycle control; mitosis; phosphoprotein; phosphotransferase; serine
F;2-255/Domain: protein kinase homology <KIN>
F;10-18/Region: protein kinase ATP-binding motif
F;33,51,127,129/Active site: Lys, Glu, Asp, Lys #status predicted

Query Match 29.9%; Score 545; DB 1; Length 298;
Best Local Similarity 46.6%; Pred. No. 4.2e-18;
Matches 102; Conservative 48; Mismatches 67; Indels 2; Gaps 2;

QY 1 MEKYELAKTSGSYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKOLKH 60
DB 1 MESFQKVEKIGSGYGVVFKCRNKTSGQVAVKFESEDDPVVKKIALREIRMLKOLKH 60

QY 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNQVAD-GVKSVLVMTQALNFC 119
DB 61 PNLVNLIEVFRKRKMHVFEYCDHTLLNELRNPNQVAD-GVKSVLVMTQALNFC 120

QY 120 HNCIHRDIKPNILITKQGIKICDFGFAQIL-IPGDAYTDVATRYRAPELLVGD 178
DB 121 HRVLRDLKPNQLIDDKGTIKLADFGARAFGIPRTFHEVTVLWYRAPELLVGS 180

QY 179 YGSSVDIWAIGCVFABLLTGQPLWPKSDVDOLYLIIRTL 217
DB 181 STAVDIWSLGCIFAEWITKALFPGDSEIDQLFRIFRIL 219

```

RESULT 15
145977
cyclin-dependent kinase 1 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
C:Accession: I45977
R:Yang, L.; Farin, C.E.
Gene 141, 283-286, 1994
A:Title: Identification of cDNAs encoding bovine cyclin B and Cdk1/cdc2.
A:Reference number: I45977; MUID:94215918; PMID:8163203
A:Accession: I45977
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-297 <YAN>
A:Cross-references: UNIPROT:P48734; GB:L26547; NID:g433155; PIDN:AAA18894.1; PID:g498173
C:Genetics:
C:Superfamily: kinase-related transforming protein; protein kinase homology
F:2-256/Domain: protein kinase homology <KIN>

Query Match      29.8%; Score 542; DB 2; Length 297;
Best Local Similarity 40.2%; Pred. No. 5.7e-18;
Matches 117; Conservative 57; Mismatches 75; Indels 42; Gaps 7;

Qy 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGOVAVKKF-VESEDDPVVKIALREIRMLKOLK 59
Db 1 MEDVTKEIKGEGTYGVVYKGRHKTGGVAMKKIRLESEEG-VPSTAIRISLLKELR 59

Qy 60 HPNLVNLIEVFRKRRKXHLVFEYCDHTLLNELERNPNG--VADGVIKSVLMQTLQALNFC 117
Db 60 HPNTVSLQDVLMDQSRLLYIFEFSLMDLKKYLSIPPGQFMDSSLVXSYLYQILQGIYVC 119

Qy 118 HHNCIHRDIKPNILITKGIKICDFGAQIL-IPGDAYTDVATRWYRAPPELLVGD 176
Db 120 HSRVLRDLKPQNLIDDKGTIKLADFGLARAFGIPRVYTHEVTVLWYRSPEVLGSA 179

Qy 177 QYSSVDIWAIGCVFAELLTGQPLWPGKSVDQLYLIIRTL----- 217
Db 180 GYSTPVDIWSIGTIFAEALATKKPLFHGDSIEDQLFRIPRALGTPNNEVWPEVESLQDYKS 239

Qy 218 -----VETGRHVDOAGLEILLTSS---DPPAVASQSAGITCKLIPRH 256
Db 240 TFPKWKPGSLASHVKNLDENGLDLLSKMLIYDP-----AKRISGKALNH 284

```

Search completed: April 22, 2005, 06:51:39
Job time : 29.3051 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 22, 2005, 01:29:40 ; Search time 91.2054 Seconds
(without alignments)
1948.255 Million cell updates/sec

Title: US-10-766-691-10
Perfect score: 1820
Sequence: 1 MEKYEKLAKTGESYGVFK.....RKARNEGRRRRQOVLPLKS 347

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1183.5	65.0	350	Q6AXJ9	Q6axj9 brachydanio
2	1180	64.8	352	Q8CEQ0	Q8ceq0 mus musculus
3	1162.5	63.9	358	Q6QUA0	Q6qua0 homo sapien
4	1158	63.6	352	Q6QHE7	Q6qhe7 rattus norv
5	1157.5	63.6	358	1 KIAA_HUMAN	Q00532 homo sapien
6	1089.5	55.5	367	Q7QBG7	Q7qbg7 anopheles g
7	1001.5	55.0	353	Q9UZH1	Q9uzh1 caenorhabdi
8	1001.5	55.0	392	Q9VMN3	Q9vmn3 drosophila
9	941.5	51.7	566	Q9TTK0	Q9ttk0 oryctolagus
10	932	51.2	385	Q675R9	Q675r9 oikopleura
11	915.5	50.3	493	Q92772	Q92772 homo sapien
12	904.5	49.7	564	Q9QYI2	Q9qyi2 mus musculus
13	904.5	49.7	568	Q9QUK0	Q9quk0 mus musculus
14	902	49.6	329	Q9QYI1	Q9qyi1 mus musculus
15	899	49.4	320	Q6GMD6	Q6gmd6 xenopus lae
16	893.5	49.1	651	Q6TXH3	Q6txh3 rattus norv
17	758.5	41.7	455	Q9PLI4	Q9pli4 homo sapien
18	758.5	41.7	592	Q9IIV4	Q9iiv4 homo sapien
19	755	41.5	657	Q9BMG2	Q9bmg2 trypanosoma
20	744	40.9	353	Q8K134	Q8k134 mus musculus
21	743.5	40.9	1106	Q9GRT9	Q9grt9 leishmania
22	741.5	40.7	457	Q9BKR2	Q9bkr2 mus musculus
23	738.5	40.6	585	Q9BLA9	Q9bla9 mus musculus
24	737.5	40.5	457	Q9JM02	Q9jmo2 rattus norv
25	737.5	40.5	505	Q9JM01	Q9jmo1 rattus norv
26	733.5	40.3	595	Q8BLF2	Q8blf2 mus musculus
27	694.5	38.2	783	Q9BWT8	Q9bwt8 mus musculus
28	694.5	38.2	831	Q8IYC7	Q8iyc7 homo sapien
29	694.5	38.2	1030	1 STK9_HUMAN	Q76039 homo sapien
30	682	37.5	993	2 Q8WXQ5	Q8wxq5 homo sapien
31	676.5	37.2	578	2 Q8BVE0	Q8bve0 mus musculus

32	618	34.0	1104	2	Q9W6R6	Q9w6r6 fugu rubrip
33	565.5	31.1	294	1	Q9ZRI1	Q9zri1 triticum ae
34	565	31.0	305	1	CDK3_HUMAN	Q00526 homo sapien
35	564	31.0	297	2	Q66IH7	Q66ih7 xenopus tro
36	563	30.9	302	1	CDK2_CARAU	P51958 carassius a
37	561	30.8	297	1	CDK2_XENLA	P23437 xenopus lae
38	558.5	30.7	292	1	CC2H_DICDI	P34117 dictyosteli
39	558.5	30.7	340	2	Q7QKF5	Q7qkf5 anopheles g
40	556.5	30.6	289	2	Q7RM49	Q7rm49 plasmodium
41	555	30.5	297	2	Q6IRQ7	Q6irq7 xenopus lae
42	555	30.5	302	2	Q7T3L7	Q7t3l7 brachydanio
43	554	30.4	298	1	CDK2_HUMAN	P24941 homo sapien
44	551.5	30.3	294	1	CC21_ORYSA	P29618 oryza sativ
45	551.5	30.3	294	1	CC2A_ARATH	P24100 arabidopsis

ALIGNMENTS

RESULT 1

Q6AXJ9 PRELIMINARY; PRT; 350 AA.
AC Q6AXJ9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Zgc:101002 protein.
GN Name=zgc:101002;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
[1]
SEQUENCE FROM N.A.
RP SFRIN=Singapore local strain; TISSUE=Embryo;
RC PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
RP SFRIN=Singapore local strain; TISSUE=Embryo;
RC Director MGC Project;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
EMBL; BC079506; AAH79506.1; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR01003; Kinase-like.
DR InterPro; IPR00719; Prot kinase.
DR InterPro; IPR002290; Ser thr kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
PFam; PF00069; Pkinase; I.

DR ProDom; PD000001; Prot Kinase; 1.
 DR SMART; SM00220; S_TK; 1.
 DR SMART; SM00219; TyK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 350 AA; 40810 MW; 9B04440EE0E38BE1 CRC64;
 Query Match 65.0%; Score 1183.5; DB 2; Length 350;
 Best Local Similarity 63.4%; Pred. No. 1.9e-72;
 Matches 220; Conservative 47; Mismatches 45; Indels 35; Gaps 3;
 QY 1 MEKYEKLAKTSGSYGVVFKCNKTSQGVAVKVFESDDPVPVKIALREIRMLKQLKH 60
 DB 1 MEKYEKISKIGESYGVVFKCNKNDTQGVAVKVFESDDPVPVKIALREIRMLKQLKH 60
 QY 61 PNLVNLIEVFRKRRKXHLVFEYCDHTLNLNLRPNVGVADGVKISVLWQTLQALNFKCH 120
 DB 61 PNLVNLMEVFRKRRKXHLVFEYCDHTLVNLDYPRGVPEHMKVSIWQTLQAVNFKCH 120
 QY 121 NCIHRIKIPENILITKQGIKIICDFGFAQILI-PGDATDYVATRWYRAPPELLVGDQY 179
 DB 121 NCIHRIKIPENILITKQGIKIICDFGFAQILITGPDYVATRWYRAPPELLVGDQY 180
 QY 180 SSVDIWAIGCVFAELITGQPLWPGKSDVDQLYLIRTLVETGPRHVDQAGLELITSSDPP 239
 DB 181 PPVDVWAGCVFAELISGAPLWPGKSDVDQLYLIRKTL----- 218
 QY 240 AVASQAGITKGLPRHOSIFKNGFPHGISIPEDMETLEKFSVHPVVALNFMKGL 299
 DB 219 -----GELIPRHQOVFSTNQFFSGVCPBPQEMPLELKYPNLSYQALSLMKGL 268
 QY 300 KNPDPDLRTCSQLLESYFDSFQF--AQIKKARNEGRNRQOVLP 344
 DB 269 RMDPAERLSCEQLLEQYFDSLREESVTRKELDRKRRKQPRKHL 315
 RESULT 2
 ID Q8CEQ0 PRELIMINARY; PRT; 352 AA.
 AC Q8CEQ0;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
 DE library, clone:4933411017 product:cyclin-dependent kinase-like 1
 DE (CDC2-related kinase), full insert sequence.
 GN Name=Cdk1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.,
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of

60,770 full-length cDNAs";
 Nature 420:563-573(2002).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes";
 Genome Res. 10:1617-1630(2000).
 [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer";
 Genome Res. 10:1757-1771(2000).
 [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hanaoka T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
 RA Inotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
 RA Kawai J., Kojima Y., Kono H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
 RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
 RA Sugabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Teijima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK016781; BAC25497.1; -;
 DR HSSP; Q00535; 1H4L.
 DR MGD; MGI:1918341; Cdk1.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0004688; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR00719; Prot kinase.
 DR InterPro; IPR002290; Ser thr kinase.
 DR InterPro; IPR008271; Ser thr_pkin_AS.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot kinase; 1.
 DR SMART; SM00220; S_TK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
 KW ATP-binding; Cyclin; Kinase; Transferase.
 SQ SEQUENCE 352 AA; 41023 MW; 6E9F56C8080F35E0 CRC64;
 Query Match 64.8%; Score 1180; DB 2; Length 352;
 Best Local Similarity 62.7%; Pred. No. 3.3e-72;
 Matches 222; Conservative 42; Mismatches 48; Indels 42; Gaps 4;
 QY 1 MEKYEKLAKTSGSYGVVFKCNKTSQGVAVKVFESDDPVPVKIALREIRMLKQLKH 60
 DB 1 MEKYEKISKIGESYGVVFKCNKNDTQGVAVKVFESDDPVPVKIALREIRMLKQLKH 60
 QY 61 PNLVNLIEVFRKRRKXHLVFEYCDHTLNLNLRPNVGVADGVKISVLWQTLQALNFKCH 120
 DB 61 PNLVNLMEVFRKRRKXHLVFEYCDHTLVNLDYPRGVPEHMKVSIWQTLQAVNFKCH 120
 QY 121 NCIHRIKIPENILITKQGIKIICDFGFAQILI-PGDATDYVATRWYRAPPELLVGDQY 179

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Db 121 NCIHRDVKPENILITKQSAIKLDFGPARLTGTGDDYDVTATRTSPPELLVGDTOYG 180
Qy 180 SSVDIWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 PPVDVWAIGCVFAELLGVLWPKGSDVDQLYLIRKTL----- 218
Qy 240 AVASQASAGITKGLIPRHQSIFKSNFGFHGISIPEDMETLEEFKFSVDHPVAFNFMKGCL 299
Db 219 -----GDLIPRHQOVFSTNQYFSGVKIPDPEDMETLEEFKFSVDHPVAFNFMKGCL 268
Qy 300 KMNPDRLTCSLLESSYFDSFQAEQIKRKARNE 333
Db 269 HMDPAERLTCEQLLHPYFDSFQAEQIKRKARNE 332

RESULT 3
Q6QUAO PRELIMINARY; PRT; 358 AA.
ID Q6QUAO
AC Q6QUAO
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cyclin-dependent kinase-like 1 (CDC2-related kinase).
GN Name=CDK1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,
RA Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,
RA Sherwood J.K., Sherwood A.M., Leithauer B.J., Nickerson D.A.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY525548; AAS000095.1; --
DR HSP; P23941; 1838.
DR GO; GO:0005534; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr_pkinase.
DR InterPro; IPR008271; Ser Thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW ATP-binding; Cyclin; Kinase; Transferase.
SQ SEQUENCE 358 AA; 41833 MW; 823E432BF84B77C6 CRC64;

Query Match 63.9%; Score 1162.5; DB 2; Length 358;
Best Local Similarity 63.8%; Pred. No. 5.2e-71;
Matches 213; Conservative 42; Mismatches 46; Indels 33; Gaps 2;

Qy 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKPFVSEDDPVVKIKALREIRMLKQLKH 60
Db 2 MEKYEKIGKIGEGSYGVVFKCRNKTSGQVAVKPFVSEDDPVVKIKALREIRMLKQLKH 61
Qy 61 PNLVNLLEVERKRMHLVPEYCDHTLLNELRNPNGVADGVIVKSLVQTLQALNFCIH 120
Db 62 PNLVNLLEVERKRMHLVPEYCDHTLLNELRNPNGVADGVIVKSLVQTLQALNFCIH 121
Qy 121 NCIHRDVKPENILITKQSAIKLDFGPARLTGTGDDYDVTATRTSPPELLVGDTOYG 179
Db 122 NCIHRDVKPENILITKQSAIKLDFGPARLTGTGDDYDVTATRTSPPELLVGDTOYG 181

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Qy 180 SSVDIWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 182 PPVDVWAIGCVFAELLGVLWPKGSDVDQLYLIRKTL----- 219
Qy 240 AVASQASAGITKGLIPRHQSIFKSNFGFHGISIPEDMETLEEFKFSVDHPVAFNFMKGCL 299
Db 220 -----GDLIPRHQOVFSTNQYFSGVKIPDPEDMETLEEFKFSVDHPVAFNFMKGCL 269
Qy 300 KMNPDRLTCSLLESSYFDSFQAEQIKRKARNE 333
Db 270 HMDPTERLTCEQLLHPYFDSFQAEQIKRKARNE 303

RESULT 4
Q66HE7 PRELIMINARY; PRT; 352 AA.
ID Q66HE7
AC Q66HE7
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Tissue=Kidney;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC081896; AAH81896.1; --
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr_pkinase.
DR InterPro; IPR008271; Ser Thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 352 AA; 40899 MW; DB9CDF5464B66E24 CRC64;

Query Match 63.6%; Score 1158; DB 2; Length 352;
Best Local Similarity 62.6%; Pred. No. 1e-70;
Matches 214; Conservative 45; Mismatches 49; Indels 34; Gaps 3;

```

QY 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGOWAVKKFVESEDDPVVKKIALREIRMLKOLKH 60
 Db 1 MEKYEKIGKIGEGSYGVVFKCRNRTGQVAKRFLETTEDDVIKKIALREIRMLKOLKH 60
 QY 61 PNLVNLIEVFRKRKXHLVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCIH 120
 Db 61 PNLVNLIEVFRKRKRLHLVFEYCHTTLHLDYRGVPEPLAVKNIWTQTLQAVNFCCHK 120
 QY 121 NCIHREDIKPENILITKQGIKICDFGFAQLI-PCDATYDVATRYRPAPELLVGDTOYG 179
 Db 121 NCIHREDIKPENILITKHSVILKICDFGFAQLITGPDYTYDVATRYRSPPELLVGDTOYG 180
 QY 180 SSVDIWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
 Db 181 PPVDVWAIGCVFAELLSGVPLWPKGSDVDQLYLIRKTL----- 218
 QY 240 AVASQAGITGKLIIPRHOSIFKSGFFHGISIPEDMETLEKPSDVHPVALNFMKGCL 299
 Db 219 -----GDLIPRHQQVFSNQYFSGVKIPDPEDMETLEKFPNISYALGFLKGCL 268
 QY 300 KNPDDRLTCSQLLESSYFDSFQB-AQIKRKARNEGRNRQ 340
 Db 269 HMDPAERLTCSQLLOHPYFDSIRVDGELARPHDKPRTKTLRQ 310

RESULT 5

QY 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGOWAVKKFVESEDDPVVKKIALREIRMLKOLKH 60
 Db 1 MEKYEKIGKIGEGSYGVVFKCRNRTGQVAKRFLETTEDDVIKKIALREIRMLKOLKH 60
 QY 61 PNLVNLIEVFRKRKXHLVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCIH 120
 Db 61 PNLVNLIEVFRKRKRLHLVFEYCHTTLHLDYRGVPEPLAVKNIWTQTLQAVNFCCHK 120
 QY 121 NCIHREDIKPENILITKQGIKICDFGFAQLI-PCDATYDVATRYRPAPELLVGDTOYG 179
 Db 121 NCIHREDIKPENILITKHSVILKICDFGFAQLITGPDYTYDVATRYRSPPELLVGDTOYG 180
 QY 180 SSVDIWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
 Db 181 PPVDVWAIGCVFAELLSGVPLWPKGSDVDQLYLIRKTL----- 218
 QY 240 AVASQAGITGKLIIPRHOSIFKSGFFHGISIPEDMETLEKPSDVHPVALNFMKGCL 299
 Db 219 -----GDLIPRHQQVFSNQYFSGVKIPDPEDMETLEKFPNISYALGFLKGCL 268
 QY 300 KNPDDRLTCSQLLESSYFDSFQB-AQIKRKARNEGRNRQ 340
 Db 269 HMDPAERLTCSQLLOHPYFDSIRVDGELARPHDKPRTKTLRQ 310

QY 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGOWAVKKFVESEDDPVVKKIALREIRMLKOLKH 60
 Db 1 MEKYEKIGKIGEGSYGVVFKCRNRTGQVAKRFLETTEDDVIKKIALREIRMLKOLKH 61
 QY 61 PNLVNLIEVFRKRKXHLVFEYCDHTLLNELRNPNGVADGVKSVLWQTLQALNFCIH 120
 Db 62 PNLVNLIEVFRKRRLHLVFEYCDHTVLHLDYRGVPEHLVKSITWTQTLQAVNFCCHK 121
 QY 121 NCIHREDIKPENILITKQGIKICDFGFAQLI-PCDATYDVATRYRPAPELLVGDTOYG 179
 Db 122 NCIHREDIKPENILITKHSVILKICDFGFAQLITGPDYTYDVATRYRSPPELLVGDTOYG 181
 QY 180 SSVDIWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPP 239
 Db 182 PPVDVWAIGCVFAELLSGVPLWPKGSDVDQLYLIRKTL----- 219
 QY 240 AVASQAGITGKLIIPRHOSIFKSGFFHGISIPEDMETLEKPSDVHPVALNFMKGCL 299
 Db 220 -----GDLIPRHQQVFSNQYFSGVKIPDPEDMETLEKFPNISYALGFLKGCL 269

QY 300 KNPDDRLTCSQLLESSYFDSFQB 325
 Db 270 HMDPTELTCEQLLHPYFENIREIE 295

RESULT 6
 QY 07QBG7 PRELIMINARY; PRT; 367 AA.
 AC 07QBG7;
 DT 01-MAR-2004 (T-EMBLrel. 26, Created)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE AGCP3044.
 GN Names=agCG55557; ORFNames=ENSGANG0000012213;
 OS Anopheles gambiae str. PE8T.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 OX NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PE8T.
 RA Anopheles Genomes Sequencing Consortium;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AAA01008879; EAA08474.1; -.
 DR HSSP; P24941; IOIO.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004672; F:protein kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; prot kinase.
 DR InterPro; IPR008271; Ser thr_pkin_AS.
 DR Pfam; PF00069; Pkinase; I.
 DR ProDom; PD000001; Prot_kinase; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PSS0011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN 1.
 KW ATP-binding; Kinase; Transferase.
 SQ SEQUENCE 367 AA; 42402 MW; F23BDB4C5D28A5E8 CRC64;

Query Match 55.5%; Score 1009.5; DB 2; Length 367;
 Best Local Similarity 52.8%; Pred. No. 1.3e-60;
 Matches 186; Conservative 62; Mismatches 67; Indels 37; Gaps 3;

Qy 1 MEKYEKLAKTGGSGVGVVFKCRNKTSGQVAVKGFVESEDDPVVKKTALRIRMLKOLKH 60
 Db 17 MDRYEKLSRLGGSGVGVVYKCRDRETGSLVAVKGFVESEDDPAIRKIALRIRLLKXKH 76
 Qy 61 PNLVNLIEVFRKRKQHLVFEYCDHTLLNELERNPNGVADGVVKSVMQTLQALNFCCHI 120
 Db 77 PNLVCLLEVFRKRRLHLVFECEHTLVLEHERPEGCPDNLTKQITVYQTQGVAYCHQ 136
 Qy 121 NCIHRIKPNILITKGGIHKICDGFPAQIILPGDAYTDVYATWYRAPPELLVGDTOYGS 180
 Db 137 GCLHRDIKPNILITKGGIHKICDGFPAQIILPGDAYTDVYATWYRAPPELLVGDTOYGT 196
 Qy 181 SVDIWAICVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 Db 197 PVDWAICVFAELVRGDLAPGSDVDQLYLIIRTL----- 233
 Qy 241 VASQAGITGKLI PRHOSIFKSGFFHGISTPEPEMETLEEKFSDFVHPVALNFMKG 297
 Db 234 -----GDLPRHLAIFNQNEFFKGITLPVPTLETLEAKMPSRTLANPLAMDFLKK 284
 Qy 298 CLKNPDDRLTCSQLLESSYFDSF--QEAQIKRKARNEGRRRQQVLPKX 347
 Db 285 CLDKDPKRWKSCERLATHPYFYEDYITKQIEQTITLQKQGTGRELKPKTS 336

RESULT 7

Q9UZH1 PRELIMINARY; PRT; 353 AA.
 AC Q9UZH1
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein Y42A5A.4.
 GN ORFNames=Y42A5A.4;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA none;
 RT "Genome sequence of the nematode C. elegans: A platform for
 investigating biology.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Steward C.A.;
 RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL032618; CAB63367.1; --
 DR HSSP; P24941; 1H00.
 DR WormBase; WBGene00012779; Y42A5A.4.
 DR WormPep; Y42A5A.4; CE20258
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_thr_kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.

DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PSS0011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00108; PROTEIN KINASE ST; UNKNOWN 1.
 KW ATP-binding; Hypothetical protein; Kinase; Transferase.
 SQ SEQUENCE 353 AA; 40665 MW; 7E32260D9849CAC9 CRC64;

Query Match 55.0%; Score 1001.5; DB 2; Length 353;
 Best Local Similarity 53.4%; Pred. No. 4.3e-60;
 Matches 187; Conservative 59; Mismatches 63; Indels 41; Gaps 3;

Qy 1 MEKYEKLAKTGGSGVGVVFKCRNKTSGQVAVKGFVESEDDPVVKKTALRIRMLKOLKH 60
 Db 1 MDKYRLSLKGGSGVGVVYKCRDRTGQIVAKKPFVETEDDPHKIKALRIRMLKOLKH 60
 Qy 61 PNLVNLIEVFRKRKQHLVFEYCDHTLLNELERNPNGVADGVVKSVMQTLQALNFCCHI 120
 Db 61 QNLVGLIEVFRKRKQHLVFEYCDHTLVLEKPNHGVNDELKIKIYQLLEALKFCHSH 120
 Qy 121 NCIHRIKPNILITKGGIHKICDGFPAQIILPGDAYTDVYATWYRAPPELLVGDTOYGS 180
 Db 121 KCIHRDVKPNIFLNRNDQVKGDFGFIARINTMTYTDVYATWYRAPPELLVGDVQYGP 180
 Qy 181 SVDIWAICVFAELLTGQPLWPKGSDVDQLYLIIRTLVETGFRHVDQAGLELLTSSDPPA 240
 Db 181 PVDIWAICVFAELLTGQPLWPKGSDVDQLYLIIRTL----- 217
 Qy 241 VASQAGITGKLI PRHOSIFKSGFFHGISTPEPEMETLEEKFSDFVHPVALNFMKG 300
 Db 218 -----GEFLPRHISIFRTNQFFGLSIPEHELEPLPSKLPNASSAQDLFQKCFE 268
 Qy 301 MNPDRLTCSQLLESSYFDSF--QEAQIKRKARNEGRRRQQVLPK 345
 Db 269 MSPDRFSCSELMHGIFSNW---ILIRQDESTPTGLTKRSPNVLPL 314

RESULT 8

Q9VMN3 PRELIMINARY; PRT; 392 AA.
 AC Q9VMN3
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE CG7236-PA.
 GN ORFNames=CG7236;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktoglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,

DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.
KW	ATP-binding; Kinase; Transferase.
SQ	SEQUENCE 392 AA; 44962 MW; C9627D077784E5DD CRC64;

Query Match		55.0%;	Score 1001.5;	DB 2;	Length 392;
Best Local Similarity		53.0%;	Pred. No. 4.9e-60;		
Matches 184; Conservative		65;	Mismatches 61;	Indels 37;	Gaps 3;

Qy	1	MEKYEKLAKTSGSYGVVFKCRNKTSGOVAVKKFVESEDDPVVKIALREIRMLKQLKH 60
Dd	1	MDRYEKLSELGSGSYGVVYKCDREDTALVAVKFVESEDDPAIRKIALREIRLLKNLKH 60
Qy	61	PNLVNLIEVFRKRKGHLVFYCHDTLLNELERNPNNGVADVTKSVLMQTLOALNFCHIH 120
Dd	61	PNLVSLLEVFRKRRLHVLFFECBLTVHELHERHQGCPEHLTKQICQYTLLGVAYCHKQ 120
Qy	121	NCIHRDIKPENILITKQGIHKIDCGPAQIILPGDAYTDYVATRWYRAPPELLVGDTQYGS 180
Dd	121	GCLHRDIKPENILLTAQQQVKLCDFGARMLSPGENTDYVATRWYRAPPELLVGDTQYGT 180
Qy	181	SVDIWAIGCVFAELLTGQPLWPKGSDVDQLYLIIRTIVETGFRHVDAQGLELTSSDPPEA 240
Dd	181	PVDVWAIGCLFAELVRGEALWPGRSDVDQLYLRKTL----- 217
Qy	241	VASQSAGITGKLI PRHQSI FKSNGFPFGISIPEDMETLEKF---SDVHPVALNPMKG 297
Dd	218	-----GDLPRHIQIFQNEYFYKGITLPVPPTLEPLEDKMPAKSQONPLTIDFLKK 268
Qy	298	CLKNNPDLRTCSQLLESSYFDSP--OEAQIKRKARNEGRRNRROQV 342
Dd	269	CLDKDPTKRWCSEKLIKHSYFDYYIAKQRELEHVSLEAANLQQQL 315

RESULT 9

Q9TTKO	PRELIMINARY;	PRT;	566 AA.
ID	Q9TTKO	AC	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DE	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Ser/Thr kinase KIAARE.		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
RX	NCBI_TaxID=9986;		
OX	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RA	Gomi H., Sun W., Finch C.E., Itohara S., Yoshimi K., Thompson R.F.;		
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
CC	-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.		
DR	EMBL; AB029045; BAA88508.1; ..		
DR	HSSP; P24941; IOIQ		
DR	GO; GO:0005524; F:ATP binding; IEA.		
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.		
DR	GO; GO:0016740; F:transferase activity; IEA.		
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.		
DR	InterPro; IPROL1009; Kinase like.		
DR	InterPro; IPR000719; Prot_kinase.		
DR	InterPro; IPR002290; Ser_thr_pkinase.		
DR	InterPro; IPR008271; Ser_thr_pkin_AS.		
DR	Ffam; PF00069; Pkinase; I.		
DR	ProDom; PD000001; Prot_kinase; 1.		
DR	SMART; SMO0220; S_TKC; 1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.		
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.		
SQ	SEQUENCE 566 AA; 64052 MW; 5D57595550902EA9 CRC64;		

Query Match		51.7%;	Score 941.5;	DB 2;	Length 566;
Best Local Similarity		49.7%;	Pred. No. 8.7e-56;		

Matches 177; Conservative 67; Mismatches 65; Indels 47; Gaps 6;

Qy 1 MEKYEKLAKTGESEGVVFKCRNKTSGOVAVKPFVESEDDPVVKKIALREIRMLKQLKH 60
 Db 1 MEKYEKLAKTGESEGVVFKCRNKTSGOVAVKPFVESEDDPVVKKIALREIRMLKQLKH 60

Qy 61 PNLYNLIEVFRKRKMHVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCCHI 120
 Db 61 ENLVNLEVCCKKRWLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCCHI 120

Qy 121 NCIRHDKPENILITKQGIKICDFGFAQIL-IPGDAYTDVATRWYRAPPELLVGDTOYG 179
 Db 121 NIHRDKPENILVQSQGVKLCDFGFARTLAAGEVYTDVATRWYRAPPELLVGDVYKG 180

Qy 180 SSVDIWAGCVFAELLTGQPLWPGKSDVDQLYLIRTLVETGFRHVDQAGLELLTSSDPP 239
 Db 181 KAVDVWAGCVFAELLTGQPLWPGKSDVDQLYLIRTLVETGFRHVDQAGLELLTSSDPP 239

Qy 240 AVASQAGITKGLIPRHSIFKSNFGFHG--ISIPEDMETLEEFSDVHPVALNFMKCL 299
 Db 240 AVASQAGITKGLIPRHSIFKSNFGFHG--ISIPEDMETLEEFSDVHPVALNFMKCL 299

Qy 300 KMPDDRLTCSQLESSEYF--DSF-----QEAQIK--RKARN-----EGRNRRQO 341
 Db 300 KMPDDRLTCSQLESSEYF--DSF-----QEAQIK--RKARN-----EGRNRRQO 341

Qy 341 HVDPRKPFCAELLHDDFFQMDGFAERFSQELQWQKQDARNISLSKKSQNRKKEK 324
 Db 341 HVDPRKPFCAELLHDDFFQMDGFAERFSQELQWQKQDARNISLSKKSQNRKKEK 324

RESULT 10

Q675R9 PRELIMINARY; PRT; 385 AA.

AC Q675R9; (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DE Cyclin-dependent kinase-like 1.

GN ORFNames=006-03;

OS Oikopleura dioica.

OC Eukaryota; Metazoa; Chordata; Urochordata; Appendicularia;

OC Oikopleuridae; Oikopleura.

OX NCBI_TaxID=34765;

RN [1]

RP SEQUENCE FROM N.A.

RX PubMed=1534333; DOI=10.1038/nature02709;

RA Seo H.C., Edvardson R.B., Maeland A.D., Bjordal M., Jensen M.F., Hansen A., Flaot M., Weissenbach J., Lehrach H., Wincker P., Reinhardt R., Chourrout D.;

RT "Hox cluster disintegration with persistent anteroposterior order of expression in Oikopleura dioica.";

RL Nature 431:67-71 (2004).

DR EMBL; AY449462; AAS21447.1; -.

DR GO; GO:0016301; F:kinase activity; IEA.

DR InterPro; IPR011009; Kinase like.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_kinase.

DR InterPro; IPR008271; Ser_thr_pkin_AS.

DR InterPro; IPR001245; Tyr_kinase.

DR Pfam; PF00069; Pkinase; 1.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00220; S_TKC; 1.

DR SMART; SM00219; TyrKC; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; UNKNOWN_1.

KW Cyclin; Kinase.

SQ SEQUENCE 385 AA; 45512 MW; 059F814421AGADAL CRC64;

Query Match 51.2%; Score 932; DB 2; Length 385;
 Best Local Similarity 52.2%; Pred. No. 2.5e-55;
 Matches 168; Conservative 58; Mismatches 62; Indels 34; Gaps 2;

Qy 2 EKYELAKTGESEGVVFKCRNKTSGOVAVKPFVESEDDPVVKKIALREIRMLKQLKHP 61
 Db 4 DYEKIEKISGSGVIVYKCRNRTTRAVAVKRFIESEELNKKIAMREIRMLKSLKHQ 63

Qy 62 NLVNLIEVFRKRKMHVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCCHI 121
 Db 64 NLVNLIEVFRKRKMHVFEYCDHTLVTELEQNPHGLPEOSIKRIIWQLKGLFEFCHAQK 123

Qy 122 CIHRDKPENILITKQGIKICDFGFAQILIPGDAYTDVATRWYRAPPELLVGDTOYGSS 181
 Db 124 CIHRDVAPENILITKQGIKLCDFGFARILNPGDDLTDVATRWYRAPPELLVGDLYKNSA 183

Qy 182 VDIWAGCVFAELLTGQPLWPGKSDVDQLYLIRTLVETGFRHVDQAGLELLTSSDPPAV 241
 Db 184 VDIWAGCVFGLNGQPIWPGKSELQDHLKQKT----- 218

Qy 242 ASQAGITKGLIPRHSIFKSNFGFHG--ISIPEDMETLEEFSDVHPVALNFMKCL 299
 Db 219 -----CGELIIQHKLLQTNKYLGRHLLTSPRERVPYEAALYKAPSHITISFLKNCL 271

Qy 300 KMPDDRLTCSQLESSEYFDSF 321
 Db 272 QMDTMRDLDCVELLDHAYFDY 293

RESULT 11

Q92772 PRELIMINARY; PRT; 493 AA.

AC Q92772; (TrEMBLrel. 02, Created)

DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE P56 KXIAMRE protein kinase.

GN Name=KXIAMRE;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97152547; PubMed=9000130;

RA Taglienti C.A., Wysek M., Davis R.J.;

RT "Molecular cloning of the epidermal growth factor-stimulated protein kinase p56 KXIAMRE.";

RT Oncogene 13:2563-2574 (1996).

CC -I- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

DR EMBL; U35146; AAC50918.1; -.

DR HSSP; P24941; LH00.

DR Genew; HGNC:1782; CDKL2.

DR GO; GO:0004672; P:protein kinase activity; TAS.

DR GO; GO:0007548; P:sex differentiation; TAS.

DR GO; GO:0007165; P:signal transduction; TAS.

DR Pfam; PF00069; Pkinase; 1.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00220; S_TKC; 1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

KW SEQUENCE 493 AA; 56018 MW; 5CC2UA91CBF89EFE CRC64;

Query Match 50.3%; Score 915.5; DB 2; Length 493;
 Best Local Similarity 48.3%; Pred. No. 4.3e-54;
 Matches 172; Conservative 68; Mismatches 69; Indels 47; Gaps 6;

Qy 1 MEKYEKLAKTGESEGVVFKCRNKTSGOVAVKPFVESEDDPVVKKIALREIRMLKQLKH 60
 Db 1 MEKYEKLAKTGESEGVVFKCRNKTSGOVAVKPFVESEDDPVVKKIALREIRMLKQLKH 60

Qy 61 PNLYNLIEVFRKRKMHVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCCHI 120
 Db 61 ENLVNLEVCCKKRWLVFEYCDHTLLNELERNPNGVADGVKSVLWQTLQALNFCCHI 120

Qy 121 NCIRHDKPENILITKQGIKICDFGFAQIL-IPGDAYTDVATRWYRAPPELLVGDTOYG 179
 Db 121 NIHRDKPENILVQSQGVKLCDFGFARTLAAGEVYTDVATRWYRAPPELLVGDVYKG 180


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QY 180 SSVDIWAIGCVFAELLTGQPLWFGKSDVDQLYLIIRTLVETGRHVDQAGLELLTSSDPP 239
Db 181 KAVDWAIGLVTEFMGEPLPGDSIDQLHIMCL----- 218
QY 240 AVASQAGITGKLIIPHQIFKSNFGFHGISIPEPEDMETLEKFSVHPVALNFMKGCL 299
Db 219 -----GNLIPRHOELFNKPNVFAVGRLPEIKEREPLRRYPKLSVVIDLAKKCL 268
QY 300 KMNPPDLRLTCSOLLESSYF--DSF-----QEAQIK--RKARN-----EGNRERROQ 341
Db 269 HIDPKRPFCAELLHHDFQMDGFAERFSQELQLKQVQDARNVSLSKSQNRKKEK 324

RESULT 12
Q9QY12
ID Q9QY12 PRELIMINARY; PRT; 564 AA.
AC Q9QY12;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Ser/Thr kinase KKIAMRE-gamma.
GN Name=Cdk12; Synonyms=Kkm;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Sassa T., Gomi H., Sun W., Ikeda T., Thompson R.F., Itohara S.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB029066; BAA88428.1; JOINED.
DR EMBL; AB029066; BAA88428.1; JOINED.
DR HSSP; P24941; IOIQ.
DR MGD; MGI:1858227; Cdk12.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 564 AA; 63640 MW; DACDEF630CCE82D5 CRC64;

Query Match 49.7%; Score 904.5; DB 2; Length 564;
Best Local Similarity 48.6%; Pred. No. 2.8e-53;
Matches 174; Conservative 66; Mismatches 69; Indels 49; Gaps 7;

QY 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKFFVESEDDPVVKKIALREIMLKQLKH 60
Db 1 MEKENLGLVGEGSYGVVFKCRNKTSGQVAVKFFVESEDDPVVKKIALREIMLKQLKH 60
QY 61 PNLVNLLEVERFRKRKMLHVFECYCDHTLLNELERNPNAGVGVKSVLWQTLQALNFCIH 120
Db 61 ENLVNLLEVCCKRWLVLFVFDVHTLDDLLKLPNGLDYQVQVKYLFQINGIGFCHSH 120
QY 121 NCIHRDIKPNILITKQGIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDTOYG 179
Db 121 NIHRDIKPNILVSGSVVKLCDFGFARTLAAGEVYTDYVATRWYRAPELLVGDVKYG 180
QY 180 SSVDIWAIGCVFAELLTGQPLWFGKSDVDQLYLIIRTLVETGRHVDQAGLELLTSSDPP 239
Db 181 KAVDWAIGLVTEFMGEPLPGDSIDQLHIMCL----- 218
QY 240 AVASQAGITGKLIIPHQIFKSNFGFHGISIPEPEDMETLEKFSVHPVALNFMKG 297
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Db 219 -----GNLIPRHOELFNKPNVFAVGRLPEIKEREPLRRYPKLSVVIDLAKK 268
QY 238 CLKMNPPDLRLTCSOLLESSYF--DSF-----QEAQIK--RKARN-----EGNRERROQ 341
Db 269 CLHIDPKRPFCAELLHHDFQMDGFAERFSQELQLKQVQDARNVSLSKSQNRKKEK 326

RESULT 13
Q9QUKO
ID Q9QUKO PRELIMINARY; PRT; 568 AA.
AC Q9QUKO;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Ser/Thr kinase KKIAMRE (Ser/Thr kinase KKIAMRE-beta).
GN Name=Cdk12; Synonyms=Kkm;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SVJ, and C57BL/6; TISSUE=Brain;
RA Sassa T., Gomi H., Sun W., Ikeda T., Thompson R.F., Itohara S.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB029073; BAA88439.1; JOINED.
DR EMBL; AB029068; BAA88439.1; JOINED.
DR EMBL; AB029070; BAA88439.1; JOINED.
DR EMBL; AB029072; BAA88439.1; JOINED.
DR EMBL; AB029071; BAA88439.1; JOINED.
DR EMBL; AB029065; BAA88427.1; JOINED.
DR HSSP; P24941; IOIQ.
DR MGD; MGI:1858227; Cdk12.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 568 AA; 64055 MW; A43B75E2E9EB86C4 CRC64;

Query Match 49.7%; Score 904.5; DB 2; Length 568;
Best Local Similarity 48.6%; Pred. No. 2.8e-53;
Matches 174; Conservative 66; Mismatches 69; Indels 49; Gaps 7;

QY 1 MEKYEKLAKTGEGSYGVVFKCRNKTSGQVAVKFFVESEDDPVVKKIALREIMLKQLKH 60
Db 1 MEKENLGLVGEGSYGVVFKCRNKTSGQVAVKFFVESEDDPVVKKIALREIMLKQLKH 60
QY 61 PNLVNLLEVERFRKRKMLHVFECYCDHTLLNELERNPNAGVGVKSVLWQTLQALNFCIH 120
Db 61 ENLVNLLEVCCKRWLVLFVFDVHTLDDLLKLPNGLDYQVQVKYLFQINGIGFCHSH 120
QY 121 NCIHRDIKPNILITKQGIKICDFGFAQIL-IPGDAYTDYVATRWYRAPELLVGDTOYG 179
Db 121 NIHRDIKPNILVSGSVVKLCDFGFARTLAAGEVYTDYVATRWYRAPELLVGDVKYG 180
QY 180 SSVDIWAIGCVFAELLTGQPLWFGKSDVDQLYLIIRTLVETGRHVDQAGLELLTSSDPP 239
Db 181 KAVDWAIGLVTEFMGEPLPGDSIDQLHIMCL----- 218
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Qy 240 AVASQSAGITGKLIPIRHSIFKSNKFFHGISIPEDMET--LEEKFSVDHVPVNLNFKG 297
Db 219 -----GNLIPRHOELFYKPNVFAGVRLPEVKOAEPLESRYPKPKPEAVISLAKK 268

Qy 298 CLKMNPDRLTCSQLLESSYF--DSF-----QEAQIK--RKARN-----EGNRNRROQ 341
Db 269 CLHIDDPKPCADLLRHDFQMDGFAERFSQELQLKIEKDARNNSLPKKSQNRKKEK 326

RESULT 14
ID Q9QY11 PRELIMINARY; PRT; 329 AA.
AC Q9QY11;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ser/Thr kinase KIAMRE-delta (Fragment).
GN Name=Cdk12; Synonyms=Kkm;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Sassa T., Gomi H., Sun W., Ikeda T., Thompson R.F., Itohara S.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AB029067; BAA88429.1; --
DR HSSP; P24941.1; IOIQ
DR MGD; MG1:1858227; Cdk12.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:proteinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 329 329
FT SEQUENCE 329 AA; 38023 MW; 72EB899E65AE8595 CRC64;

Query Match 49.6%; Score 902; DB 2; Length 329;
Best Local Similarity 49.0%; Pred. No. 2.3e-53;
Matches 173; Conservative 63; Mismatches 73; Indels 44; Gaps 6;

Qy 1 MEKYEKLAKTCEGSGYGVFKCRNTSGOVAVKFESEDDPVVKKIALREIRMLKQKH 60
Db 1 MEKYNLGLVGEISGYGMKCRNDSGRIVAIFKPLESDDDDKMKVKIAMREIKLKQLRH 60

Qy 61 PNLVNLIEVFRKRRKMLVPEYCDHTLLNELRNPNGVADGVKSLWQTLQALNFCIH 120
Db 61 ENLVNLIEVCKKRWLVFEFVDHTILDDKLKLPNGLDYGVQVKYLFQINGIGFCHSH 120

Qy 121 NCIHRIKPNILITKQGIKICDPGFAQIL-IPGDAYTDYVATRWYRAPPELLVGD7QYG 179
Db 121 NIHRIKPNILVSQSGWVKLCDFGARTLAAPGEVVDYVATRWYRAPPELLVGDVKYG 180

Qy 180 SSVDIWAIGCVFALLTGQPLWPKGSVDQYLYLIRTLVETGFRHVDQAGLELLTSSDPP 239
Db 181 KAVDIWAIGCVLIVEMLQGLPFGESDQLDHLHMTCL----- 218

Qy 240 AVASQSAGITGKLIPIRHSIFKSNKFFHGISIPEDMET--LEEKFSVDHVPVNLNFKG 297
Db 219 -----GNLIPRHOELFYKPNVFAGVRLPEVKOAEPLESRYPKPKPEAVISLAKK 268
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Qy 298 CLKMNPDRLTCSQLLESSYF--DSF-----QEAQIK--RKARNEGRRRRROQ 341
Db 269 CLHIDDPKPCADLLRHDFQMDGFAERFSQELQLKIEKDARNNSLPKKSQK 321

RESULT 15
ID Q6GMD6 PRELIMINARY; PRT; 320 AA.
AC Q6GMD6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE LOC443693 protein (Fragment).
GN Name=LOC443693;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalak U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP [2]
RC TISSUE=Kidney;
RA MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RX Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC074132; AAH74132.1; --
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TyKc; 1.
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